GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 08:51:42 ; Search time 189 Seconds
(without alignments)
2531.659 Million cell updates/sec

Title: US-08-439-095-1
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5652	100.0	1089	5	AAU84300	Aau84300 Human end
2	5652	100.0	1089	6	ABG72449	Abg72449 Human pla
3	5652	100.0	1089	6	ABP96312	Abp96312 Human pla
4	5652	100.0	1089	7	ABR84718	Abr84718 Human PDG
5	5652	100.0	1089	7	ADF45081	Adf45081 Human kin
6	5652	100.0	1089	7	ADF90896	Adf90896 Human hep
7	5652	100.0	1089	8	ADM69012	Adm69012 Human pla
8	5652	100.0	1089	8	ADQ17833	Adq17833 Human sof
9	5652	100.0	1089	8	ADQ59532	Adq59532 Human can
10	5652	100.0	1089	8	ADQ39641	Adq39641 Human myo
11	5652	100.0	1089	9	ADY59389	Ady59389 Human PDG
12	5652	100.0	1089	9	ADZ13915	Adz13915 Human can
13	5649	99.9	1089	2	AAR06910	Aar06910 Alpha typ
14	5649	99.9	1089	6	ABG72453	Abg72453 Human pla
15	5648	99.9	1089	6	ABG72450	Abg72450 Human pla
16	5647	99.9	1089	6	ABG72452	Abg72452 Human pla
17	5646	99.9	1089	6	ABG72451	Abg72451 Human pla
18	5645	99.9	1089	2	AAR08267	Aar08267 Platelet
19	5645	99.9	1089	8	ADM69031	Adm69031 Human PDG
20	5643	99.8	1089	8	ADM69014	Adm69014 Human PDG
21	5640	99.8	1089	8	ADM69035	Adm69035 Human PDG
22	5637	99.7	1090	8	ADM69020	Adm69020 Human PDG
23	5636.5	99.7	1088	5	AAO17356	Aao17356 Human pla
24	5617.5	99.4	1084	8	ADM69033	Adm69033 Human PDG
25	5617	99.4	1085	8	ADM69016	Adm69016 Human PDG
26	5614.5	99.3	1086	8	ADM69018	Adm69018 Human PDG
27	5602.5	99.1	1084	8	ADM69022	Adm69022 Human PDG
28	5533	97.9	1089	8	ADM69037	Adm69037 Human PDG
29	5232	92.6	1089	9	ADZ13910	Adz13910 Murine ca
30	5232	92.6	1096	8	ADQ59529	Adq59529 Human can
31	5154	91.2	1009	2	AAR26206	Aar26206 Type B hu
32	3046	53.9	589	6	ABG72454	Abg72454 Human pla
33	2693.5	47.7	834	8	ADJ93550	Adj93550 NM_030917
34	2692	47.6	849	8	ADJ93549	Adj93549 NM_030917
35	2676.5	47.4	811	8	ADJ93552	Adj93552 NM_030917
36	2676.5	47.4	826	8	ADJ93551	Adj93551 NM_030917
37	2380.5	42.1	457	9	ADY85492	Ady85492 Catalytic
38	2359.5	41.7	1106	2	AAR26205	Aar26205 Type B hu
39	2354.5	41.7	1106	1	AAP90127	Aap90127 Platelet
40	2354.5	41.7	1106	2	AAR99690	Aar99690 Platelet-
41	2354.5	41.7	1106	6	ABG72459	Abg72459 Human pla
42	2354.5	41.7	1106	6	ABP96311	Abp96311 Human pla
43	2354.5	41.7	1106	7	ABR84719	Abr84719 Human PDG
44	2354.5	41.7	1106	7	ADF45082	Adf45082 Human kin
45	2354.5	41.7	1106	8	ABO84679	Abo84679 Human can
46	2354.5	41.7	1106	9	ADY59381	Ady59381 Human PDG
47	2354.5	41.7	1106	9	ADY70691	Ady70691 Human BAC
48	2351	41.6	1107	8	ABO84677	Abo84677 Human can
49	2351	41.6	1107	9	ADY70656	Ady70656 Human BAC
50	2350.5	41.6	1106	6	ABG72456	Abg72456 Human pla
51	2349.5	41.6	1106	6	ABG72458	Abg72458 Human pla
52	2348.5	41.6	1106	6	ABG72457	Abg72457 Human pla
53	2347	41.5	1090	6	ABG72455	Abg72455 Human pla
54	2339.5	41.4	1098	8	ABO84676	Abo84676 Mouse can
55	2336.5	41.3	1098	5	ABB57338	Abb57338 Mouse isc
56	2332	41.3	1158	8	ABO84675	Abo84675 Mouse can
57	2323.5	41.1	1106	1	AAP90646	Aap90646 Human pla
58	2309	40.9	1089	4	ABG20753	Abg20753 Novel hum
59	2008	35.5	383	9	ADZ64611	Adz64611 Tyrosine
60	1965.5	34.8	2129	4	ABG15478	Abg15478 Novel hum
61	1965.5	34.8	2129	4	ABG20749	Abg20749 Novel hum
62	1612.5	28.5	821	2	AAY28935	Aay28935 Platelet-
63	1481.5	26.2	977	3	AAY51322	Aay51322 Bovine c-
64	1473	26.1	972	8	ADT55100	Adt55100 Amino aci
65	1458	25.8	978	7	ADE55805	Ade55805 Rat Prote
66	1458	25.8	978	7	ADD48368	Add48368 Rat Prote
67	1458	25.8	978	9	AEA80344	Aea80344 Rat KIT t
68	1457.5	25.8	972	8	ADO59940	Ado59940 Human KIT
69	1454.5	25.7	976	4	AAE07145	Aae07145 Human Kit
70	1454.5	25.7	976	4	AAU00375	Aau00375 Human ste
71	1454.5	25.7	976	6	ABR43623	Abr43623 Human c-k
72	1454.5	25.7	976	6	ABP72342	Abp72342 Human c-k
73	1454.5	25.7	976	6	ABP57094	Abp57094 Human c-k
74	1454.5	25.7	976	6	ABP72341	Abp72341 Human c-k
75	1454.5	25.7	976	6	AAO27192	Aao27192 Human c-k
76	1454.5	25.7	976	6	ABP72761	Abp72761 Human c-k
77	1454.5	25.7	976	6	AAO19912	Aao19912 Human c-k
78	1454.5	25.7	976	6	ABP57092	Abp57092 Human c-k
79	1454.5	25.7	976	6	ABP57418	Abp57418 Human c-k
80	1454.5	25.7	976	6	ABP96025	Abp96025 Human c-k
81	1454.5	25.7	976	6	ABR39481	Abr39481 Human c-k
82	1454.5	25.7	976	6	ABP57411	Abp57411 Human c-k
83	1454.5	25.7	976	6	ABR42763	Abr42763 Human c-k
84	1454.5	25.7	976	7	AAO29520	Aao29520 Human c-k
85	1454.5	25.7	976	7	ADC98648	Adc98648 Human tyr
86	1454.5	25.7	976	7	ABR83074	Abr83074 Human c-k
87	1454.5	25.7	976	7	ABR83119	Abr83119 Human c-k
88	1454.5	25.7	976	7	ADD48370	Add48370 Human Pro
89	1454.5	25.7	976	7	ADE55807	Ade55807 Human Pro
90	1454.5	25.7	976	7	ADN39390	Adn39390 Cancer/an
91	1454.5	25.7	976	8	ADI33412	Adi33412 Human KIT
92	1454.5	25.7	976	8	ADP12414	Adp12414 Protein e
93	1454.5	25.7	976	8	ADQ82892	Adq82892 Human cKI
94	1454.5	25.7	976	8	ADP55988	Adp55988 Human PRO
95	1454.5	25.7	976	8	ADS92967	Ads92967 v-kit Har
96	1454.5	25.7	976	8	ADU06733	Adu06733 Novel bro
97	1454.5	25.7	976	8	ADU48584	Adu48584 Human c-k

98	1454.5	25.7	976	9	ADY27719	Ady27719 Human c-k
99	1454.5	25.7	976	9	ADY15474	Ady15474 PRO polyp
100	1454.5	25.7	976	9	AEA80340	Aea80340 Human KIT
101	1450.5	25.7	976	4	AAE07149	Aae07149 Mutant hu
102	1447.5	25.6	976	6	ABP72766	Abp72766 Human act
103	1447.5	25.6	976	6	ABP72765	Abp72765 Human act
104	1447.5	25.6	976	6	ABP57420	Abp57420 Human c-k
105	1447.5	25.6	976	6	ABP96027	Abp96027 Human c-k
106	1447.5	25.6	976	6	ABP57413	Abp57413 Human c-k
107	1447.5	25.6	976	7	AAO29526	Aao29526 Human c-k
108	1447.5	25.6	976	7	AAO29525	Aao29525 Human c-k
109	1446.5	25.6	975	4	AAE07144	Aae07144 Murine Ki
110	1446.5	25.6	975	9	AEA19289	Aea19289 Mouse c-k
111	1446.5	25.6	975	9	AEA80342	Aea80342 Mouse KIT
112	1445.5	25.6	976	6	ABP72762	Abp72762 Human act
113	1445.5	25.6	976	6	ABP72764	Abp72764 Human act
114	1445.5	25.6	976	6	ABP72763	Abp72763 Human act
115	1445.5	25.6	976	7	AAO29524	Aao29524 Human c-k
116	1445.5	25.6	976	7	AAO29523	Aao29523 Human c-k
117	1445.5	25.6	976	7	AAO29522	Aao29522 Human c-k
118	1442.5	25.5	975	4	AAE07148	Aae07148 Mutant mu
119	1440.5	25.5	976	6	ABR43624	Abr43624 Human c-k
120	1440.5	25.5	976	6	ABP57093	Abp57093 Human c-k
121	1440.5	25.5	976	6	ABP57419	Abp57419 Human c-k
122	1440.5	25.5	976	6	ABP96026	Abp96026 Human c-k
123	1440.5	25.5	976	6	ABP57412	Abp57412 Human c-k
124	1420	25.1	936	8	ADS98080	Ads98080 Protein f
125	1354.5	24.0	972	5	AAU11935	Aau11935 Colony st
126	1347.5	23.8	972	5	AAU11941	Aau11941 Colony st
127	1347.5	23.8	972	6	ABU89777	Abu89777 Protein d
128	1347.5	23.8	972	7	ADM29260	Adm29260 Human noe
129	1347.5	23.8	972	8	ADO71659	Ado71659 Amino aci
130	1347.5	23.8	1055	4	ABG15479	Abg15479 Novel hum
131	1346.5	23.8	972	5	AAU11936	Aau11936 Colony st
132	1346.5	23.8	972	5	AAU73585	Aau73585 Colony st
133	1346.5	23.8	972	5	AAU79039	Aau79039 Human mac
134	1346.5	23.8	972	8	ADQ19495	Adq19495 Human sof
135	1346.5	23.8	972	8	ADQ39907	Adq39907 Human myo
136	1346.5	23.8	972	8	ADQ39908	Adq39908 Human myo
137	1346.5	23.8	972	9	AEB31949	Aeb31949 Macrophag
138	1345.5	23.8	972	5	AAU11940	Aau11940 Colony st
139	1345.5	23.8	972	5	AAU11939	Aau11939 Colony st
140	1344.5	23.8	972	5	AAU11934	Aau11934 Colony st
141	1342.5	23.8	972	5	AAU11937	Aau11937 Colony st
142	1342.5	23.8	972	7	ADM29258	Adm29258 Human nov
143	1342.5	23.8	972	7	ADM29262	Adm29262 Human nov
144	1340.5	23.7	806	7	ADJ70529	Adj70529 Human hea
145	1340.5	23.7	972	5	AAU11938	Aau11938 Colony st
146	1300.5	23.0	917	7	ADM29420	Adm29420 Mouse mac
147	1296.5	22.9	411	9	ADZ64612	Adz64612 Tyrosine
148	1287	22.8	1273	3	AAY70751	Aay70751 Human tyr
149	1287	22.8	1338	4	AAG67625	Aag67625 Amino aci
150	1287	22.8	1338	4	AAG67446	Aag67446 Amino aci
151	1287	22.8	1338	6	ABU03562	Abu03562 Angiogene
152	1287	22.8	1338	6	ABR43696	Abr43696 Human vas
153	1287	22.8	1338	7	ABM79008	Abm79008 Human VEG
154	1287	22.8	1338	7	ADN95710	Adn95710 Human BEC
155	1287	22.8	1338	7	ADN95933	Adn95933 Human BEC
156	1287	22.8	1338	8	ADT92355	Adt92355 Human vas
157	1287	22.8	1338	9	ADV90284	Adv90284 Protease-
158	1287	22.8	1338	9	ADY59383	Ady59383 Human VEG
159	1287	22.8	1338	9	ADZ26559	Adz26559 Human VEG
160	1287	22.8	1421	4	ABG06099	Abg06099 Novel hum
161	1286.5	22.8	1339	4	AAY97784	Aay97784 Human FLT
162	1280	22.6	1333	6	ABR43697	Abr43697 Mouse vas
163	1280	22.6	1333	7	ADE61408	Ade61408 Rat Prote
164	1280	22.6	1333	7	ADF45096	Adf45096 Rat kinas
165	1280	22.6	1333	9	AEA55046	Aea55046 Mouse VEG
166	1251	22.1	1311	2	ADP90839	Adp90839 Human fms
167	1251	22.1	1311	3	AAY71001	Aay71001 Alternati
168	1219	21.6	314	5	ABB81191	Abb81191 Human PDG
169	1218.5	21.6	1356	4	AAB62475	Aab62475 Human VEG
170	1218.5	21.6	1356	4	AAY97783	Aay97783 Human KDR
171	1218.5	21.6	1356	4	AAY97576	Aay97576 Human Flk
172	1218.5	21.6	1356	5	AAU79429	Aau79429 Human Kin
173	1218.5	21.6	1356	6	ABR40196	Abr40196 Human vas
174	1218.5	21.6	1356	7	ADD08954	Add08954 Human VEG
175	1218.5	21.6	1356	7	ABM79007	Abm79007 Human VEG
176	1218.5	21.6	1356	7	ADF45097	Adf45097 Human kin
177	1218.5	21.6	1356	8	ADH17130	Adh17130 Human vas
178	1218.5	21.6	1356	8	ADQ39806	Adq39806 Human myo
179	1218.5	21.6	1356	8	ADQ39808	Adq39808 Human myo
180	1218.5	21.6	1356	8	ADR46648	Adr46648 Cancer-as
181	1218.5	21.6	1356	8	ADT92353	Adt92353 Human vas
182	1218.5	21.6	1356	9	ADV90285	Adv90285 Protease-
183	1218.5	21.6	1356	9	ADY59385	Ady59385 Human VEG
184	1218.5	21.6	1356	9	ADZ26561	Adz26561 Human VEG
185	1217.5	21.5	1355	2	AAW80997	Aaw80997 Human rec
186	1217.5	21.5	1356	5	AAU79426	Aau79426 Human Kin
187	1217.5	21.5	1356	8	ADG70543	Adg70543 Human KDR
188	1216.5	21.5	1356	7	ABU64302	Abu64302 Human KDR
189	1216	21.5	1356	5	AAU79430	Aau79430 Human Kin
190	1214.5	21.5	1356	5	AAU79427	Aau79427 Human Kin
191	1206.5	21.3	1354	9	ADZ00446	Adz00446 VEGFR-2.
192	1206.5	21.3	1356	2	AAR26999	Aar26999 Novel typ
193	1206.5	21.3	1356	2	AAW59275	Aaw59275 Human KDR
194	1192.5	21.1	917	8	ADH48350	Adh48350 Human KPP
195	1188	21.0	1343	8	ADR32338	Adr32338 Rat optim
196	1183	20.9	1343	8	ADR32351	Adr32351 Rat recep
197	1177.5	20.8	1306	8	ADQ39807	Adq39807 Human myo
198	1177	20.8	993	8	ADQ39992	Adq39992 Human myo
199	1177	20.8	993	9	ADZ12552	Adz12552 Human can
200	1174	20.8	993	6	ADA00001	Ada00001 Human FMS
201	1174	20.8	993	9	AEA19275	Aea19275 Human Flt
202	1173	20.8	993	2	AAR75961	Aar75961 Human STK
203	1171	20.7	993	2	AAR81869	Aar81869 Human Flk
204	1168.5	20.7	1000	7	ADE47736	Ade47736 Human NOV
205	1168.5	20.7	1000	8	ADJ79006	Adj79006 Human NOV
206	1167.5	20.7	993	2	AAR37503	Aar37503 Human flk
207	1166.5	20.6	1167	2	AAR31376	Aar31376 Human flk
208	1166.5	20.6	1302	7	ADD93316	Add93316 Zebrafish
209	1166	20.6	992	2	ADP90723	Adp90723 Human foe
210	1166	20.6	993	2	AAR44995	Aar44995 Human flk
211	1166	20.6	993	2	AAR67536	Aar67536 Human flk
212	1166	20.6	993	2	AAR67816	Aar67816 Flk2 rece
213	1166	20.6	993	2	AAR97419	Aar97419 Murine fo
214	1166	20.6	993	2	AAW19873	Aaw19873 Human flk
215	1166	20.6	993	2	AAY08617	Aay08617 Human flk
216	1166	20.6	993	5	ABG70916	Abg70916 Human rec
217	1166	20.6	993	5	AAE25819	Aae25819 Human rec
218	1166	20.6	993	7	ADF45089	Adf45089 Human kin
219	1166	20.6	993	8	ADI33418	Adi33418 Human FMS
220	1166	20.6	993	8	ADP12454	Adp12454 Protein e
221	1166	20.6	993	8	ADQ39993	Adq39993 Human myo
222	1166	20.6	993	9	ADW87789	Adw87789 Human fet
223	1166	20.6	993	9	ADY97854	Ady97854 FMS-like
224	1166	20.6	993	9	AEB46054	Aeb46054 Human flk
225	1165.5	20.6	1002	9	ADZ12549	Adz12549 Murine ca
226	1164.5	20.6	1000	2	AAR81868	Aar81868 Flk2/flt3
227	1163.5	20.6	1298	2	AAR85937	Aar85937 Protein t
228	1163.5	20.6	1298	2	AAR90528	Aar90528 FLT4 rece
229	1163.5	20.6	1298	2	ADP90836	Adp90836 Human fms
230	1163.5	20.6	1298	3	AAY90365	Aay90365 Human Flt
231	1163.5	20.6	1298	3	AAY70746	Aay70746 Human tyr
232	1163.5	20.6	1298	5	ABG32043	Abg32043 Human Flt
233	1163.5	20.6	1298	6	ABU04292	Abu04292 Human exp
234	1163.5	20.6	1298	6	ABU04307	Abu04307 Human exp
235	1163.5	20.6	1298	6	ABU04296	Abu04296 Human exp
236	1163.5	20.6	1298	6	ABU04274	Abu04274 Human exp
237	1163.5	20.6	1298	6	ABU04294	Abu04294 Human exp
238	1163.5	20.6	1298	6	ABU04293	Abu04293 Human exp
239	1163.5	20.6	1298	7	ADD08956	Add08956 Human VEG
240	1163.5	20.6	1298	7	ADF45098	Adf45098 Human kin
241	1163.5	20.6	1298	8	ADT92356	Adt92356 Human vas
242	1163.5	20.6	1298	9	ADZ00448	Adz00448 VEGFR-3.
243	1163.5	20.6	1304	6	ABU04279	Abu04279 Human exp

244	1163.5	20.6	1363	2	ADP90838	Adp90838	Human fms
245	1163.5	20.6	1363	3	AAY90366	Aay90366	Human Flt
246	1163.5	20.6	1363	3	AAY70747	Aay70747	Human tyr
247	1163.5	20.6	1363	3	AAB29047	Aab29047	Human Flt
248	1163.5	20.6	1363	4	AAB37604	Aab37604	Human Flt
249	1163.5	20.6	1363	5	ABG32044	Abg32044	Human Flt
250	1163.5	20.6	1363	6	ABU04297	Abu04297	Human exp
251	1163.5	20.6	1363	6	ABU04284	Abu04284	Human exp
252	1163.5	20.6	1363	6	ABU04282	Abu04282	Human exp
253	1163.5	20.6	1363	6	ABU04295	Abu04295	Human exp
254	1162	20.6	1345	7	ABM79009	Abm79009	Murine Fl
255	1162	20.6	1367	6	ABR40197	Abr40197	Murine va
256	1160.5	20.5	1298	3	AAB30542	Aab30542	Amino aci
257	1160.5	20.5	1298	4	AAY97785	Aay97785	Mouse Flt
258	1160.5	20.5	1298	4	AAY97575	Aay97575	Human Flt
259	1160.5	20.5	1298	6	ABU07853	Abu07853	Human vas
260	1160.5	20.5	1298	6	ABU04298	Abu04298	Human exp
261	1160.5	20.5	1298	6	ABU04304	Abu04304	Human exp
262	1160.5	20.5	1298	6	ABU04277	Abu04277	Human exp
263	1160.5	20.5	1298	6	ABU04283	Abu04283	Human exp
264	1160.5	20.5	1298	7	ADN95352	Adn95352	Human BEC
265	1160.5	20.5	1298	8	ADQ91191	Adq91191	Human vas
266	1160.5	20.5	1298	8	ADR05211	Adr05211	Human fms
267	1160.5	20.5	1298	9	ADY16409	Ady16409	PRO polyp
268	1160.5	20.5	1363	7	ADC64992	Adc64992	Human VEG
269	1152.5	20.4	992	2	AAR31375	Aar31375	Murine fl
270	1152.5	20.4	992	2	AAR37502	Aar37502	Murine fl
271	1152.5	20.4	992	2	AAR44994	Aar44994	Murine fl
272	1152.5	20.4	992	2	AAR67535	Aar67535	Mouse flk
273	1152.5	20.4	992	2	AAR67815	Aar67815	Flk2 rece
274	1152.5	20.4	992	2	AAR97418	Aar97418	Human foe
275	1152.5	20.4	992	2	AAW19874	Aaw19874	Murine fl
276	1152.5	20.4	992	2	ADP90721	Adp90721	Mouse foe
277	1152.5	20.4	992	2	AAY08616	Aay08616	Murine fl
278	1152.5	20.4	992	5	ABG70915	Abg70915	Mouse rec
279	1152.5	20.4	992	5	AAE25818	Aae25818	Murine re
280	1152.5	20.4	992	9	ADW87787	Adw87787	Murine fe
281	1152.5	20.4	992	9	AEB46052	Aeb46052	Murine fl
282	1152.5	20.4	1363	4	AAB37607	Aab37607	Human pro
283	1152.5	20.4	1363	6	ABU04285	Abu04285	Human exp
284	1152	20.4	1367	2	AAR31377	Aar31377	Human flk
285	1152	20.4	1367	2	AAR37504	Aar37504	Murine fl
286	1152	20.4	1367	2	AAR44996	Aar44996	Murine fl
287	1152	20.4	1367	2	AAR67537	Aar67537	Mouse flk
288	1152	20.4	1367	2	AAR97420	Aar97420	Murine fo
289	1152	20.4	1367	2	AAW19875	Aaw19875	Murine fl
290	1152	20.4	1367	2	ADP90725	Adp90725	Mouse foe
291	1152	20.4	1367	2	AAY08618	Aay08618	Murine fl
292	1152	20.4	1367	5	ABG70917	Abg70917	Mouse rec
293	1152	20.4	1367	5	AAE25820	Aae25820	Murine re
294	1152	20.4	1367	9	ADW87791	Adw87791	Murine fe
295	1152	20.4	1367	9	AEB46056	Aeb46056	Murine fl
296	1149.5	20.3	983	2	AAW63588	Aaw63588	Human rec
297	1149	20.3	1367	2	AAR28041	Aar28041	flk-1. 3/
298	1148	20.3	986	2	AAW63589	Aaw63589	Human rec
299	1147	20.3	986	2	AAW63587	Aaw63587	Human rec
300	1146	20.3	1367	2	AAR67817	Aar67817	Flk1 rece
301	1145	20.3	994	2	AAW63586	Aaw63586	Human rec
302	1140.5	20.2	1373	4	AAY97782	Aay97782	Mouse Flk
303	1139	20.2	1367	2	AAR54046	Aar54046	Sequence
304	1136	20.1	433	9	ADZ64610	Adz64610	Kinase do
305	1132.5	20.0	992	2	AAR28038	Aar28038	Murine fl
306	1105	19.6	217	9	ADY28130	Ady28130	Receptor
307	1105	19.6	218	8	ADQ39642	Adq39642	Human myo
308	1105	19.6	218	9	ADY28131	Ady28131	Receptor
309	1105	19.6	218	9	ADZ13913	Adz13913	Human can
310	1069	18.9	917	7	ADM29419	Adm29419	Rat macro
311	1031.5	18.3	427	7	ADM29268	Adm29268	Human nov
312	1031.5	18.3	427	7	ADM29270	Adm29270	Human nov
313	1031.5	18.3	427	7	ADM29264	Adm29264	Human nov
314	1031.5	18.3	427	7	ADM29266	Adm29266	Human nov
315	1018	18.0	312	5	ABB81190	Abb81190	Human KIT
316	1007.5	17.8	343	8	ADI79350	Adi79350	Colony st
317	1000.5	17.7	329	8	ADI79351	Adi79351	Colony st
318	997.5	17.6	270	2	AAY43977	Aay43977	Mouse pro
319	976	17.3	1474	7	AAE39593	Aae39593	Drosophil
320	973.5	17.2	1503	7	AAE39594	Aae39594	Drosophil
321	972.5	17.2	952	7	ADE47734	Ade47734	Human NOV
322	972.5	17.2	952	8	ADJ79004	Adj79004	Human NOV
323	965	17.1	1500	4	ABB63715	Abb63715	Drosophil
324	960.5	17.0	1509	7	AAE39592	Aae39592	Drosophil
325	953.5	16.9	551	9	ADY52646	Ady52646	Human tra
326	950.5	16.8	392	9	ADY52579	Ady52579	Human onc
327	938	16.6	548	9	ADY52647	Ady52647	Human tra
328	933	16.5	307	5	ABB81198	Abb81198	Human FLT
329	932.5	16.5	389	9	ADY52580	Ady52580	Human onc
330	928.5	16.4	367	8	ADT92363	Adt92363	Human VEG
331	918	16.2	820	8	ADR32354	Adr32354	GST-rat K
332	912.5	16.1	558	8	ADR32352	Adr32352	Rat recep
333	908.5	16.1	713	7	ADD90617	Add90617	Human VEG
334	908.5	16.1	713	8	ADO34223	Ado34223	Human VEG
335	903.5	16.0	429	9	ADY85472	Ady85472	Catalytic
336	902.5	16.0	364	8	ADT92365	Adt92365	Human VEG
337	897	15.9	366	3	AAY87421	Aay87421	Human VEG
338	897	15.9	366	8	ADT92364	Adt92364	Human VEG
339	867.5	15.3	815	8	ADO26856	Ado26856	Human rec
340	862	15.3	819	2	AAR10648	Aar10648	Chicken b
341	859.5	15.2	270	2	AAY43979	Aay43979	Human pro
342	859.5	15.2	820	8	ADS18132	Ads18132	Human FGF
343	859.5	15.2	822	2	AAR13549	Aar13549	Basic FGF
344	859.5	15.2	822	2	AAR20750	Aar20750	flg recep
345	859.5	15.2	822	2	AAR26337	Aar26337	N-sam. 2/
346	859.5	15.2	822	6	AAE34488	Aae34488	Human FGF
347	859.5	15.2	822	7	ABR56164	Abr56164	Human Fib
348	859.5	15.2	822	7	ADE61700	Ade61700	Human Pro
349	859.5	15.2	822	7	ADF45057	Adf45057	Human kin
350	859.5	15.2	822	7	ADP65260	Adp65260	Human fib
351	859.5	15.2	822	7	ADP65261	Adp65261	Human fib
352	859.5	15.2	822	8	ADQ17658	Adq17658	Human sof
353	859.5	15.2	822	8	ADP24447	Adp24447	PRO polyp
354	859.5	15.2	822	9	ADW12711	Adw12711	Human fib
355	859.5	15.2	822	9	ADY16516	Ady16516	PRO polyp
356	858.5	15.2	820	9	ADW12710	Adw12710	Human fib
357	857.5	15.2	759	9	ADY57312	Ady57312	Human fib
358	857.5	15.2	820	2	AAR47233	Aar47233	Human fib
359	857.5	15.2	820	4	AAB84383	Aab84383	Amino aci
360	857.5	15.2	820	9	AEB87746	Aeb87746	Human fib
361	855.5	15.1	816	2	AAR39647	Aar39647	Human fib
362	855.5	15.1	830	8	ABM83108	Abm83108	Human dia
363	855	15.1	822	7	ADE61698	Ade61698	Rat Prote
364	855	15.1	822	7	ADE55803	Ade55803	Rat Prote
365	853.5	15.1	561	6	ABG72460	Abg72460	Human pla
366	853	15.1	316	3	AAY87417	Aay87417	Human VEG
367	853	15.1	316	8	ADT92354	Adt92354	Human VEG
368	852.5	15.1	820	2	AAY06458	Aay06458	Fibroblas
369	852.5	15.1	820	8	ADO49087	Ado49087	Human ded
370	852.5	15.1	820	8	ADS18125	Ads18125	Human fib
371	852.5	15.1	820	8	ADS18122	Ads18122	Human FGF
372	852.5	15.1	822	4	AAU04694	Aau04694	Mouse fib
373	851.5	15.1	820	9	ADZ12913	Adz12913	Human can
374	851	15.1	804	8	ABM83110	Abm83110	Human dia
375	845	15.0	316	9	ADY85454	Ady85454	Catalytic
376	845	15.0	316	9	ADZ64614	Adz64614	Tyrosine
377	844.5	14.9	822	8	ADO42159	Ado42159	Human NOV
378	844	14.9	299	8	ADR15782	Adr15782	Kinase lv
379	844	14.9	764	3	AAB58376	Aab58376	Lung canc
380	843	14.9	831	8	ABM83107	Abm83107	Human dia
381	842	14.9	824	8	ADO42155	Ado42155	Human NOV
382	841	14.9	832	8	ABM83109	Abm83109	Human dia
383	839	14.8	838	9	ADZ13071	Adz13071	Human can
384	839	14.8	838	9	ADZ13115	Adz13115	Human can
385	837.5	14.8	820	2	AAW63844	Aaw63844	Mouse bFG
386	837	14.8	804	9	ADZ13079	Adz13079	Human can
387	833.5	14.7	821	7	ADE57113	Ade57113	Human Pro
388	833.5	14.7	821	7	ADD45446	Add45446	Human Pro
389	833.5	14.7	821	7	ADF45058	Adf45058	Human kin

390	833.5	14.7	821	7	ADH63155
391	833.5	14.7	821	8	ADO49089
392	833.5	14.7	821	9	ADY57311
393	833.5	14.7	821	9	AEA81232
394	833	14.7	822	8	ADN03976
395	833	14.7	822	9	ADY15139
396	833	14.7	822	9	AEA81236
397	832.5	14.7	735	8	ADO42157
398	831.5	14.7	768	9	AEA81237
399	831.5	14.7	821	2	AAR21080
400	831	14.7	788	9	AEA81241
401	830.5	14.7	733	9	ADW12713
402	829.5	14.7	731	2	AAR21686
403	828.5	14.7	729	9	ADZ12919
404	828	14.6	822	7	ADH63164
405	828	14.6	822	8	ADL61330
406	828	14.6	822	8	ADQ80367
407	828	14.6	822	9	AEA81233
408	826.5	14.6	731	2	AAR10649
409	826.5	14.6	731	9	ADW12712
410	826	14.6	769	9	AEA81238
411	821.5	14.5	291	8	ADR88389
412	821	14.5	769	2	AAR15268
413	821	14.5	821	7	ADH63156
414	818	14.5	768	7	ADH63160
415	818	14.5	771	7	ADH63158
416	818	14.5	817	7	ADH63159
417	818	14.5	819	7	ADH63157
418	815.5	14.4	709	8	ADU24336
419	814.5	14.4	270	2	AAY43978
420	807	14.3	806	4	AAE21976
421	807	14.3	806	6	ABJ38646
422	807	14.3	806	6	ADA89050
423	807	14.3	806	6	AAE36462
424	807	14.3	806	7	ADF45059
425	807	14.3	806	7	ADG74302
426	807	14.3	806	7	ADK51038
427	807	14.3	806	9	ADV73201
428	807	14.3	806	9	ADY57310
429	807	14.3	806	9	ADZ12673
430	807	14.3	806	9	ADZ12685
431	807	14.3	806	9	ADZ12675
432	807	14.3	806	9	AEB29730
433	806.5	14.3	749	8	ABM83559
434	804	14.2	732	9	AEA81242
435	802	14.2	782	9	ADZ12664
436	801.5	14.2	729	2	AAW37804
437	801.5	14.2	729	2	AAY23631
438	801	14.2	750	9	ADZ13087
439	799.5	14.1	731	8	ABM83558
440	799.5	14.1	731	9	AEA81239
441	799	14.1	701	9	ADZ13065
442	799	14.1	701	9	ADZ13073
443	798	14.1	808	7	ADK51040
444	798	14.1	808	9	ADZ12679
445	797.5	14.1	679	2	AAR41517
446	797.5	14.1	682	7	ADH63162
447	797.5	14.1	682	9	ADX69301
448	796	14.1	724	9	ADZ13075
449	796	14.1	724	9	ADZ13111
450	796	14.1	724	9	ADZ13097
451	796	14.1	800	9	ADZ12666
452	794	14.0	724	9	ADZ13059
453	794	14.0	724	9	ADZ13049
454	794	14.0	724	9	ADZ13067
455	794	14.0	856	8	ABM83858
456	792	14.0	726	2	AAR14280
457	792	14.0	726	2	AAR10933
458	791.5	14.0	705	7	ADH63163
459	791.5	14.0	705	9	AEA81234
460	791	14.0	652	2	AAR15269
461	791	14.0	654	7	ADD47011
462	790.5	14.0	672	8	ADO26840

Adh63155	Human fib
Ado49089	Human ded
Ady57311	Human fib
Aea81232	Human fib
Adn03976	Antipsori
Ady15139	PRO polyp
Aea81236	Human fib
Ado42157	Human NOV
Aea81237	Human fib
Aar21080	flg recep
Aea81241	Human fib
Adw12713	Human fib
Aar21686	Human bFG
Adz12919	Human can
Adh63164	Human FGF
Adl61330	Human fib
Adq80367	Fibroblas
Aea81233	Human fib
Aar10649	Chicken b
Adw12712	Human fib
Aea81238	Human fib
Adr88389	KDR tyros
Aar15268	Clone pTB
Adh63156	Murine fi
Adh63160	Human FGF
Adh63158	Human FGF
Adh63159	Human FGF
Adh63157	Human FGF
Adu24336	Human FGF
Aay43978	Human pro
Aae21976	Human fib
Abj38646	FGFR3 pro
Ada89050	Human FGF
Aae36462	Human FGF
Adf45059	Human kin
Adg74302	Fibroblas
Adk51038	Human NOV
Adv73201	Human col
Ady57310	Human fib
Adz12673	Human can
Adz12685	Human can
Adz12675	Human can
Aeb29730	Human fib
Abm83559	Human dia
Aea81242	Human fib
Adz12664	Murine ca
Aaw37804	Fibroblas
Aay23631	Bek-like
Adz13087	Human can
Abm83558	Human dia
Aea81239	Human fib
Adz13065	Human can
Adz13073	Human can
Adk51040	Human NOV
Adz12679	Human can
Aar41517	K-sam. 3/
Adh63162	Human FGF
Adx69301	Human hep
Adz13075	Human can
Adz13111	Human can
Adz13097	Human can
Adz12666	Murine ca
Adz13059	Human can
Adz13049	Human can
Adz13067	Human can
Abm83858	Human dia
Aar14280	Murine KG
Aar10933	KGF recep
Adh63163	Human FGF
Aea81234	Human fib
Aar15269	Clone pTB
Add47011	Human Pro
Ado26840	Human rec

463	786.5	13.9	731	2	AAY23633
464	786.5	13.9	750	2	AAW37806
465	786	13.9	705	9	AEA81244
466	785	13.9	707	9	AEA81243
467	779.5	13.8	801	4	AAE21977
468	766.5	13.6	1052	4	ABB71502
469	763	13.5	694	5	ABG66739
470	763	13.5	694	8	ADO49091
471	763	13.5	694	9	ADW38877
472	763	13.5	694	9	ADZ12683
473	763	13.5	694	9	ADZ12669
474	763	13.5	694	9	ADZ12681
475	761.5	13.5	310	9	ADZ64613
476	761.5	13.5	315	2	AAW56001
477	761.5	13.5	351	2	AAW56000
478	760	13.4	687	2	AAY06456
479	760	13.4	1072	6	ABU03993
480	760	13.4	1089	6	ABU03998
481	760	13.4	1106	6	ABU03992
482	760	13.4	1114	5	AAE24148
483	760	13.4	1114	5	ABG95125
484	760	13.4	1114	6	ABP97192
485	760	13.4	1114	6	ABU03994
486	760	13.4	1114	6	ABU03995
487	760	13.4	1114	6	ABU03996
488	760	13.4	1114	7	ADE61505
489	759.5	13.4	299	8	ADR15783
490	759.5	13.4	386	9	ADZ12917
491	758.5	13.4	650	7	ADE58201
492	758.5	13.4	650	7	ADE58205
493	758.5	13.4	650	7	ADE58197
494	758.5	13.4	650	7	ADE58193
495	758.5	13.4	650	7	ADE03534
496	758	13.4	388	2	AAW37803
497	758	13.4	388	2	AAY23630
498	758	13.4	783	8	ABM83106
499	757.5	13.4	310	2	AAW55999
500	757.5	13.4	379	9	ADY85473

Aay23633	Newt kera
Aaw37806	Keratinoc
Aea81244	Human fib
Aea81243	Human fib
Aae21977	Mouse fib
Abb71502	Drosophil
Abg66739	Human nov
Ado49091	Human ded
Adw38877	T-cell me
Adz12683	Human can
Adz12669	Human can
Adz12681	Human can
Adz64613	Tyrosine
Aaw56001	Protein t
Aaw56000	Fibroblas
Aay06456	ZNF198-FG
Abu03993	Human exp
Abu03998	Human exp
Abu03992	Human exp
Aae24148	Human kin
Abg95125	Human onc
Abp97192	Tumour-as
Abu03994	Human exp
Abu03995	Human exp
Abu03996	Human exp
Ade61505	Human Pro
Adr15783	Kinase la
Adz12917	Human can
Ade58201	Rat Prote
Ade58205	Rat Prote
Ade58197	Rat Prote
Ade58193	Rat Prote
Ade03534	Rat fibro
Aaw37803	Truncated
Aay23630	Truncated
Abm83106	Human dia
Aaw55999	Protein t
Ady85473	Catalytic

ALIGNMENTS

RESULT 1
AAU84300
ID AAU84300 standard; protein; 1089 AA.
XX
AC AAU84300;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human endometrial cancer related protein, PDGFRA.
XX
KW Human; endometrial cancer; differential expression; DNA microarray;
KW protein microarray.
XX
OS Homo sapiens.
XX
PN WO200209573-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US024104.
XX
PR 31-JUL-2000; 2000US-0221735P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI; 2002-179967/23.
DR N-PSDB; ABK35520.
XX

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PT   Diagnosing endometrial cancer comprises determining expression of nucleic
PT   acid molecules or expression products that are differentially expressed
PT   in normal and malignant endometrium.
XX
PS   Claim 33; Page 214-217; 233pp; English.
XX
CC   The invention relates to diagnosing endometrial cancer in a subject
CC   suspected of having endometrial cancer comprising determining the
CC   expression of a set of nucleic acid molecules or expression products in
CC   an endometrial sample suspected of being cancerous, where the set of
CC   nucleic acid molecules comprises at least 2 nucleic acid molecules
CC   selected from 50 fully defined sequences as given in the specification.
CC   The nucleic acids are used as an array of at least 2 of the 50 nucleic
CC   acids bound to a solid substrate. Also included is a solid-phase protein
CC   microarray comprising at least 2 antibodies or its antigen binding
CC   fragments, that specifically bind at least 2 different polypeptides from
CC   the 50 fully defined sequences as given in the specification, fixed to a
CC   solid substrate. The methods and arrays are useful for the diagnosis of
CC   endometrial cancer, selecting and monitoring treatment regimes and
CC   identification of lead compounds useful for the treatment of endometrial
CC   cancer. The present sequence is one of 50 proteins differentially
CC   expressed between cancerous and non-cancerous samples
XX
SQ   Sequence 1089 AA;

  Query Match             100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 2
ABG72449
ID   ABG72449 standard; protein; 1089 AA.
XX
AC   ABG72449;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .490
FT                   /label= Extracellular_domain
FT   Peptide         1. .24
FT                   /label= Signal_peptide_sequence_2
FT   Peptide         1. .20
FT                   /label= Signal_peptide_sequence_1
FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
FT                   /label= Immunoglobulin-like_domain
FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
FT                   /label= Immunoglobulin-like_domain
FT   Domain          338. .399
FT                   /label= Immunoglobulin-like_domain
```

```
FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .661
FT                   /note= "Split tyrosine kinase domain segment 1"
FT   Domain          760. .900
FT                   /note= "Split tyrosine kinase domain segment 2"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   N-PSDB; ABS57780.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 1; Page 38-41; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This is the amino
CC   acid sequence of human platelet derived growth factor receptor (PDGFR)
CC   alpha used to make mutant PDGFR alpha proteins for use in treating
CC   fibrotic diseases
XX
SQ   Sequence 1089 AA;

  Query Match             100.0%;  Score 5652;  DB 6;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 3
ABP96312
ID   ABP96312 standard; protein; 1089 AA.
XX
AC   ABP96312;
XX
DT   20-MAY-2003  (first entry)
XX
DE   Human platelet-derived growth factor receptor alpha protein.
XX
```

```
KW   Humanised baculovirus; cytostatic; gene therapy; baculovirus; cancer;
KW   prostate cancer; platelet-derived growth factor receptor alpha;
KW   chromosome 4.
XX
OS   Homo sapiens.
XX
PN   WO2003016540-A2.
XX
PD   27-FEB-2003.
XX
PF   15-AUG-2002; 2002WO-GB003791.
XX
PR   15-AUG-2001; 2001GB-00019852.
XX
PA   (UYYO-) UNIV YORK.
XX
PI   Maitland N;
XX
DR   WPI; 2003-268336/26.
XX
PT   New baculovirus having a modified genome encoding a therapeutic agent,
PT   useful in the manufacture of a medicament for the treatment of cancer,
PT   particularly prostate cancer.
XX
PS   Claim 33; Page; 34pp; English.
XX
CC   The present invention describes a humanised baculovirus (I) which
CC   comprises a modified baculovirus genome having a nucleic acid molecule
CC   encoding a therapeutic agent and a polypeptide which functions to target
CC   the baculovirus to at least one cell type. Also described is a
CC   pharmaceutical composition comprising (I). (I) has cytostatic activity,
CC   and can be used in gene therapy. The baculovirus is useful in the
CC   manufacture of a medicament for the treatment of cancer, particularly
CC   prostate cancer. The present sequence represents the human platelet-
CC   derived growth factor receptor alpha protein, which is specified in the
CC   exemplification of the present invention. N.B. The present sequence is
CC   not given in the specification but is referred to in Claim 33 as Genbank
CC   accession number NM_006206
XX
SQ   Sequence 1089 AA;

  Query Match          100.0%;  Score 5652;  DB 6;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 4
ABR84718
ID   ABR84718 standard; protein; 1089 AA.
XX
AC   ABR84718;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PDGF alpha receptor protein.
XX
KW   Tissue vascularisation; aging; mouse; human; PDGF A; PDGF B;
KW   PDGF alpha receptor; PDGF beta receptor; endothelial precursor cell;
KW   vascular disease; cardiant; cell therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003070083-A2.
XX
PD   28-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-US004244.
XX
PR   15-FEB-2002; 2002US-0357328P.
PR   08-AUG-2002; 2002WO-US025175.
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XX
PA   (CORR ) CORNELL RES FOUND INC.
PA   (EDEL/) EDELBERG J M.
PA   (RAFI/) RAFII S.
PA   (HONG/) HONG M K.
PA   (LANZ/) LANZA R P.
PA   (WEST/) WEST M D.
XX
PI   Edelberg JM,  Rafii S,  Hong MK,  Lanza RP,  West MD;
XX
DR   WPI; 2003-697548/66.
XX
PT   Treating a vascular condition, e.g. myocardial infarction,
PT   atherosclerosis, ischemia, congestive heart failure, hypertension,
PT   stroke, thrombosis, arrhythmia or tachycardia, by administering
PT   endothelial precursor cells.
XX
PS   Claim 24; Page 47; 110pp; English.
XX
CC   The present invention relates to a method of treating a vascular
CC   condition in a mammal, which comprises administering to the mammal a
CC   therapeutic amount of endothelial precursor cells. The method and cells
CC   of the invention are useful for treating a vascular condition, e.g.
CC   myocardial infarction, atherosclerosis, ischaemia, tachycardia,
CC   congestive heart failure, peripheral vasculature disorder, hypertension,
CC   stroke, thrombosis, arrhythmia or tachycardia. The present sequence is a
CC   protein shown in the exemplification of the invention
XX
SQ   Sequence 1089 AA;

  Query Match             100.0%;  Score 5652;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 5
ADF45081
ID   ADF45081 standard; protein; 1089 AA.
XX
AC   ADF45081;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human kinase PDGFR-a.
XX
KW   Human; protein kinase; enzyme; inhibitor; PDGFR-a.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC,  Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 50; 260pp; English.
XX
```

```
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 1089 AA;

  Query Match             100.0%;  Score 5652;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 6
ADF90896
ID   ADF90896 standard; protein; 1089 AA.
XX
AC   ADF90896;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human hepatic-fibrosis disease marker protein SEQ ID 358.
XX
KW   Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
KW   hepatic carcinoma; human.
XX
OS   Homo sapiens.
XX
PN   JP2003259877-A.
XX
PD   16-SEP-2003.
XX
PF   11-MAR-2002; 2002JP-00065013.
XX
PR   11-MAR-2002; 2002JP-00065013.
XX
PA   (SUMU ) SUMITOMO SEIYAKU KK.
XX
DR   WPI; 2003-821598/77.
XX
PT   Hepatic fibrosis disease markers comprising polynucleotides or
PT   antibodies, useful for improved diagnosis, screening and developing drugs
PT   to treat hepatitis, to control cirrhosis and carcinoma.
XX
PS   Claim 3; SEQ ID NO 358; 313pp; Japanese.
XX
CC   The present invention relates to hepatic-fibrosis disease markers
CC   (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The
CC   sequences are useful for detecting and treating hepatic fibrosis caused
CC   by alcohol consumption, virus infection, etc., and the associated chronic
CC   hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC   markers allow the cause of hepatic fibrosis to be clarified (diagnostic
CC   precision), so more suitable treatments can be developed and given.
XX
SQ   Sequence 1089 AA;

  Query Match             100.0%;  Score 5652;  DB 7;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Qy       1081 SDLVEDSFL 1089
Db       1081 SDLVEDSFL 1089

RESULT 7
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```
ADM69012
ID   ADM69012 standard; protein; 1089 AA.
XX
AC   ADM69012;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha wild-type protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; wild-type.
XX
OS   Homo sapiens.
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69011, ADM69029.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Example 1; SEQ ID NO 2; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA wild-type
CC   protein of the invention.
XX
SQ   Sequence 1089 AA;
```

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  Query Match           100.0%;  Score 5652;  DB 8;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
                |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 8
ADQ17833
ID   ADQ17833 standard; protein; 1089 AA.
XX
AC   ADQ17833;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 650.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 650; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   protein of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 1089 AA;

  Query Match           100.0%;  Score 5652;  DB 8;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
```

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Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

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RESULT 9
ADQ59532
ID   ADQ59532 standard; protein; 1089 AA.
XX
AC   ADQ59532;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human cancer-associated (CA) protein sequence SEQ ID NO:168.
XX
KW   human; cancer-associated gene; cancer-associated protein; cytostatic;
KW   gene therapy; vaccine; tyrosine kinase antagonist;
KW   G-protein coupled receptor antagonist; cancer; lymphoma.
XX
OS   Homo sapiens.
XX
PN   WO2004058288-A1.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040082.
XX
PR   17-DEC-2002; 2002US-00322696.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-543349/52.
DR   N-PSDB; ADQ59530, ADQ59531.
XX
PT   New cancer-associated nucleic acid for diagnosing, preventing or treating
PT   cancer (e.g. lymphoma) or for screening agents that may be used for
PT   treating or preventing cancer.
XX
PS   Claim 19; SEQ ID NO 168; 143pp; English.
XX
CC   The present invention describes human cancer-associated (CA) nucleotide
CC   sequences (I). Also described: (1) an expression vector comprising (I);
CC   (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC   for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC   within an open reading frame of a CA sequence; (5) an isolated antibody,
CC   or its antigen binding fragment, that binds to the above polypeptide; (6)
CC   a hybridoma that produces the monoclonal antibody described above; (7) a
CC   pharmaceutical composition comprising the antibody and a pharmaceutical
CC   excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC   the above (monoclonal) antibody or polynucleotide that selectively
CC   hybridises to any of the polynucleotide sequences mentioned above; (9)
CC   methods for diagnosing cancer or for detecting the presence or absence of
CC   cancer cells in an individual; (10) a method for inhibiting growth of
CC   cancer cells in an individual; (11) a method for delivering a therapeutic
CC   agent to cancer cells in an individual; (12) an electronic library
CC   comprising the polynucleotide or polypeptide, or their fragments,
CC   mentioned above; (13) a method of screening for anticancer activity; (14)
CC   methods for detecting cancer associated with expression of a polypeptide
CC   or the presence of the antibody in a test cell or serum sample; (15) a
CC   method for screening for a bioactive agent capable of modulating the
CC   activity of a CA protein encoded by the above nucleic acid molecule; and
CC   (16) a method for treating cancers. (I) has cytostatic activity, and can
CC   be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC   and as a G-protein coupled receptor antagonist. The compositions and
CC   methods of the present invention can be used for diagnosing, preventing
CC   and treating cancer, especially lymphomas. They may also be used in
CC   screening for agents that may be used for treating or preventing cancer.
CC   The present sequence represents a human CA gene amino acid sequence,
CC   which is given in the exemplification of the present invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1089 AA;
```

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  Query Match           100.0%;  Score 5652;  DB 8;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
```

```
Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 10
ADQ39641
ID ADQ39641 standard; protein; 1089 AA.
XX
AC ADQ39641;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1304.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
DR N-PSDB; ADQ38813.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 10; SEQ ID NO 1304; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC sequence represents the protein of a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1089 AA;

Query Match 100.0%; Score 5652; DB 8; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 11
ADY59389
ID ADY59389 standard; protein; 1089 AA.
XX
AC ADY59389;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human PDGFR-A.
XX
KW PDGF antagonist; VEGF antagonist; psoriasis; rheumatoid arthritis;
KW age-related macular degeneration; antipsoriatic; dermatological disease;
KW immune disorder; antiarthritic; antirheumatic; immune disorder;
KW inflammation; musculoskeletal disease; age related macular degeneration;
KW ophthalmological; ocular disease; diabetic retinopathy; antidiabetic;
KW ophthalmological; cardiovascular disease; ocular disease.
XX
OS Homo sapiens.
XX
PN WO2005020972-A2.
XX
PD 10-MAR-2005.
XX
PF 26-AUG-2004; 2004WO-US027612.
XX
PR 27-AUG-2003; 2003US-0498407P.
PR 26-MAR-2004; 2004US-0556837P.
XX
PA (EYET-) EYETECH PHARM INC.
XX
PI Shima D, Calias P, Adamis AP;
XX
DR WPI; 2005-214423/22.
DR N-PSDB; ADY59388.
XX
PT Treating an ocular neovascular disorder, comprises administering a
PT platelet derived growth factor antagonist and a vascular endothelial
PT growth factor antagonist, simultaneously or within ninety days of each
PT other.
XX
PS Disclosure; SEQ ID NO 14; 112pp; English.
XX
CC The invention relates to a method of treating a patient diagnosed with or
CC at risk for developing a neovascular disorder, or suppressing a
CC neovascular disorder in a patient. The method is useful for treating a
CC patient diagnosed with or at risk for developing a neovascular disorder
CC or suppressing a neovascular disorder in a patient. The neovascular
CC disorder is an ocular neovascular disorder, psoriasis or rheumatoid
CC arthritis. The ocular neovascular disorder is ischemic retinopathy, iris
CC neovascularization, intraocular neovascularization, age-related macular
CC degeneration, corneal neovascularization, retinal neovascularization,
CC choroidal neovascularization, diabetic retinal ischemia, or proliferative
CC diabetic retinopathy. The present sequence represents a human PDGFR
CC protein.
XX
SQ Sequence 1089 AA;

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  Query Match             100.0%;  Score 5652;  DB 9;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 12
ADZ13915
ID ADZ13915 standard; protein; 1089 AA.
XX
AC ADZ13915;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated protein #436.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
DR N-PSDB; ADZ13914.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1435; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a human cancer-associated protein of the
CC invention.
XX
SQ Sequence 1089 AA;

Query Match 100.0%; Score 5652; DB 9; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
```

```
Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 13
AAR06910
ID AAR06910 standard; protein; 1089 AA.
XX
AC AAR06910;
XX
DT 25-MAR-2003 (revised)
DT 16-JAN-1991 (first entry)
XX
DE Alpha type PDGF receptor deduced from TR4 cDNA clone.
XX
KW Platelet derived growth factor; T11.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Domain	1. .23
FT		/label= signal peptide
FT	Domain	24. .524
FT		/label= ligand binding domain
FT	Modified-site	42. .44
FT		/label= N-glycos_site
FT	Modified-site	76. .78
FT		/label= N-glycos_site
FT	Modified-site	103. .105
FT		/label= N-glycos_site
FT	Modified-site	179. .181
FT		/label= N-glycos_site
FT	Modified-site	353. .355
FT		/label= N-glycos_site
FT	Modified-site	359. .361
FT		/label= N-glycos_site
FT	Modified-site	458. .460
FT		/label= N-glycos_site
FT	Modified-site	468. .470
FT		/label= N-glycos_site
FT	Domain	525. .548
FT		/label= transmembrane region
FT	Domain	549. .599
FT		/label= juxtamembrane domain
FT	Binding-site	600. .627
FT		/label= ATP binding site
FT	Modified-site	849
FT		/label= tyrosine autophosphorylation site

XX
PN WO9010013-A.
XX
PD 07-SEP-1990.
XX
PF 09-FEB-1989; 89US-00308282.
XX
PR 09-FEB-1989; 89US-00308282.
XX
PA (USDC) US SEC OF COMMERCE.
PA (USSH) US NAT CANCER INST.
XX
PI Matsui T, Aaronson SA, Pierce J;
XX
DR WPI; 1990-290306/38.
DR N-PSDB; AAQ05989.
XX
PT Type alpha platelet-derived growth factor receptor gene - useful for
PT transforming cells to express novel protein receptor and also susceptible
PT to genetic engineering.
XX
PS Claim 7; Fig 3; 64pp; English.
XX
CC The TR4 clone is the largest cDNA clone related to the T11 genomic clone,
CC isolated from a library prepd. from human thymus DNA. The T4 cDNA clone
CC was isolated from a M426 human embryo fibroblast cDNA library. The coding
CC region can be introduced into the pSV2 gpt vector with a simian sarcoma
CC virus LTR as a promoter and expressed in a host. The resulting protein is
CC a novel PDGF receptor designated type alpha (the known receptor is
CC designated type beta). The polypeptide has a calculated molecular mass of
CC 120 kD and has all the characteristics of a membrane spanning tyrosine
CC kinase receptor. The extracellular region comprises a hydrophobic signal
CC peptide and a ligand binding domain which has structural homology with
CC the PDGF-R/CSF1-R subfamily. Ten Cys residues are spaced at the same
CC positions as in other receptors of the sub- family and eight potential N-
CC linked glycosylation sites are also present. A hydrophobic segment spans
CC the membrane and the cyto- plasmic region comprises a juxtamembrane
CC region, a tyrosine kinase region split into TK1 and TK2 by a hydrophilic
CC interkinase region and a hydrophilic C-terminal tail. The TK region
CC includes the consensus ATP binding sequence (G-X-G-X-X-G. . .K) and a
CC tyrosine autophosphorylation site homologous to that of pp60(v-src).
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1089 AA;

```
  Query Match             99.9%;  Score 5649;  DB 2;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
```

```
Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPQKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 14
ABG72453
ID   ABG72453 standard; protein; 1089 AA.
XX
AC   ABG72453;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha mutant V859M.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .490
FT                   /label= Extracellular_domain
FT   Peptide         1. .24
FT                   /label= Signal_peptide_sequence_2
FT   Peptide         1. .20
FT                   /label= Signal_peptide_sequence_1
FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
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FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
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FT   Domain          338. .399
FT                   /label= Immunoglobulin-like_domain
FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .661
FT                   /note= "Split tyrosine kinase domain segment 1"
FT   Domain          760. .900
FT                   /note= "Split tyrosine kinase domain segment 2"
FT   Misc-difference 859
FT                   /note= "Wild type Val substituted by Met"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   N-PSDB; ABS57784.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 7; Page 64-67; 127pp; English.
XX
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CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This is the amino
CC   acid sequence of human platelet derived growth factor receptor (PDGFR)
CC   alpha mutant V859M
XX
SQ   Sequence 1089 AA;

  Query Match             99.9%;  Score 5649;  DB 6;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPMKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 15
ABG72450
ID   ABG72450 standard; protein; 1089 AA.
XX
AC   ABG72450;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha mutant E587K.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT   Peptide         1. .20
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FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
FT                   /label= Immunoglobulin-like_domain
FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
FT                   /label= Immunoglobulin-like_domain
FT   Domain          338. .399
FT                   /label= Immunoglobulin-like_domain
FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
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FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .661
FT                   /note= "Split tyrosine kinase domain segment 1"
FT   Misc-difference 587
FT                   /note= "Wild type Glu substituted by Lys"
FT   Domain          760. .900
FT                   /note= "Split tyrosine kinase domain segment 2"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   N-PSDB; ABS57781.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 7; Page 45-47; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This is the amino
CC   acid sequence of human platelet derived growth factor receptor (PDGFR)
CC   alpha mutant E587K
XX
SQ   Sequence 1089 AA;

  Query Match             99.9%;  Score 5648;  DB 6;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWKFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 16
ABG72452
ID   ABG72452 standard; protein; 1089 AA.
XX
AC   ABG72452;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha mutant D818N.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
```

```
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .490
FT                   /label= Extracellular_domain
FT   Peptide         1. .24
FT                   /label= Signal_peptide_sequence_2
FT   Peptide         1. .20
FT                   /label= Signal_peptide_sequence_1
FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
FT                   /label= Immunoglobulin-like_domain
FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
FT                   /label= Immunoglobulin-like_domain
FT   Domain          338. .399
FT                   /label= Immunoglobulin-like_domain
FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .661
FT                   /note= "Split tyrosine kinase domain segment 1"
FT   Domain          760. .900
FT                   /note= "Split tyrosine kinase domain segment 2"
FT   Misc-difference 818
FT                   /note= "Wild type Asp substituted by Asn"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   N-PSDB; ABS57783.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 7; Page 58-60; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This is the amino
CC   acid sequence of human platelet derived growth factor receptor (PDGFR)
CC   alpha mutant D818N
XX
SQ   Sequence 1089 AA;
```

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  Query Match             99.9%;  Score 5647;  DB 6;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRNLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 17
ABG72451
ID   ABG72451 standard; protein; 1089 AA.
XX
AC   ABG72451;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha mutant T665M.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .490
FT                   /label= Extracellular_domain
FT   Peptide         1. .24
FT                   /label= Signal_peptide_sequence_2
FT   Peptide         1. .20
FT                   /label= Signal_peptide_sequence_1
FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
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FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
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FT   Domain          338. .399
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FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .661
FT                   /note= "Split tyrosine kinase domain segment 1"
FT   Misc-difference 665
FT                   /note= "Wild type Thr substituted by Met"
FT   Domain          760. .900
FT                   /note= "Split tyrosine kinase domain segment 2"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   N-PSDB; ABS57782.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 7; Page 51-54; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This is the amino
CC   acid sequence of human platelet derived growth factor receptor (PDGFR)
CC   alpha mutant T665M
XX
SQ   Sequence 1089 AA;

  Query Match             99.9%;  Score 5646;  DB 6;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
```

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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACMKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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```
RESULT 18
AAR08267
ID   AAR08267 standard; protein; 1089 AA.
XX
AC   AAR08267;
XX
DT   25-MAR-2003  (revised)
DT   07-MAR-1991  (first entry)
XX
DE   Platelet derived growth factor (PDGF) receptor protein.
XX
KW   Atherosclerosis; fibrotic diseases.
XX
OS   Homo sapiens.
XX
PN   WO9014425-A.
XX
PD   29-NOV-1990.
XX
PF   22-MAY-1989;   89US-00355018.
XX
PR   22-MAY-1989;   89US-00355018.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Kelly JD,  Murray MJ;
XX
DR   WPI; 1990-375992/50.
DR   N-PSDB; AAQ06869.
XX
PT   DNA encoding platelet-derived growth factor - used to transform cells for
PT   culturing to detect PDG agonists and antagonists.
XX
PS   Claim 1; Fig 1; 30pp; English.
XX
CC   Gene product may be expressed from a transformed cell. It has utility in
CC   dection of PDGF agonist and antagonist analogues, binding AA, AB and BB
CC   isoforms. PDGF agonists may be used to enhance wound healing, and
CC   antagonists may be used to block the effects of PDGF eg. in treatment of
CC   atherosclerosis or fibrotic diseases. (Updated on 25-MAR-2003 to correct
CC   PA field.)
XX
SQ   Sequence 1089 AA;
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Query Match 99.9%; Score 5645; DB 2; Length 1089;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1087; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTLLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 19
ADM69031
ID ADM69031 standard; protein; 1089 AA.
XX
AC ADM69031;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant V561D protein.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 561
FT /note= "Wild-type Val substituted by Asp"
XX
PN WO2003105773-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018901.
XX
PR 13-JUN-2002; 2002US-0389107P.
PR 08-JAN-2003; 2003US-0438899P.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
XX
PI Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
DR WPI; 2004-082052/08.
DR N-PSDB; ADM69030.
XX
PT New isolated variant platelet derived growth factor alpha (PDGFRA)
PT polypeptide, useful for screening for a compound useful in influencing
PT PDGFRA-mediated neoplasia in a mammal.
XX
PS Claim 2; SEQ ID NO 21; 302pp; English.
XX
CC The invention relates to a novel isolated variant platelet derived growth
CC factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC for screening for a compound that may influence PDGFRA-mediated neoplasia
CC in a mammal. The current sequence is that of the human PDGFRA cancer-
CC related activating mutant V561D protein of the invention.
XX
SQ Sequence 1089 AA;

```
  Query Match             99.9%;  Score 5645;  DB 8;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRDIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 20
ADM69014
ID ADM69014 standard; protein; 1089 AA.
XX
AC ADM69014;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant D842V protein.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW cancer.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 842
FT   /note= "Wild-type Asp substituted by Val"
XX
PN WO2003105773-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018901.
XX
PR 13-JUN-2002; 2002US-0389107P.
PR 08-JAN-2003; 2003US-0438899P.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
XX
PI Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
DR WPI; 2004-082052/08.
DR N-PSDB; ADM69013.
XX
PT New isolated variant platelet derived growth factor alpha (PDGFRA)
PT polypeptide, useful for screening for a compound useful in influencing
PT PDGFRA-mediated neoplasia in a mammal.
XX
PS Claim 2; SEQ ID NO 4; 302pp; English.
XX
CC The invention relates to a novel isolated variant platelet derived growth
CC factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC for screening for a compound that may influence PDGFRA-mediated neoplasia
CC in a mammal. The current sequence is that of the human PDGFRA cancer-
CC related activating mutant D842V protein of the invention.
XX
SQ Sequence 1089 AA;

Query Match 99.8%; Score 5643; DB 8; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RVIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
             |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 21
ADM69035
ID   ADM69035 standard; protein; 1089 AA.
XX
AC   ADM69035;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant Del RD841-842KI protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 841. .842
FT                   /note= "Wild-type Arg,Asp substituted by Lys,Ile"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69034.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 25; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant Deletion RD841-842KI protein of the invention.
XX
SQ   Sequence 1089 AA;

  Query Match             99.8%;  Score 5640;  DB 8;  Length 1089;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1087;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 KIIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 22
ADM69020
```

```
ID   ADM69020 standard; protein; 1090 AA.
XX
AC   ADM69020;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant ER561-562 protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 561. .562
FT                   /note= "Absent in wild-type"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69019.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 10; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant ER561-562 protein of the invention.
XX
SQ   Sequence 1090 AA;
```

Query Match 99.7%; Score 5637; DB 8; Length 1090;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

```
Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRW--RVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRV 598
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRERVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRV 600

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 660

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 720

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 780

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 840

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 900

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 960

Qy        959 KKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGY 1018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 KKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGY 1020

Qy       1019 IIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGI 1078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 IIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGI 1080

Qy       1079 DSSDLVEDSF 1088
              ||||||||||
Db       1081 DSSDLVEDSF 1090
```

```
RESULT 23
AAO17356
ID   AAO17356 standard; protein; 1088 AA.
XX
AC   AAO17356;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha.
XX
KW   Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
KW   aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
KW   insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
```

```
KW   transmembrane receptor PTK7; collagen type XVIII alpha 1;
KW   platelet derived growth factor receptor alpha; laminin M chain;
KW   subtilisin like protein PACE4; nidogen.
XX
OS   Homo sapiens.
XX
PN   EP1191107-A2.
XX
PD   27-MAR-2002.
XX
PF   21-AUG-2001; 2001EP-00250300.
XX
PR   25-SEP-2000; 2000DE-01048633.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Hess-Stumpp H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E;
PI   Regidor P, Scotti S;
XX
DR   WPI; 2002-317413/36.
XX
PT   In vitro diagnosis and monitoring of endometriosis, comprises detecting
PT   reduced expression of specific gene products, e.g. from the fibronectin
PT   gene.
XX
PS   Claim 1; Page 11-12; 21pp; German.
XX
CC   The present invention relates to a method for the in vitro diagnosis of
CC   endometriosis by determining the amount of gene product from at least one
CC   specific gene in a patient sample and comparing this with the amount of
CC   gene product in a control sample. A reduced level is indicative of
CC   endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
CC   aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
CC   insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
CC   transmembrane receptor PTK7, collagen type XVIII alpha 1, platelet
CC   derived growth factor receptor alpha, laminin M chain, subtilisin like
CC   protein PACE4 or nidogen. The method is useful for initial diagnosis of
CC   endometriosis, and also for monitoring progress and treatment of the
CC   disease. The present sequence is human platelet derived growth factor
CC   receptor alpha
XX
SQ   Sequence 1088 AA;

  Query Match             99.7%;  Score 5636.5;  DB 5;  Length 1088;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARM-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1019

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1079

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1080 SDLVEDSFL 1088


RESULT 24
ADM69033
ID   ADM69033 standard; protein; 1084 AA.
XX
AC   ADM69033;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant RVIES560-564 protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 559. .560
FT                   /note= "Wild-type RVIES deleted"
XX
PN   WO2003105773-A2.
XX
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PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69032.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 23; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant RVIES560-564 protein of the invention.
XX
SQ   Sequence 1084 AA;

  Query Match             99.4%;  Score 5617.5;  DB 8;  Length 1084;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1084;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRW-----ISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 595

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 655

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 715

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 775

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 835

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 895

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 955

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1015

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1075

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1076 SDLVEDSFL 1084


RESULT 25
ADM69016
ID   ADM69016 standard; protein; 1085 AA.
XX
AC   ADM69016;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant DIMH842-845 protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 841. .842
FT                   /note= "Wild-type DIMH deleted"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
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XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69015.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 6; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant DIMH842-845 protein of the invention.
XX
SQ   Sequence 1085 AA;

  Query Match             99.4%;  Score 5617;  DB 8;  Length 1085;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              |    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 R----DSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 896

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 956

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1016

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1076

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1077 SDLVEDSFL 1085


RESULT 26
ADM69018
ID   ADM69018 standard; protein; 1086 AA.
XX
AC   ADM69018;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant HSDN845-848P protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 845
FT                   /note= "Wild-type HDSN substituted by Pro"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69017.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 8; 302pp; English.
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XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant HSDN845-848P protein of the invention.
XX
SQ   Sequence 1086 AA;

  Query Match             99.3%;  Score 5614.5;  DB 8;  Length 1086;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIM---PYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 897

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 957

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1017

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1077

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1078 SDLVEDSFL 1086


RESULT 27
ADM69022
ID   ADM69022 standard; protein; 1084 AA.
XX
AC   ADM69022;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant SPDGHE566-571R protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 566
FT                   /note= "Wild-type SPDGHE substituted by Pro"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69021.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 2; SEQ ID NO 12; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant SPDGHE566-571R protein of the invention.
XX
SQ   Sequence 1084 AA;

  Query Match             99.1%;  Score 5602.5;  DB 8;  Length 1084;
```

```
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1083;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESI-----PYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 595

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 655

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 715

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 775

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 835

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 895

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 955

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1015

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1075

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1076 SDLVEDSFL 1084
```

```
RESULT 28
ADM69037
ID   ADM69037 standard; protein; 1089 AA.
XX
AC   ADM69037;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant consensus protein.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; enzyme; receptor; mutant; mutein;
KW   cancer.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 560. .564
FT                   /label= OTHER
FT                   /note= "OTHER = Any naturally-occurring amino acid"
FT   Misc-difference 566. .571
FT                   /label= OTHER
FT                   /note= "OTHER = Any naturally-occurring amino acid"
FT   Misc-difference 841
FT                   /label= Lys, Arg, Thr, Ile
FT   Misc-difference 842. .847
FT                   /label= OTHER
FT                   /note= "OTHER = Any naturally-occurring amino acid"
FT   Misc-difference 848
FT                   /label= Asn, Ser, Thr, Ile, Asp, Gly, Ala, Val, His, Arg,
FT                   Pro, Leu, Tyr, Cys, Phe
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   N-PSDB; ADM69036.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 1; SEQ ID NO 27; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant consensus protein of the invention.
XX
SQ   Sequence 1089 AA;
```

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  Query Match             97.9%;  Score 5533;  DB 8;  Length 1089;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 1070;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||| |      ||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWXXXXXIXXXXXXYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 XXXXXXXXYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 29
ADZ13910
ID ADZ13910 standard; protein; 1089 AA.
XX
AC ADZ13910;
XX
DT 16-JUN-2005 (first entry)
XX
DE Murine cancer-associated protein #157.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic.
XX
OS Mus sp.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
DR N-PSDB; ADZ13909.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1430; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents a murine cancer-associated protein of
CC the invention.
XX
SQ Sequence 1089 AA;

```
  Query Match             92.6%;  Score 5232;  DB 9;  Length 1089;
  Best Local Similarity   91.8%;  Pred. No. 0;
```

```
  Matches 1000;  Conservative   48;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| |||||  || ||| ||||||||||:|||||||||| ||||||||:|
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:||||||||||||| :|||||| ||||||||||:|:|:||||||||
Db         61 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:|||||||||||||| |||||:  :|||||||||||||
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:||||||||||||: |:|  ||||||||||||:|||:| :||||:|||||||||||||
Db        181 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:|||||||||||||:|||||||:|||||||||:|||
Db        241 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:||||||||||:||:|||  |||||||||: |||||:||| |||||||:||||||||
Db        301 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:|||||||||||||||||: |||| |||||||| | ||:|||||
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||||:|:||||| ||||||:||||:||:|||||||:  |
Db        421 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||| |    |||||||||||||||||||||||||||||:
Db        481 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 30
ADQ59529
ID   ADQ59529 standard; protein; 1096 AA.
XX
AC   ADQ59529;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human cancer-associated (CA) protein sequence SEQ ID NO:165.
XX
KW   human; cancer-associated gene; cancer-associated protein; cytostatic;
KW   gene therapy; vaccine; tyrosine kinase antagonist;
KW   G-protein coupled receptor antagonist; cancer; lymphoma.
XX
OS   Homo sapiens.
XX
PN   WO2004058288-A1.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040082.
XX
PR   17-DEC-2002; 2002US-00322696.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-543349/52.
DR   N-PSDB; ADQ59527, ADQ59528.
XX
PT   New cancer-associated nucleic acid for diagnosing, preventing or treating
PT   cancer (e.g. lymphoma) or for screening agents that may be used for
PT   treating or preventing cancer.
XX
PS   Disclosure; SEQ ID NO 165; 143pp; English.
XX
CC   The present invention describes human cancer-associated (CA) nucleotide
CC   sequences (I). Also described: (1) an expression vector comprising (I);
CC   (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC   for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC   within an open reading frame of a CA sequence; (5) an isolated antibody,
CC   or its antigen binding fragment, that binds to the above polypeptide; (6)
CC   a hybridoma that produces the monoclonal antibody described above; (7) a
CC   pharmaceutical composition comprising the antibody and a pharmaceutical
CC   excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC   the above (monoclonal) antibody or polynucleotide that selectively
CC   hybridises to any of the polynucleotide sequences mentioned above; (9)
CC   methods for diagnosing cancer or for detecting the presence or absence of
CC   cancer cells in an individual; (10) a method for inhibiting growth of
CC   cancer cells in an individual; (11) a method for delivering a therapeutic
CC   agent to cancer cells in an individual; (12) an electronic library
CC   comprising the polynucleotide or polypeptide, or their fragments,
CC   mentioned above; (13) a method of screening for anticancer activity; (14)
CC   methods for detecting cancer associated with expression of a polypeptide
CC   or the presence of the antibody in a test cell or serum sample; (15) a
CC   method for screening for a bioactive agent capable of modulating the
CC   activity of a CA protein encoded by the above nucleic acid molecule; and
CC   (16) a method for treating cancers. (I) has cytostatic activity, and can
CC   be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC   and as a G-protein coupled receptor antagonist. The compositions and
CC   methods of the present invention can be used for diagnosing, preventing
CC   and treating cancer, especially lymphomas. They may also be used in
CC   screening for agents that may be used for treating or preventing cancer.
CC   The present sequence represents a human CA gene amino acid sequence,
CC   which is given in the exemplification of the present invention. Note: The
CC   sequence data for this patent did not form part of the printed
```

```
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1096 AA;

  Query Match             92.6%;  Score 5232;  DB 8;  Length 1096;
  Best Local Similarity   91.8%;  Pred. No. 0;
  Matches 1000;  Conservative   48;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  ||||  |||||  || ||| ||||||||||:|||||||||| ||||||||:|
Db          8 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 67

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:|||||||||||||| :||||||| ||||||||||:|:|:|||||||||
Db         68 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 127

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:||||||||| |||||:|||||||||||||||| |||||:  :|||||||||||||
Db        128 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 187

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:|||||||||||||: |:|  |||||||||||||:|||:| :||||:|||||||||||||
Db        188 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 247

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||||:|||||||||||||:|||||||:|||||||||:|||
Db        248 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 307

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:|||||||||:||:|||  ||||||||||: |||||:||| |||||||:||||||||
Db        308 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 367

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:||||||||||||||||: |||| |||||||| | ||:|||||
Db        368 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 427

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||||:|:|||||| ||||||:||||:||:|||||||:  |
Db        428 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 487

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||| |     ||||||||||||||||||||||||||||:
Db        488 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 547

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        548 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 607

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 667

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||||||
Db        668 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 727

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 787

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 847

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 907

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        908 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 967

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1027

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1087

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1088 SDLVEDSFL 1096


RESULT 31
AAR26206
ID   AAR26206 standard; protein; 1009 AA.
XX
AC   AAR26206;
XX
DT   25-MAR-2003  (revised)
DT   09-FEB-1993  (first entry)
XX
DE   Type B human platelet-derived growth factor receptor.
XX
KW   PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .1009
FT                   /label= Mature_PDGF-A
XX
PN   WO9213867-A1.
XX
PD   20-AUG-1992.
XX
PF   28-JAN-1992;   92WO-US000730.
XX
PR   31-JAN-1991;   91US-00650793.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Escobedo JA,  Williams LT,  Wolf D,  Tomlinson JE,  Fretto LJ;
PI   Giese NA;
XX
DR   WPI; 1992-299970/36.
DR   N-PSDB; AAQ27451.
XX
PT   Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful
PT   as therapeutic and diagnostic agents e.g. for assaying PDGF activity in
PT   sample.
XX
PS   Disclosure; Page 90; 109pp; English.
XX
CC   The sequence given is one allele of type A human platelet-derived growth
CC   factor (PDGF) receptor (PDGF-R). This receptor is typically found on
CC   cells of mesenchymal origin. It acts while in the form of two
CC   transmembrane glycoproteins, each of which is about 180 kD. This receptor
CC   has three major regions. The first is a transmembrane region, which spans
CC   the membrane once, separating the regions of the receptor exterior to the
CC   cell from those interior to the cell. The second region is an
CC   extracellular region which contains the domains which bind the PDGF. The
CC   third region is an intracellular region which posseses a tyrosine kinase
CC   activity. This tyrosine kinase domain is notable in having an insert of
CC   approx. 100 amino acids, as compared with most other receptor tyrosine
CC   kinase domains which are contiguous or have shorter insert sequences.
CC   Fragments of this sequence between 8 and 400 amino acids comprising one
CC   or more PDGF ligand binding region from the extracellular domain may be
CC   used to bind a PDGF ligand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 1009 AA;
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  Query Match           91.2%;  Score 5154;  DB 2;  Length 1009;
  Best Local Similarity  92.5%;  Pred. No. 0;
  Matches 1007;  Conservative    1;  Mismatches    1;  Indels   80;  Gaps    2;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||:
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLF---------------------- 98

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
                          ||||||||||||||||||||||||||||||||||||||||||||
Db         99 ------------------IVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 140

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 200

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 260

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 320

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 380

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 440

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 500

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 560

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 620

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 680

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 740

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||
Db        741 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR---------------------- 777

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
                          ||||||||||||||||||||||||||||||||||||||||||||
Db        778 ----------------AVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 820

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 880

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        881 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 940

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        941 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1000

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1001 SDLVEDSFL 1009
```

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RESULT 32
ABG72454
ID   ABG72454 standard; protein; 589 AA.
XX
AC   ABG72454;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha truncation mutant.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .490
FT                   /label= Extracellular_domain
FT   Peptide         1. .24
FT                   /label= Signal_peptide_sequence_2
FT   Peptide         1. .20
FT                   /label= Signal_peptide_sequence_1
FT   Protein         21
FT                   /label= Mature_PDGFR_sequence_1
FT   Protein         25
FT                   /label= Mature_PDGFR_sequence_2
FT   Domain          42. .102
FT                   /label= Immunoglobulin-like_domain
FT   Domain          143. .191
FT                   /label= Immunoglobulin-like_domain
FT   Domain          228. .292
FT                   /label= Immunoglobulin-like_domain
FT   Domain          338. .399
FT                   /label= Immunoglobulin-like_domain
FT                   /note= "6"
FT   Domain          428. .503
FT                   /label= Immunoglobulin-like_domain
FT   Domain          525. .548
FT                   /label= Transmembrane_domain
FT   Domain          549. .1055
FT                   /label= Intracellular_domain
FT   Domain          556. .589
FT                   /note= "Truncated split tyrosine kinase domain segment 1"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
```

PI Kazlauskas A, Ikuno Y;
XX
DR WPI; 2003-066697/06.
DR N-PSDB; ABS57785.
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 3; Page 69-71; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)
CC alpha truncation mutant
XX
SQ Sequence 589 AA;

Query Match 53.9%; Score 3046; DB 6; Length 589;
Best Local Similarity 100.0%; Pred. No. 6.8e-204;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
```

RESULT 33
ADJ93550
ID ADJ93550 standard; protein; 834 AA.
XX
AC ADJ93550;
XX
DT 06-MAY-2004 (first entry)
XX
DE NM_030917-PDGFR-alpha fusion protein splice variant #1.
XX
KW NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase; chromosome 4;
KW translocation; hyperproliferation; cancer; atherosclerosis;
KW graft coronary vascular disease; transplantation; restenosis;
KW angioplasty; stent replacement; epidermal hyperproliferation;
KW tissue remodeling; repair; psoriasis; multiple sclerosis;
KW rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 324. .328
FT /note= "Encoded by CAGGAC"
XX
PN WO2004015082-A2.
XX
PD 19-FEB-2004.
XX
PF 08-AUG-2003; 2003WO-US024992.
XX
PR 09-AUG-2002; 2002US-0402330P.
PR 16-JAN-2003; 2003US-0440491P.
XX
PA (THER-) THERAVANCE INC.
XX
PI Briesewitz R, Griffin JH;
XX
DR WPI; 2004-180662/17.
DR N-PSDB; ADJ93554.
XX
PT New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT conditions associated with the fusion polypeptide, and for identifying
PT agents for treating associated hyperproliferative disease conditions,
PT e.g. cancer or psoriasis.
XX
PS Claim 10; SEQ ID NO 2; 95pp; English.
XX
CC This sequence represents an NM_030917-PDGFR-alpha fusion protein splice
CC variant. The fusion polypeptide of the invention comprises a C-terminal
CC tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC constitutively activated kinase activity, and is present in other than
CC its naturally occurring environment. The N- and C-terminal domains are
CC from chromosome 4 encoded proteins, and the fusion protein is not a
CC product of a translocation event. The fusion polypeptide or the
CC polynucleotide encoding it, are useful for determining whether a host
CC suffers from a disease condition, e.g. a hyperproliferative disease
CC condition. An agent that inhibits the activity or expression of the
CC fusion polypeptide is useful for treating a hyperproliferative disease
CC condition, such as cancer, atherosclerosis, graft coronary vascular
CC disease after transplantation, restenosis after angioplasty or stent
CC replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC or inflammatory bowel disease. The polynucleotides are also useful as
CC probes and primers in hybridization applications, or in the
CC identification of homologues, expression regulatory factors or expression
CC patterns in biological specimens.
XX
SQ Sequence 834 AA;

Query Match 47.7%; Score 2693.5; DB 8; Length 834;
Best Local Similarity 74.6%; Pred. No. 4.9e-179;
Matches 551; Conservative 28; Mismatches 61; Indels 99; Gaps 12;

```
Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
              | :|  :   |:|   | ||: |:     | : ::  :|:    :: | |: |   |  |
Db        194 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRTGN----SEKETALPSTKAE-FT 243

Qy        412 QVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVS 470
                ||     :      ||  |:   ||                 :| |:    |
Db        244 SPPSLFKTGLPPSRNSTSSQSQTSTAS--------------RKANSSVGKW-------- 280

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
                     :||        : : |                       :| ||    :  |
Db        281 --------QDR--------YGRAE----------------------SPDLR---RLPGA 298

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
              : |:   : ||             | | | |  |: :           :||||||||||||
Db        299 IDVIGQTITIS------------RVEGRRRANENSN-----------IQLPYDSRWEFPR 335

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 395

Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 455

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 515

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 575

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 635

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 695

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 755

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 815

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
              |||||||||||||||||||
Db        816 DMMDDIGIDSSDLVEDSFL 834
```

```
RESULT 34
ADJ93549
ID   ADJ93549 standard; protein; 849 AA.
XX
AC   ADJ93549;
XX
DT   06-MAY-2004  (first entry)
XX
DE   NM_030917-PDGFR-alpha fusion protein.
XX
KW   NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase; chromosome 4;
KW   translocation; hyperproliferation; cancer; atherosclerosis;
KW   graft coronary vascular disease; transplantation; restenosis;
KW   angioplasty; stent replacement; epidermal hyperproliferation;
KW   tissue remodeling; repair; psoriasis; multiple sclerosis;
KW   rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 339. .343
FT                   /note= "Encoded by CAGGAC"
XX
PN   WO2004015082-A2.
XX
PD   19-FEB-2004.
XX
PF   08-AUG-2003; 2003WO-US024992.
XX
PR   09-AUG-2002; 2002US-0402330P.
PR   16-JAN-2003; 2003US-0440491P.
XX
PA   (THER-) THERAVANCE INC.
XX
PI   Briesewitz R,  Griffin JH;
XX
DR   WPI; 2004-180662/17.
DR   N-PSDB; ADJ93553.
XX
PT   New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT   conditions associated with the fusion polypeptide, and for identifying
PT   agents for treating associated hyperproliferative disease conditions,
PT   e.g. cancer or psoriasis.
XX
PS   Claim 10; Page 63; 95pp; English.
XX
CC   This sequence represents an NM_030917-PDGFR-alpha fusion protein. The
CC   fusion polypeptide of the invention comprises a C-terminal tyrosine
CC   kinase domain and an N-terminal domain. The fusion protein has a
CC   constitutively activated kinase activity, and is present in other than
CC   its naturally occurring environment. The N- and C-terminal domains are
CC   from chromosome 4 encoded proteins, and the fusion protein is not a
CC   product of a translocation event. The fusion polypeptide or the
CC   polynucleotide encoding it, are useful for determining whether a host
CC   suffers from a disease condition, e.g. a hyperproliferative disease
CC   condition. An agent that inhibits the activity or expression of the
CC   fusion polypeptide is useful for treating a hyperproliferative disease
CC   condition, such as cancer, atherosclerosis, graft coronary vascular
CC   disease after transplantation, restenosis after angioplasty or stent
CC   replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC   psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC   or inflammatory bowel disease. The polynucleotides are also useful as
CC   probes and primers in hybridization applications, or in the
CC   identification of homologues, expression regulatory factors or expression
CC   patterns in biological specimens.
XX
SQ   Sequence 849 AA;
```

```
  Query Match             47.6%;  Score 2692;  DB 8;  Length 849;
  Best Local Similarity   74.6%;  Pred. No. 6.4e-179;
  Matches  551;  Conservative   28;  Mismatches   61;  Indels   99;  Gaps   12;

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
              | :|  :   |:|   | ||: |:     | : ::  :|:    :: | |: |   |  |
Db        209 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRTGN----SEKETALPSTKAE-FT 258

Qy        412 QVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVS 470
                ||     :      ||  |:   ||                 :| |:    |
Db        259 SPPSLFKTGLPPSRNSTSSQSQTSTAS--------------RKANSSVGKW-------- 295

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
                     :||        : : |                       :| ||    :  |
Db        296 --------QDR--------YGRAE----------------------SPDLR---RLPGA 313

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
              : |:   : ||             | | | |  |: :           :||||||||||||
Db        314 IDVIGQTITIS------------RVEGRRRANENSN-----------IQLPYDSRWEFPR 350

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 410
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```
Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 470

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 530

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 590

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 650

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 710

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 770

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 830

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
              |||||||||||||||||||
Db        831 DMMDDIGIDSSDLVEDSFL 849
```

```
RESULT 35
ADJ93552
ID   ADJ93552 standard; protein; 811 AA.
XX
AC   ADJ93552;
XX
DT   06-MAY-2004  (first entry)
XX
DE   NM_030917-PDGFR-alpha fusion protein splice variant #3.
XX
KW   NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase; chromosome 4;
KW   translocation; hyperproliferation; cancer; atherosclerosis;
KW   graft coronary vascular disease; transplantation; restenosis;
KW   angioplasty; stent replacement; epidermal hyperproliferation;
KW   tissue remodeling; repair; psoriasis; multiple sclerosis;
KW   rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 301. .305
FT                   /note= "Encoded by CAGGAC"
XX
PN   WO2004015082-A2.
XX
PD   19-FEB-2004.
XX
PF   08-AUG-2003; 2003WO-US024992.
XX
PR   09-AUG-2002; 2002US-0402330P.
PR   16-JAN-2003; 2003US-0440491P.
XX
PA   (THER-) THERAVANCE INC.
XX
PI   Briesewitz R,  Griffin JH;
XX
DR   WPI; 2004-180662/17.
DR   N-PSDB; ADJ93556.
XX
PT   New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT   conditions associated with the fusion polypeptide, and for identifying
PT   agents for treating associated hyperproliferative disease conditions,
PT   e.g. cancer or psoriasis.
XX
PS   Claim 10; SEQ ID NO 4; 95pp; English.
XX
CC   This sequence represents an NM_030917-PDGFR-alpha fusion protein splice
CC   variant. The fusion polypeptide of the invention comprises a C-terminal
CC   tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC   constitutively activated kinase activity, and is present in other than
CC   its naturally occurring environment. The N- and C-terminal domains are
CC   from chromosome 4 encoded proteins, and the fusion protein is not a
CC   product of a translocation event. The fusion polypeptide or the
CC   polynucleotide encoding it, are useful for determining whether a host
CC   suffers from a disease condition, e.g. a hyperproliferative disease
CC   condition. An agent that inhibits the activity or expression of the
CC   fusion polypeptide is useful for treating a hyperproliferative disease
CC   condition, such as cancer, atherosclerosis, graft coronary vascular
CC   disease after transplantation, restenosis after angioplasty or stent
CC   replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC   psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC   or inflammatory bowel disease. The polynucleotides are also useful as
CC   probes and primers in hybridization applications, or in the
CC   identification of homologues, expression regulatory factors or expression
CC   patterns in biological specimens.
XX
SQ   Sequence 811 AA;
```

```
  Query Match             47.4%;  Score 2676.5;  DB 8;  Length 811;
  Best Local Similarity   99.8%;  Pred. No. 7.3e-178;
  Matches  511;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        578 MQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 637
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 IQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 359

Qy        638 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 419

Qy        698 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 479

Qy        758 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 539

Qy        818 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 599

Qy        878 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 659

Qy        938 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 719

Qy        998 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 779

Qy       1058 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||||||||||||||||||||||||||||||||
Db        780 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 811
```

```
RESULT 36
ADJ93551
ID   ADJ93551 standard; protein; 826 AA.
XX
```

```
AC   ADJ93551;
XX
DT   06-MAY-2004  (first entry)
XX
DE   NM_030917-PDGFR-alpha fusion protein splice variant #2.
XX
KW   NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase; chromosome 4;
KW   translocation; hyperproliferation; cancer; atherosclerosis;
KW   graft coronary vascular disease; transplantation; restenosis;
KW   angioplasty; stent replacement; epidermal hyperproliferation;
KW   tissue remodeling; repair; psoriasis; multiple sclerosis;
KW   rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 316. .320
FT                   /note= "Encoded by CAGGAC"
XX
PN   WO2004015082-A2.
XX
PD   19-FEB-2004.
XX
PF   08-AUG-2003; 2003WO-US024992.
XX
PR   09-AUG-2002; 2002US-0402330P.
PR   16-JAN-2003; 2003US-0440491P.
XX
PA   (THER-) THERAVANCE INC.
XX
PI   Briesewitz R,  Griffin JH;
XX
DR   WPI; 2004-180662/17.
DR   N-PSDB; ADJ93555.
XX
PT   New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT   conditions associated with the fusion polypeptide, and for identifying
PT   agents for treating associated hyperproliferative disease conditions,
PT   e.g. cancer or psoriasis.
XX
PS   Claim 10; SEQ ID NO 3; 95pp; English.
XX
CC   This sequence represents an NM_030917-PDGFR-alpha fusion protein splice
CC   variant. The fusion polypeptide of the invention comprises a C-terminal
CC   tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC   constitutively activated kinase activity, and is present in other than
CC   its naturally occurring environment. The N- and C-terminal domains are
CC   from chromosome 4 encoded proteins, and the fusion protein is not a
CC   product of a translocation event. The fusion polypeptide or the
CC   polynucleotide encoding it, are useful for determining whether a host
CC   suffers from a disease condition, e.g. a hyperproliferative disease
CC   condition. An agent that inhibits the activity or expression of the
CC   fusion polypeptide is useful for treating a hyperproliferative disease
CC   condition, such as cancer, atherosclerosis, graft coronary vascular
CC   disease after transplantation, restenosis after angioplasty or stent
CC   replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC   psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC   or inflammatory bowel disease. The polynucleotides are also useful as
CC   probes and primers in hybridization applications, or in the
CC   identification of homologues, expression regulatory factors or expression
CC   patterns in biological specimens.
XX
SQ   Sequence 826 AA;

  Query Match             47.4%;  Score 2676.5;  DB 8;  Length 826;
  Best Local Similarity   99.8%;  Pred. No. 7.5e-178;
  Matches  511;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        578 MQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 637
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 IQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 374

Qy        638 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 434

Qy        698 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 494

Qy        758 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 554

Qy        818 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 614

Qy        878 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 674

Qy        938 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 734

Qy        998 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 794

Qy       1058 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||||||||||||||||||||||||||||||||
Db        795 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 826


RESULT 37
ADY85492
ID   ADY85492 standard; protein; 457 AA.
XX
AC   ADY85492;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Catalytic domain of PIM kinase-like protein PDGFR.
XX
KW   Kinase; protein co-ordinate data; protein structure; cancer; cytostatic;
KW   neoplasm; inflammation; antiinflammatory.
XX
OS   Unidentified.
XX
PN   WO2005028624-A2.
XX
PD   31-MAR-2005.
XX
PF   15-SEP-2004; 2004WO-US030360.
XX
PR   15-SEP-2003; 2003US-0503277P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Artis DR,  Bremer RE,  Gillette SJ,  Hurt CR,  Ibrahim PL;
PI   Zuckerman RL;
XX
DR   WPI; 2005-273155/28.
XX
PT   New scaffold library used for identifying and developing ligands for
PT   protein kinases and treating kinase associated disorders e.g. cancer,
PT   comprises set of compounds comprising N-heterocyclic compounds.
XX
PS   Disclosure; Page 170-174; 236pp; English.
XX
CC   The invention relates to a new kinase scaffold library comprises at least
CC   1 set of compounds, each set comprising at least 1 N-heterocyclic
CC   compound of formulae (I)-(VII) given in the specification. Also included
CC   are a system for fitting compounds in binding sites of protein kinases
CC   (comprising an electronic kinase scaffold, and a scaffold library
```

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CC   comprising at least 1 collection of electronic representations of (I)-
CC   (VII), where the scaffold library is embedded in a computer device and
CC   the electronic representations of the compounds can be selectively
CC   retrieved and functionally connected with computer software adapted to
CC   fit electronic representations of compounds in an electronic
CC   representation of a binding site of a kinase), obtaining improved ligands
CC   binding to a protein kinase (which comprises determining if a derivative
CC   of (I)-(VII) binds to the kinase with greater affinity and/or specificity
CC   than (I)-(VII)), developing ligands specific for a particular kinase
CC   (which comprises determining if a derivative of (I)-(VII) that binds to
CC   kinases has greater for specificity for the particular kinase than (I)-
CC   (VII), developing ligands binding to a kinase (which comprises
CC   determining the orientation of at least 1 molecular scaffold of (I)-(VII)
CC   in co-crystals with the kinase, identifying chemical structures of the
CC   scaffolds, that, when modified, change the binding affinity and/or
CC   specificity between the scaffold and kinase and synthesizing a ligand in
CC   which at least 1 chemical structure of the scaffold is modified),
CC   developing ligands with increased specificity on a kinase (which
CC   comprises testing a derivative of a kinase binding compound (I)-(VII) for
CC   increased specificity on the kinase), identifying a ligand binding to a
CC   kinase (which comprises determining if a derivative compound including a
CC   core structure (I)-(VII) binds to the kinase with changed binding
CC   affinity and/or specificity), a co-crystal of a kinase and a binding
CC   compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII),
CC   identifying potential kinase binding compounds (which comprises fitting
CC   electronic representations of (I)-(VII) in an electronic representation
CC   of a kinase binding site), attaching a kinase binding compound to an
CC   attachment component (which comprises identifying energetically allowed
CC   sites for attachment of the component on a kinase binding compound (I)-
CC   (VII) and attaching the compound or derivative to the attachment
CC   component at the allowed site), modified compounds (comprising (I)-(VIII)
CC   with an attached linker group, and developing a ligand for a kinase
CC   comprising conserved residues matching at least on of Pim-1 residues 49,
CC   52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds
CC   to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,
CC   vascular endothelial growth factor receptor, endothelial growth factor
CC   receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold
CC   library is used for identifying and developing ligands binding to
CC   kinases, for modulating kinase activity and for treating disease
CC   condition associated with abnormal kinase activity e.g. cancer,
CC   inflammatory disease. The method identifies improved ligands binding to a
CC   kinase resulting in ligands having high affinity and specificity towards
CC   kinase. The co-crystals of kinase and the binding compound are of
CC   sufficient size and quality to allow structural determination of at least
CC   2 Angstroms. The present sequence is a catalytic domain from a PIM-like
CC   kinase. NOTE: It is not clear whether the sequence as presented
CC   represents a continuous amino acid sequence.
XX
SQ   Sequence 457 AA;

  Query Match             42.1%;  Score 2380.5;  DB 9;  Length 457;
  Best Local Similarity   98.9%;  Pred. No. 1.6e-157;
  Matches  455;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy        543 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 60

Qy        603 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 120

Qy        663 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 180

Qy        723 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 240

Qy        783 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 300

Qy        843 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVD 902
              ||||||||||||||||||||||||||||||||||||||||||||||| |||    ||||||
Db        301 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIXSLG---XPGMMVD 357

Qy        903 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 417

Qy        963 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 1002
              |||||||||||||||||||||||||||||||||||||||||
Db        418 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 457


RESULT 38
AAR26205
ID   AAR26205 standard; protein; 1106 AA.
XX
AC   AAR26205;
XX
DT   25-MAR-2003  (revised)
DT   09-FEB-1993  (first entry)
XX
DE   Type B human platelet-derived growth factor receptor.
XX
KW   PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .32
FT                   /label= Signal_peptide
FT   Protein         24. .1106
FT                   /label= Mature_PDGF-B
XX
PN   WO9213867-A1.
XX
PD   20-AUG-1992.
XX
PF   28-JAN-1992;   92WO-US000730.
XX
PR   31-JAN-1991;   91US-00650793.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Escobedo JA,  Williams LT,  Wolf D,  Tomlinson JE,  Fretto LJ;
PI   Giese NA;
XX
DR   WPI; 1992-299970/36.
DR   N-PSDB; AAQ27447.
XX
PT   Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful
PT   as therapeutic and diagnostic agents e.g. for assaying PDGF activity in
PT   sample.
XX
PS   Disclosure; Page 75; 109pp; English.
XX
CC   The sequence given is one allele of type B human platelet-derived growth
CC   factor (PDGF) receptor (PDGF-R). This receptor is typically found on
CC   cells of mesenchymal origin. It acts while in the form of two
CC   transmembrane glycoproteins, each of which is about 180 kD. This receptor
CC   has three major regions. The first is a transmembrane region, which spans
CC   the membrane once, separating the regions of the receptor exterior to the
CC   cell from those interior to the cell. The second region is an
CC   extracellular region which contains the domains which bind the PDGF. The
CC   third region is an intracellular region which posseses a tyrosine kinase
CC   activity. This tyrosine kinase domain is notable in having an insert of
CC   approx. 100 amino acids, as compared with most other receptor tyrosine
CC   kinase domains which are contiguous or have shorter insert sequences.
CC   Fragments of this sequence between 8 and 400 amino acids comprising one
CC   or more PDGF ligand binding region from the extracellular domain may be
CC   used to bind a PDGF ligand. (Updated on 25-MAR-2003 to correct PN field.)
XX
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SQ   Sequence 1106 AA;

  Query Match             41.7%;  Score 2359.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 1.6e-155;
  Matches  504;  Conservative  196;  Mismatches  340;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :    |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| |||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| || | ||| |::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGGGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                |: |||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 39
AAP90127
ID   AAP90127 standard; protein; 1106 AA.
XX
AC   AAP90127;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Platelet derived growth factor receptor.
XX
KW   Platelet derived growth factor receptor; human;
KW   ligand binding receptor analogues; isoforms; assays; antibodies;
KW   atherosclerosis; wound healing; peptide dimer; cDNA.
XX
OS   Homo sapiens.
XX
PN   EP325224-A.
XX
PD   26-JUL-1989.
XX
PF   18-JAN-1989;   89EP-00100787.
XX
PR   22-JAN-1988;   88US-00146877.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Siedziewsk AZ,  Bell LA,  Kindsvogel WR;
XX
DR   WPI; 1989-214434/30.
DR   N-PSDB; AAN90355.
XX
PT   Secreted ligand-binding receptor analogues e.g. PDGF receptor - used in
PT   assays, in purifications and as or with therapeutic agents.
XX
PS   Claim 2; Fig 1; 45pp; English.
XX
CC   Platelet derived growth factor receptor (see corresp. AAN90355). Used in
CC   the invention to make analogues that are secreted (pref. Ile-29 - Met-
CC   441, and Ile-29 - Lys-531; see specification for details). These
CC   analogues are easily purified, produced in large quantities
CC   recombinantly, used to produce antibodies, to screen ligands as imaging
CC   agents, as (ant-)agonists, or therapeutically for atherosclerosis and
CC   wound healing, and assays. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1106 AA;

  Query Match             41.7%;  Score 2354.5;  DB 1;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120
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Qy      122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db      121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy      180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db      181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy      240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db      240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy      296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db      297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy      356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db      357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy      415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
Db      417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy      475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
Db      470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy      520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db      527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy      580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db      587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy      640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db      647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy      700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db      707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy      757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db      766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy      817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db      825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy      877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db      885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy      937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
Db      945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy      985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db     1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy     1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db     1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy     1087 SFL 1089
Db     1104 SFL 1106
```

```
RESULT 40
AAR99690
ID   AAR99690 standard; protein; 1106 AA.
XX
AC   AAR99690;
XX
DT   25-MAR-2003  (revised)
DT   11-OCT-1996  (first entry)
XX
DE   Platelet-derived growth factor receptor.
XX
KW   Platelet-derived growth factor receptor; PDGF-R; peptide dimer;
KW   protein secretion; agonist; antagonist.
XX
OS   Homo sapiens.
XX
PN   EP721983-A1.
XX
PD   17-JUL-1996.
XX
PF   18-JAN-1989;   95EP-00118567.
XX
PR   22-JAN-1988;   88US-00146877.
PR   18-JAN-1989;   89EP-00100787.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sledziewski AZ,  Bell LA,  Kindsvogel WR;
XX
DR   WPI; 1996-322833/33.
DR   N-PSDB; AAT34552.
XX
PT   Prodn. of biologically active peptide dimers, esp. platelet-derived
PT   growth factor receptor analogues - useful for systematic designing of
PT   novel (ant)agonists.
XX
PS   Disclosure; Fig 1; 45pp; English.
XX
CC   The amino acid sequence (AAR99690) of human platelet-derived growth
CC   factor receptor (PDGF-R) was deduced from a cDNA clone (AAT34552)
CC   isolated from a human diploid dermal fibroblast library. The cDNA can be
CC   used in novel constructs that allow the prodn. of secreted biologically
CC   active PDGF-R analogues. This may comprise linking a sequence coding for
CC   PDGR-R, or the ligand- binding domain of the PDGF-R extracellular region,
CC   to a protein secretion signal (e.g. SUC2) and promoter, and expression in
CC   transformed host cells, esp. Saccharomyces cerevisiae. The secreted PDGF-
CC   R analogues are used in ligand screening procedures, to screen for
CC   (ant)agonists, and in diagnostic assays. (Updated on 25-MAR-2003 to
CC   correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1106 AA;

  Query Match             41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy        6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
Db        8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy       62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db       66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy      122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db      121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy      180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db      181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy      240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
```

```
                ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
                : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
                | ::   ||      : | || |:| |:| |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
                  :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                  | : | :|  ||:                |:  ::|||  :| :|  : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
                :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
                ||||| || ||| |||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
                |||||||||:|||||||:|||||||| |||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
                |   |  ||    | |     |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
                |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
                ||||||||| :||:|||||||||||| ||||:|||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
                ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
                | || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
                :        ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
                |  | :   ::|||      :: :||         :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
                |||
Db       1104 SFL 1106
```

RESULT 41
ABG72459
ID ABG72459 standard; protein; 1106 AA.
XX
AC ABG72459;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human platelet derived growth factor receptor beta mutant L867M.
XX
KW Human; platelet derived growth factor receptor beta; PDGFRbeta;
KW hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .32
FT /label= Signal_peptide
FT Protein 33. .1106
FT /label= Mature_PDGFR_beta
FT Domain 227. .298
FT /label= Immunoglobulin-like_domain
FT Domain 335. .398
FT /label= Immunogobulin-like_domain
FT Domain 532. .556
FT /label= Transmembrane_domain
FT Domain 604. .694
FT /note= "Split tyrosine kinase domian segment 1"
FT Domain 799. .951
FT /note= "Split tyrosine kinase domain segment 2"
FT Misc-difference 867
FT /note= "Wild type Leu substituted by Met"
XX
PN US2002111304-A1.
XX
PD 15-AUG-2002.
XX
PF 25-MAY-2001; 2001US-00866510.
XX
PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
XX
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
XX
PI Kazlauskas A, Ikuno Y;
XX
DR WPI; 2003-066697/06.
DR N-PSDB; ABS57790.
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 101-104; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)
CC beta mutant L867M
XX
SQ Sequence 1106 AA;

```
  Query Match           41.7%;  Score 2354.5;  DB 6;  Length 1106;
  Best Local Similarity  44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    : : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |  |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||       : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| |||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   | ||   | |     |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::|||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPMKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:|  ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
                :    ||                        |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 42
ABP96311
ID   ABP96311 standard; protein; 1106 AA.
XX
AC   ABP96311;
XX
DT   20-MAY-2003  (first entry)
XX
DE   Human platelet-derived growth factor receptor beta protein.
XX
KW   Humanised baculovirus; cytostatic; gene therapy; baculovirus; cancer;
KW   prostate cancer; platelet-derived growth factor receptor beta;
KW   chromosome 5.
XX
OS   Homo sapiens.
XX
PN   WO2003016540-A2.
XX
PD   27-FEB-2003.
XX
PF   15-AUG-2002; 2002WO-GB003791.
XX
PR   15-AUG-2001; 2001GB-00019852.
XX
PA   (UYYO-) UNIV YORK.
XX
PI   Maitland N;
XX
DR   WPI; 2003-268336/26.
XX
PT   New baculovirus having a modified genome encoding a therapeutic agent,
PT   useful in the manufacture of a medicament for the treatment of cancer,
PT   particularly prostate cancer.
XX
PS   Claim 33; Page; 34pp; English.
XX
CC   The present invention describes a humanised baculovirus (I) which
CC   comprises a modified baculovirus genome having a nucleic acid molecule
CC   encoding a therapeutic agent and a polypeptide which functions to target
CC   the baculovirus to at least one cell type. Also described is a
CC   pharmaceutical composition comprising (I). (I) has cytostatic activity,
CC   and can be used in gene therapy. The baculovirus is useful in the
CC   manufacture of a medicament for the treatment of cancer, particularly
CC   prostate cancer. The present sequence represents the human platelet-
CC   derived growth factor receptor beta protein, which is specified in the
CC   exemplification of the present invention. N.B. The present sequence is
CC   not given in the specification but is referred to in Claim 33 as Genbank
CC   accession number NM_002609
XX
SQ   Sequence 1106 AA;

  Query Match           41.7%;  Score 2354.5;  DB 6;  Length 1106;
  Best Local Similarity  44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
```

```
Db        66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy       122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db       121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy       180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db       181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy       240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db       240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy       296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db       297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy       356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db       357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy       415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db       417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy       475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db       470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy       520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db       527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy       580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db       587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy       640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db       647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy       700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db       707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy       757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db       766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy       817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db       825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy       877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db       885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy       937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984

Db       945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy       985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db      1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy      1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db      1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy      1087 SFL 1089

Db       1104 SFL 1106
```

RESULT 43
ABR84719
ID ABR84719 standard; protein; 1106 AA.
XX
AC ABR84719;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PDGF beta receptor protein.
XX
KW Tissue vascularisation; aging; mouse; human; PDGF A; PDGF B;
KW PDGF alpha receptor; PDGF beta receptor; endothelial precursor cell;
KW vascular disease; cardiant; cell therapy.
XX
OS Homo sapiens.
XX
PN WO2003070083-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004244.
XX
PR 15-FEB-2002; 2002US-0357328P.
PR 08-AUG-2002; 2002WO-US025175.
XX
PA (CORR) CORNELL RES FOUND INC.
PA (EDEL/) EDELBERG J M.
PA (RAFI/) RAFII S.
PA (HONG/) HONG M K.
PA (LANZ/) LANZA R P.
PA (WEST/) WEST M D.
XX
PI Edelberg JM, Rafii S, Hong MK, Lanza RP, West MD;
XX
DR WPI; 2003-697548/66.
XX
PT Treating a vascular condition, e.g. myocardial infarction,
PT atherosclerosis, ischemia, congestive heart failure, hypertension,
PT stroke, thrombosis, arrhythmia or tachycardia, by administering
PT endothelial precursor cells.
XX
PS Claim 24; Page 47-48; 110pp; English.
XX
CC The present invention relates to a method of treating a vascular
CC condition in a mammal, which comprises administering to the mammal a
CC therapeutic amount of endothelial precursor cells. The method and cells
CC of the invention are useful for treating a vascular condition, e.g.
CC myocardial infarction, atherosclerosis, ischaemia, tachycardia,
CC congestive heart failure, peripheral vasculature disorder, hypertension,
CC stroke, thrombosis, arrhythmia or tachycardia. The present sequence is a
CC protein shown in the exemplification of the invention
XX
SQ Sequence 1106 AA;

Query Match 41.7%; Score 2354.5; DB 7; Length 1106;
Best Local Similarity 44.1%; Pred. No. 3.7e-155;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;

```
Qy         6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db         8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy        62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db        66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy       122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db       121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180
```

```
Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106
```

RESULT 44
ADF45082
ID   ADF45082 standard; protein; 1106 AA.
XX
AC   ADF45082;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human kinase PDGFR-b.
XX
KW   Human; protein kinase; enzyme; inhibitor; PDGFR-b.
XX
OS   Homo sapiens.
XX
PN   WO2003081210-A2.
XX
PD   02-OCT-2003.
XX
PF   20-MAR-2003; 2003WO-US008725.
XX
PR   21-MAR-2002; 2002US-0366892P.
XX
PA   (SUNE-) SUNESIS PHARM INC.
XX
PI   Prescott JC, Braisted A;
XX
DR   WPI; 2003-865136/80.
XX
PT   Identifying ligand binding to inactive conformation of target protein
PT   kinase (T) comprises contacting the conformation modified (T) which
PT   contains reactive group at binding site, with ligands and detecting
PT   kinase-ligand conjugate formation.
XX
PS   Disclosure; SEQ ID NO 51; 260pp; English.
XX
CC   The present invention relates to a method for identifying a ligand (L),
CC   which binds to an inactive conformation of target protein kinase (T). The
CC   method involves contacting inactive conformation of (T), which contains
CC   or is modified to contain a reactive group at or near a binding site of
CC   interest, with one or more ligand candidates capable of covalently
CC   bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC   The method is useful for identifying protein kinase inhibitors that
CC   preferentially bind to inactive conformation of a target protein kinase.
CC   The present sequence is a protein kinase which may be modified via an
CC   amino acid substitution, for use in the method of the invention.
XX
SQ   Sequence 1106 AA;

Query Match 41.7%; Score 2354.5; DB 7; Length 1106;
Best Local Similarity 44.1%; Pred. No. 3.7e-155;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;

```
Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
```

```
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984

Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 45
ABO84679
ID   ABO84679 standard; protein; 1106 AA.
XX
AC   ABO84679;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human cancer-associated protein HP20-018.3.
XX
KW   Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW   lymphoma; CAP.
XX
OS   Homo sapiens.
XX
PN   WO2004074320-A2.
XX
PD   02-SEP-2004.
XX
PF   17-FEB-2004; 2004WO-US004730.
XX
PR   14-FEB-2003; 2003US-00367094.
PR   14-MAR-2003; 2003US-00388838.
PR   15-APR-2003; 2003US-00417375.
PR   13-JUN-2003; 2003US-00461862.
PR   15-SEP-2003; 2003US-00663431.
PR   15-DEC-2003; 2003US-00737318.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Morris DW,  Malandro MS;
XX
DR   WPI; 2004-652914/63.
DR   N-PSDB; ABD32965.
XX
PT   New isolated cancer-associated polynucleotides and polypeptides useful
PT   for diagnosing, preventing or treating cancers, especially lymphoma and
PT   leukemia, or in screening for agents that modulate cancer.
XX
PS   claim 18; seqid 710; 310pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising at least 10
CC   contiguous nucleotides of any of the 233 polynucleotide sequences given
CC   in the specification, or its complement. The nucleic acids encode cancer-
CC   associated proteins. Also included are an expression vector comprising
CC   the isolated nucleic acid cited above, a host cell comprising the above
CC   recombinant nucleic acid or expression vector, a microarray for detecting
CC   a cancer-associated (CA) nucleic acid comprising at least one probe
CC   comprising at least 10 contiguous nucleotides of any of the above-
CC   mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC   an open reading frame of a CA sequence selected from any of the 95
CC   polynucleotide sequences as mentioned in the specification, or its
CC   complement), an isolated antibody, (or its antigen binding fragment) that
CC   binds to the above polypeptide, a hybridoma that produces the above
CC   monoclonal antibody, a pharmaceutical composition comprising the above
CC   antibody and a pharmaceutical excipient, a kit for detecting cancer
CC   cells(comprising the antibody cited above, methods for diagnosing cancer
CC   or for detecting the presence or absence of cancer cells in an
CC   individual, a method for inhibiting growth of cancer cells in an
CC   individual, a method for delivering a therapeutic agent to cancer cells
CC   in an individual, an electronic library comprising the above
CC   polynucleotide or polypeptide (or their fragments), methods of screening
CC   for anticancer activity or for a bioactive agent capable of modulating
CC   the activity of a CA protein (CAP), methods for detecting cancer
CC   associated with expression of a polypeptide in a test cell sample, a
CC   method for treating cancers and a method for inhibiting the expression of
CC   CA gene in a cell. The composition and methods are useful for detecting,
CC   diagnosing, preventing and treating cancers, especially lymphoma and
CC   leukaemia. These may also be used in screening for agents that modulate
CC   cancer. The present sequence is a human CAP protein sequence. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1106 AA;

  Query Match             41.7%;  Score 2354.5;  DB 8;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

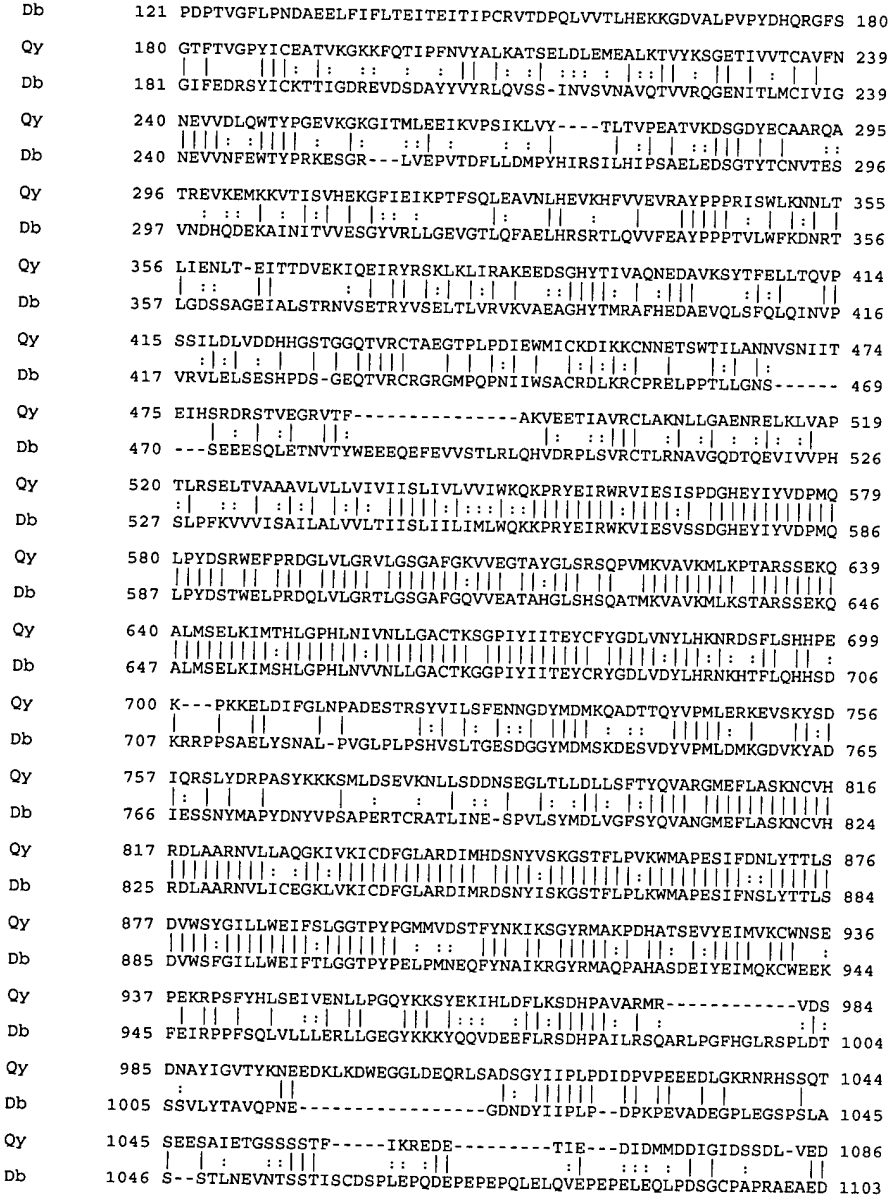
Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

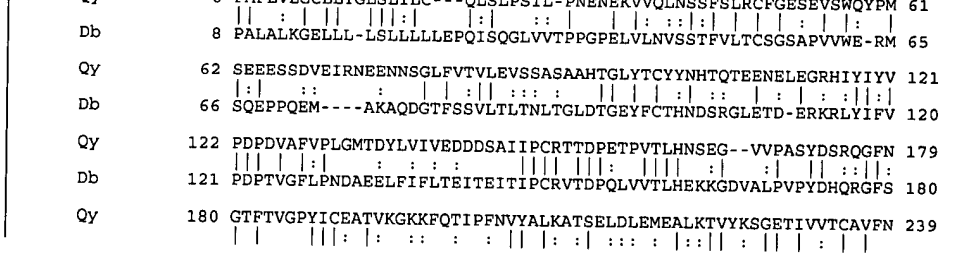
Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
```



RESULT 46
ADY59381

ID ADY59381 standard; protein; 1106 AA.
XX
AC ADY59381;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human PDGFR-B.
XX
KW PDGF antagonist; VEGF antagonist; psoriasis; rheumatoid arthritis;
KW age-related macular degeneration; antipsoriatic; dermatological disease;
KW immune disorder; antiarthritic; antirheumatic; immune disorder;
KW inflammation; musculoskeletal disease; age related macular degeneration;
KW ophthalmological; ocular disease; diabetic retinopathy; antidiabetic;
KW ophthalmological; cardiovascular disease; ocular disease.
XX
OS Homo sapiens.
XX
PN WO2005020972-A2.
XX
PD 10-MAR-2005.
XX
PF 26-AUG-2004; 2004WO-US027612.
XX
PR 27-AUG-2003; 2003US-0498407P.
PR 26-MAR-2004; 2004US-0556837P.
XX
PA (EYET-) EYETECH PHARM INC.
XX
PI Shima D, Calias P, Adamis AP;
XX
DR WPI; 2005-214423/22.
DR N-PSDB; ADY59380.
XX
PT Treating an ocular neovascular disorder, comprises administering a
PT platelet derived growth factor antagonist and a vascular endothelial
PT growth factor antagonist, simultaneously or within ninety days of each
PT other.
XX
PS Disclosure; SEQ ID NO 6; 112pp; English.
XX
CC The invention relates to a method of treating a patient diagnosed with or
CC at risk for developing a neovascular disorder, or suppressing a
CC neovascular disorder in a patient. The method is useful for treating a
CC patient diagnosed with or at risk for developing a neovascular disorder
CC or suppressing a neovascular disorder in a patient. The neovascular
CC disorder is an ocular neovascular disorder, psoriasis or rheumatoid
CC arthritis. The ocular neovascular disorder is ischemic retinopathy, iris
CC neovascularization, intraocular neovascularization, age-related macular
CC degeneration, corneal neovascularization, retinal neovascularization,
CC choroidal neovascularization, diabetic retinal ischemia, or proliferative
CC diabetic retinopathy. The present sequence represents a human PDGFR
CC protein.
XX
SQ Sequence 1106 AA;

Query Match 41.7%; Score 2354.5; DB 9; Length 1106;
Best Local Similarity 44.1%; Pred. No. 3.7e-155;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;



```
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| : |:|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||  | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| |||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::|||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
               | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              | | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106
```

```
RESULT 47
ADY70691
ID   ADY70691 standard; protein; 1106 AA.
XX
AC   ADY70691;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human BACE1-complex member, PDGFRB protein.
XX
KW   protein interaction; neurological disease; neurodegenerative disease;
KW   Alzheimer's disease; PDGFRB.
XX
OS   Homo sapiens.
XX
PN   WO2005023833-A2.
XX
PD   17-MAR-2005.
XX
PF   02-SEP-2004; 2004WO-EP009771.
XX
PR   05-SEP-2003; 2003EP-00019642.
PR   10-DEC-2003; 2003WO-EP013980.
PR   29-JAN-2004; 2004EP-00001894.
PR   29-JAN-2004; 2004EP-00001895.
PR   26-MAR-2004; 2004EP-00007447.
PR   07-MAY-2004; 2004WO-EP004889.
PR   07-MAY-2004; 2004WO-EP004891.
PR   09-AUG-2004; 2004EP-00018874.
XX
PA   (CELL-) CELLZOME AG.
XX
PI   Hopf C;
XX
DR   WPI; 2005-223334/23.
XX
PT   Use of a FADS2 interacting molecule for preparing a pharmaceutical
PT   composition for treating neurodegenerative diseases.
XX
PS   Claim 13; SEQ ID NO 78; 488pp; English.
XX
CC   The invention relates to a novel FADS2 (fatty acid delta6 desaturase)
CC   interacting molecule to be used in the preparation of a pharmaceutical
CC   composition for treating neurodegenerative diseases. FADS2 has been found
CC   to form part of different intracellular protein complexes that are
CC   involved in the aberrant gamma secretase processing of amyloid precursor
CC   protein (APP) in Alzheimer's disease. In particular, it has been found
CC   that FADS2 is a component of the nicastrin-complex, the BACE1 (beta-site
CC   APP-cleaving enzyme 1)-complex, the Psen2 (presenilin 2)-complex and the
CC   PTK7 (protein tyrosine kinase 7)-complex. The molecule of the invention
CC   demonstrates neuroprotective activity and may be useful for modulating
CC   gamma secretase and/or beta secretase activity in vitro. Thus the FADS2
CC   interacting molecule may be useful for preparing a pharmaceutical
CC   composition for diagnosing, treating or preventing neurodegenerative
CC   diseases, particularly, Alzheimer's disease. The complex provided by the
CC   invention which comprises FADS2 and one or more proteins may be useful as
CC   a target for the active agent of such a pharmaceutical composition. The
CC   current sequence is that of the human FADS2-interacting BACE1-complex
CC   member, PDGFRB protein of the invention. The BACE1 complex is involved in
CC   APP processing by beta-secretase.
XX
SQ   Sequence 1106 AA;
```

```
  Query Match           41.7%;  Score 2354.5;  DB 9;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3.7e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180
```

```
Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106
```

RESULT 48
ABO84677
ID ABO84677 standard; protein; 1107 AA.
XX
AC ABO84677;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated protein HP20-018.1.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
DR N-PSDB; ABD32963.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 18; seqid 706; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells(comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1107 AA;

 Query Match   41.6%; Score 2351; DB 8; Length 1107;

```
  Best Local Similarity   44.2%;  Pred. No. 6.5e-155;
  Matches  506;  Conservative  194;  Mismatches  340;  Indels  104;  Gaps   26;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   ::  |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : ||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYP-GEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQ 294
              ||||: :||||  || |:   ::| :    : : |     | :| | ::||| | |   :
Db        240 NEVVNPEWTYPRKEVIGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTE 296

Qy        295 ATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNL 354
              :  : :: | : |:| | |:: :      |:   ||  :   |   |||||  : | |:|
Db        297 SVNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNR 356

Qy        355 TLIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQV 413
              || ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   |
Db        357 TLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINV 416

Qy        414 PSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII 473
              |  :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 PVRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS----- 470

Qy        474 TEIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVA 518
                  | : | :|  ||:                 |:  ::||| :| :| : :|: :|
Db        471 ----SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVP 526

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
              :|  :: | :|:| |:|: ||||||:|:::|::|||||||:||||:| ||||||||||
Db        527 HSLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPM 586

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
              |||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| |||||||
Db        587 QLPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEK 646

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
              |||||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :|| ||
Db        647 QALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHS 706

Qy        699 EK---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 755
              :|   |  ||     | |      |:| |: |::| |||| : ::  |||||: |   ||:
Db        707 DKRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYA 765

Qy        756 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 815
              ||: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 DIESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCV 824

Qy        816 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 875
              ||||||||||: :||:|||||||||||||| ||||:||||||||:||||||||::|||||
Db        825 HRDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTL 884

Qy        876 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 935
              |||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||
Db        885 SDVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEE 944

Qy        936 EPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VD 983
              : | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|
Db        945 KFEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLD 1004

Qy        984 SDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQ 1043
              : :        ||                  |: ||||||  || ||  | |      |

Db       1005 TSSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSL 1045

Qy       1044 TSEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VE 1085
                |  | :   ::|||      :: :||          :|   ::: : | |  :     |
Db       1046 AS--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAE 1103

Qy       1086 DSFL 1089
                ||||
Db       1104 DSFL 1107
```

RESULT 49
ADY70656
ID   ADY70656 standard; protein; 1107 AA.
XX
AC   ADY70656;
XX
DT   02-JUN-2005 (first entry)
XX
DE   Human BACE1-complex member, PDGFRB protein.
XX
KW   protein interaction; neurological disease; neurodegenerative disease;
KW   Alzheimer's disease; PDGFRB.
XX
OS   Homo sapiens.
XX
PN   WO2005023833-A2.
XX
PD   17-MAR-2005.
XX
PF   02-SEP-2004; 2004WO-EP009771.
XX
PR   05-SEP-2003; 2003EP-00019642.
PR   10-DEC-2003; 2003WO-EP013980.
PR   29-JAN-2004; 2004EP-00001894.
PR   29-JAN-2004; 2004EP-00001895.
PR   26-MAR-2004; 2004EP-00007447.
PR   07-MAY-2004; 2004WO-EP004889.
PR   07-MAY-2004; 2004WO-EP004891.
PR   09-AUG-2004; 2004EP-00018874.
XX
PA   (CELL-) CELLZOME AG.
XX
PI   Hopf C;
XX
DR   WPI; 2005-223334/23.
XX
PT   Use of a FADS2 interacting molecule for preparing a pharmaceutical
PT   composition for treating neurodegenerative diseases.
XX
PS   Claim 13; SEQ ID NO 43; 488pp; English.
XX
CC   The invention relates to a novel FADS2 (fatty acid delta6 desaturase)
CC   interacting molecule to be used in the preparation of a pharmaceutical
CC   composition for treating neurodegenerative diseases. FADS2 has been found
CC   to form part of different intracellular protein complexes that are
CC   involved in the aberrant gamma secretase processing of amyloid precursor
CC   protein (APP) in Alzheimer's disease. In particular, it has been found
CC   that FADS2 is a component of the nicastrin-complex, the BACE1 (beta-site
CC   APP-cleaving enzyme 1)-complex, the Psen2 (presenilin 2)-complex and the
CC   PTK7 (protein tyrosine kinase 7)-complex. The molecule of the invention
CC   demonstrates neuroprotective activity and may be useful for modulating
CC   gamma secretase and/or beta secretase activity in vitro. Thus the FADS2
CC   interacting molecule may be useful for preparing a pharmaceutical
CC   composition for diagnosing, treating or preventing neurodegenerative
CC   diseases, particularly, Alzheimer's disease. The complex provided by the
CC   invention which comprises FADS2 and one or more proteins may be useful as
CC   a target for the active agent of such a pharmaceutical composition. The
CC   current sequence is that of the human FADS2-interacting BACE1-complex
CC   member, PDGFRB protein of the invention. The BACE1 complex is involved in
CC   APP processing by beta-secretase.
XX
SQ   Sequence 1107 AA;

Query Match 41.6%; Score 2351; DB 9; Length 1107;
Best Local Similarity 44.2%; Pred. No. 6.5e-155;
Matches 506; Conservative 194; Mismatches 340; Indels 104; Gaps 26;

```
Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|    ::  |    | |: ::|:|  | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::      :   | | :|| ::: :   || | | :| ::   | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|     :  : : :        |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYP-GEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQ 294
              ||||: :||||  || |:   ::| :    : : |     | :| | ::||| | |   :
Db        240 NEVVNFEWTYPRKEVIGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTE 296

Qy        295 ATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNL 354
              :  : :: | : |:| | |:: :       |:   ||  :   |  |||||  : | |:|
Db        297 SVNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNR 356

Qy        355 TLIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQV 413
              || ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   |
Db        357 TLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINV 416

Qy        414 PSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNII 473
              |  :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 PVRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS----- 470

Qy        474 TEIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVA 518
                | : | :|  ||:                |:  ::|||  :| :|  : :|: :|
Db        471 ----SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVP 526

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||
Db        527 HSLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPM 586

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
              |||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| |||||||
Db        587 QLPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEK 646

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| ||
Db        647 QALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHS 706

Qy        699 EK---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 755
              :|    |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:
Db        707 DKRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYA 765

Qy        756 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 815
              ||: | | |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 DIESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCV 824

Qy        816 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 875
              ||||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::|||||
Db        825 HRDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTL 884

Qy        876 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 935
              |||||:|||||||:|||||||  : ::  ||| || |||||:| ||: |:|||| |||
Db        885 SDVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEE 944

Qy        936 EPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VD 983
              : | || |  |  ::| ||   ||| |::  :||:|||||: | :             :|
Db        945 KFEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLD 1004

Qy        984 SDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQ 1043
              : :          ||                   |: ||||||  || ||  | |      |
Db       1005 TSSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSL 1045

Qy       1044 TSEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VE 1085
                |  | :   ::|||      :: :||          :|   ::: : | |  :     |
Db       1046 AS--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAE 1103

Qy       1086 DSFL 1089
                ||||
Db       1104 DSFL 1107
```

RESULT 50
ABG72456
ID ABG72456 standard; protein; 1106 AA.
XX
AC ABG72456;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human platelet derived growth factor receptor beta mutant E594K.
XX
KW Human; platelet derived growth factor receptor beta; PDGFRbeta;
KW hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .32
FT		/label= Signal_peptide
FT	Protein	33. .1106
FT		/label= Mature_PDGFR_beta
FT	Domain	227. .298
FT		/label= Immunoglobulin-like_domain
FT	Domain	335. .398
FT		/label= Immunogobulin-like_domain
FT	Domain	532. .556
FT		/label= Transmembrane_domain
FT	Misc-difference	594
FT		/note= "Wild type Glu substituted by Lys"
FT	Domain	604. .694
FT		/note= "Split tyrosine kinase domian segment 1"
FT	Domain	799. .951
FT		/note= "Split tyrosine kinase domain segment 2"

XX
PN US2002111304-A1.
XX
PD 15-AUG-2002.
XX
PF 25-MAY-2001; 2001US-00866510.
XX
PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
XX
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
XX
PI Kazlauskas A, Ikuno Y;
XX
DR WPI; 2003-066697/06.
DR N-PSDB; ABS57787.
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell

PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 7; Page 81-84; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This is the amino
CC acid sequence of human platelet derived growth factor receptor (PDGFR)
CC beta mutant E594K
XX
SQ Sequence 1106 AA;

Query Match 41.6%; Score 2350.5; DB 6; Length 1106;
Best Local Similarity 44.0%; Pred. No. 7e-155;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

```
Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::    :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :   : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| |: ||| ||||| ||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWKLPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:|||||||  : ::  ||| || |||||:|  ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :   ||                |: |||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106
```

Search completed: May 15, 2006, 08:55:27
Job time : 217 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 08:51:48 ; Search time 29 Seconds
(without alignments)
3613.105 Million cell updates/sec

Title: US-08-439-095-1
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5652	100.0	1089	1	PFHUGA	platelet-derived g
2	5190.5	91.8	1088	1	PFRTGA	platelet-derived g
3	5177	91.6	1089	1	S33727	platelet-derived g
4	4246	75.1	1087	2	I51552	platelet-derived g
5	2354.5	41.7	1106	1	PFHUGB	platelet-derived g
6	2336.5	41.3	1098	1	PFMSRB	platelet-derived g
7	2182.5	38.6	1048	2	T30815	platelet-derived g
8	1914.5	33.9	457	2	S44269	platelet-derived g
9	1481.5	26.2	977	2	I45877	protein-tyrosine k
10	1461.5	25.9	960	1	JN0677	protein-tyrosine k
11	1458	25.8	978	1	A49814	protein-tyrosine k
12	1454.5	25.7	976	1	TVHUKT	protein-tyrosine k
13	1446.5	25.6	975	1	TVMSKT	protein-tyrosine k
14	1416.5	25.1	954	2	I51703	c-kit-related kina
15	1412.5	25.0	980	1	TVCTMD	macrophage colony-
16	1400.5	24.8	941	1	TVMVMD	protein-tyrosine k
17	1395	24.7	975	2	T30816	macrophage colony-
18	1352.5	23.9	978	2	S16385	macrophage colony-
19	1346.5	23.8	972	1	TVHUMD	macrophage colony-
20	1344	23.8	976	1	TVMSMD	macrophage colony-
21	1287	22.8	1338	2	S09982	protein-tyrosine k
22	1280	22.6	1333	2	I78875	receptor tyrosine
23	1278	22.6	1336	2	I60598	Fit-1 tyrosine kin
24	1231.5	21.8	1330	2	S49010	embryonic receptor
25	1226	21.7	1348	2	S51656	vascular endotheli
26	1206.5	21.3	1356	2	JC1402	protein-tyrosine k
27	1198.5	21.2	1379	2	JC4954	vascular endotheli
28	1164.5	20.6	1000	2	S18827	Flt3 protein - mou
29	1163.5	20.6	1298	2	A48999	protein-tyrosine k
30	1152.5	20.4	992	2	A39931	protein-tyrosine k
31	1152.5	20.4	1363	2	I58375	protein-tyrosine k
32	1152	20.4	1367	2	A41228	protein-tyrosine k
33	1151	20.4	993	2	A36873	protein-tyrosine k
34	1067	18.9	790	1	FOMVHZ	gag-kit polyprotei
35	863	15.3	819	1	TVCHFG	fibroblast growth
36	859.5	15.2	822	1	TVHUFG	fibroblast growth
37	855	15.1	822	2	S29840	fibroblast growth
38	854	15.1	812	1	A36477	fibroblast growth
39	852.5	15.1	822	2	I49289	fibroblast growth
40	849.5	15.0	822	1	TVMSFG	fibroblast growth
41	846	15.0	814	1	A39752	fibroblast growth
42	843.5	14.9	832	2	JH0393	fibroblast growth
43	841.5	14.9	816	2	A49151	fibroblast growth
44	841	14.9	797	2	S38579	fibroblast growth
45	833.5	14.7	821	1	TVHUF2	fibroblast growth
46	830.5	14.7	729	2	A56795	fibroblast growth
47	829.5	14.7	733	2	I49293	fibroblast growth
48	828	14.6	822	2	B54846	fibroblast growth
49	828	14.6	822	2	A45081	fibroblast growth
50	827.5	14.6	824	2	S36439	fibroblast growth
51	826	14.6	769	2	S16236	fibroblast growth
52	821	14.5	821	1	TVMSBK	fibroblast growth
53	821	14.5	823	2	B35963	protein-tyrosine k
54	820	14.5	822	2	A41794	keratinocyte growt
55	814	14.4	820	2	S17295	fibroblast growth
56	811	14.3	824	2	S24108	protein-tyrosine k
57	808	14.3	822	2	B49151	fibroblast growth
58	807	14.3	806	1	TVHUF3	fibroblast growth
59	806.5	14.3	818	2	JC4058	fibroblast growth
60	802	14.2	822	2	S19947	fibroblast growth
61	801.5	14.2	748	2	S41050	fibroblast growth
62	798	14.1	806	2	A35963	protein-tyrosine k
63	797.5	14.1	682	2	A35969	heparin-binding gr
64	796	14.1	800	2	A48991	heparin-binding gr
65	795	14.1	800	1	TVHU2F	fibroblast growth
66	792	14.0	707	2	A38429	keratinocyte growt
67	792	14.0	707	2	A54846	fibroblast growth
68	790	14.0	705	2	S51635	fibroblast growth
69	788.5	14.0	750	2	S41051	fibroblast growth
70	784	13.9	1064	1	S57450	protein-tyrosine k
71	781.5	13.8	829	2	JC4583	fibroblast growth
72	778.5	13.8	801	2	I55363	fibroblast growth
73	771.5	13.7	713	2	I50128	fibroblast growth
74	767.5	13.6	813	1	A49123	fibroblast growth
75	763	13.5	799	2	S18209	fibroblast growth
76	760	13.4	1114	1	S05582	protein-tyrosine k
77	758.5	13.4	650	1	JC1450	fibroblast growth
78	758.5	13.4	1052	2	B49120	protein-tyrosine k
79	758	13.4	388	2	I51023	fibroblast growth
80	749.5	13.3	1115	1	S29926	protein-tyrosine k
81	744	13.2	802	1	TVHUF4	fibroblast growth
82	739	13.1	499	2	S33766	platelet-derived g
83	737.5	13.0	415	2	I65223	heparin-binding fi
84	710	12.6	801	4	TVHURE	transforming prote
85	700.5	12.4	435	2	JN0290	protein-tyrosine k
86	700.5	12.4	477	2	JN0291	protein-tyrosine k
87	700	12.4	899	2	I38153	gene retII protein
88	696	12.3	402	2	B34735	protein-tyrosine k
89	693.5	12.3	790	2	A39627	protein-tyrosine k
90	689.5	12.2	1040	2	A57638	receptor tyrosine
91	689	12.2	729	2	A49120	fibroblast growth
92	685	12.1	1103	2	T22889	hypothetical prote
93	641.5	11.3	1227	2	T23004	hypothetical prote
94	597.5	10.6	871	1	I48696	protein-tyrosine k
95	597.5	10.6	881	1	I48697	protein-tyrosine k
96	593.5	10.5	903	2	T33177	hypothetical prote
97	583.5	10.3	1199	2	T23005	hypothetical prote
98	581.5	10.3	1123	1	JN0712	protein-tyrosine k
99	581	10.3	367	2	B56598	endothelial kinase
100	581	10.3	1122	2	I54237	protein-tyrosine k
101	580	10.3	2311	1	TVCHSR	kinase-related pro
102	578	10.2	1124	1	I58388	protein-tyrosine k

103	574.5	10.2	1081	2	T31329	receptor tyrosine
104	573.5	10.1	1125	1	S57846	protein-tyrosine k
105	571	10.1	1607	2	T43212	insulin-like growt
106	569	10.1	160	2	A39061	protein-tyrosine k
107	556	9.8	1125	1	JH0771	protein-tyrosine k
108	556	9.8	1134	1	JN0711	protein-tyrosine k
109	550	9.7	1136	1	S57845	protein-tyrosine k
110	549	9.7	2338	2	I73957	kinase-related pro
111	545.5	9.7	821	1	A39667	brain-derived neur
112	545.5	9.7	923	2	S03900	gene torso protein
113	545	9.6	495	2	I44329	protein-tyrosine k
114	543.5	9.6	430	2	T33178	hypothetical prote
115	543.5	9.6	818	1	S44098	brain-derived neur
116	542.5	9.6	2347	1	TVHURS	kinase-related pro
117	542	9.6	821	1	S06943	brain-derived neur
118	540.5	9.6	1138	1	S24066	protein-tyrosine k
119	540	9.6	822	1	A56853	brain-derived neur
120	540	9.6	1477	2	T18534	protein-tyrosine k
121	537.5	9.5	402	1	TVFVUR	protein-tyrosine k
122	537	9.5	1363	2	T43220	insulin-like growt
123	534.5	9.5	666	1	JE0201	protein-tyrosine k
124	533	9.4	825	2	A55178	neurotrophin recep
125	532	9.4	2340	2	I48310	kinase-related pro
126	531.5	9.4	1367	1	IGHUR1	insulin-like growt
127	525	9.3	202	2	A44876	protein-tyrosine k
128	524	9.3	946	1	A47299	ror-related recept
129	521	9.2	994	2	I49276	c-mer tyrosine kin
130	521	9.2	1070	2	JC4593	protein-tyrosine k
131	518	9.2	839	1	I73632	neurotrophin-3 rec
132	517.5	9.2	880	1	JC4166	protein-tyrosine k
133	514.5	9.1	974	1	A49714	protein-tyrosine k
134	514	9.1	825	1	A40026	neurotrophin-3 rec
135	513	9.1	822	1	TVHUFE	protein-tyrosine k
136	513	9.1	894	1	A41527	protein-tyrosine k
137	512.5	9.1	1146	2	B35962	protein-tyrosine k
138	512.5	9.1	1182	2	A35962	protein-tyrosine k
139	512	9.1	1390	2	T30346	insulin receptor -
140	511.5	9.0	882	2	I38912	receptor tyrosine
141	511	9.0	880	2	B53743	protein-tyrosine k
142	509.5	9.0	799	1	TVRTTB	nerve growth facto
143	509	9.0	876	2	I49152	protein-tyrosine k
144	508.5	9.0	640	2	S23008	insulin-like growt
145	506.5	9.0	890	1	A53743	protein-tyrosine k
146	503.5	8.9	991	2	I78843	receptor protein-t
147	502.5	8.9	803	1	S35695	neurotrophin-3 rec
148	502.5	8.9	1383	2	A36080	insulin receptor p
149	502	8.9	323	2	S04328	protein-tyrosine k
150	502	8.9	1051	2	A39712	kinase-like protei
151	501	8.9	1371	2	A33837	insulin-like growt
152	500.5	8.9	852	2	I51259	tyrosine kinase C
153	499	8.8	2148	1	A56081	insulin receptor -
154	498.5	8.8	856	2	I58411	protein-tyrosine k
155	498	8.8	888	2	S23065	ufo protein - mous
156	497	8.8	453	2	I49663	tyrosine kinase (f
157	496.5	8.8	1372	2	A34157	insulin receptor p
158	496	8.8	1382	1	INHUR	insulin receptor p
159	495	8.8	143	2	B39061	protein-tyrosine k
160	494.5	8.7	1005	2	S49015	receptor tyrosine
161	494.5	8.7	1013	2	I50615	receptor-type prot
162	494.5	8.7	1123	2	A39962	kinase-related tra
163	493.5	8.7	981	2	S51604	receptor-like tyro
164	493	8.7	790	1	TVHUTT	nerve growth facto
165	493	8.7	1520	1	TVFFA	protein-tyrosine k
166	492.5	8.7	981	1	FOMVGM	gag-abl polyprotei
167	491.5	8.7	484	2	C88264	protein kin-15 [im
168	491.5	8.7	488	2	I44330	protein-tyrosine k
169	491.5	8.7	507	1	A39939	protein-tyrosine k
170	491.5	8.7	576	2	S12792	protein-tyrosine k
171	491.5	8.7	888	2	I58378	tyrosine kinase -
172	490	8.7	820	1	TVCTFF	protein-tyrosine k
173	489.5	8.7	803	1	OKFFPS	protein-tyrosine k
174	489	8.7	942	2	S23251	protein-tyrosine k
175	489	8.7	1130	1	TVHUA	protein-tyrosine k
176	489	8.7	1621	2	T30200	protein-tyrosine k
177	487	8.6	2594	2	A35774	kinase-related pro
178	486.5	8.6	502	2	T19108	hypothetical prote
179	486	8.6	697	2	A26132	gag-abl-pol polypr
180	485	8.6	609	1	TVMVGC	protein-tyrosine k
181	481	8.5	2554	1	TVFF7L	kinase-related pro
182	480	8.5	498	2	T28115	hypothetical prote
183	477.5	8.4	276	2	T16765	hypothetical prote
184	477.5	8.4	512	1	I56160	protein-tyrosine k
185	476.5	8.4	1196	2	T23832	protein-tyrosine k
186	474.5	8.4	2101	2	S57245	insulin receptor (
187	473.5	8.4	1268	2	B36502	insulin receptor-r
188	473	8.4	503	4	S23741	hypothetical TPR/T
189	473	8.4	685	1	A48289	neurotrophic recep
190	472.5	8.4	478	2	T32476	probable protein-t
191	472.5	8.4	590	1	TVFFDS	protein-tyrosine k
192	472.5	8.4	820	2	I48347	protein-tyrosine k
193	472.5	8.4	898	2	S47489	receptor tyrosine
194	472	8.4	680	4	I38491	nucleophosmin/anap
195	471.5	8.3	512	1	TVHULY	protein-tyrosine k
196	471.5	8.3	893	2	S51603	receptor-like tyro
197	471	8.3	1300	2	A36502	insulin receptor-r
198	470	8.3	505	1	TVHUHC	protein-tyrosine k
199	470	8.3	983	2	A38224	protein-tyrosine k
200	468.5	8.3	509	1	OKHULK	protein-tyrosine k
201	468	8.3	442	1	B43362	protein-tyrosine k
202	468	8.3	506	1	S24553	protein-tyrosine k
203	467.5	8.3	512	1	A39719	protein-tyrosine k
204	467	8.3	477	1	TVMVCS	protein-tyrosine k
205	467	8.3	822	1	TVHUFF	protein-tyrosine k
206	466.5	8.3	999	2	I38547	novel cellular pro
207	464.5	8.2	334	2	S24552	protein-tyrosine k
208	463.5	8.2	675	2	S60612	protein-tyrosine k
209	463.5	8.2	1369	1	JC4860	protein-tyrosine k
210	463	8.2	568	1	TVFVS1	protein-tyrosine k
211	462.5	8.2	824	2	I50618	c-fps proto oncoge
212	462	8.2	505	2	I37206	protein-tyrosine k
213	461.5	8.2	505	2	I38396	protein-tyrosine k
214	461	8.2	1375	1	JC5148	hepatocyte growth
215	460.5	8.1	450	2	A41973	protein-tyrosine k
216	460.5	8.1	877	2	I48967	brain-specific kin
217	459.5	8.1	509	1	I48845	protein-tyrosine k
218	459.5	8.1	1052	2	JC4200	protein-tyrosine k
219	458	8.1	503	1	TVMSHC	protein-tyrosine k
220	458	8.1	512	2	I49552	protein-tyrosine k
221	458	8.1	864	2	A48266	protein-tyrosine k
222	458	8.1	943	2	B45082	neurotrophic recep
223	458	8.1	983	2	B45583	receptor tyrosine
224	457.5	8.1	509	1	TVHAST	protein-tyrosine k
225	457	8.1	503	1	JQ1321	protein-tyrosine k
226	455.5	8.1	450	1	JH0559	protein-tyrosine k
227	455.5	8.1	587	1	TVFVPR	protein-tyrosine k
228	455.5	8.1	1052	2	A46166	protein-tyrosine k
229	455.5	8.1	1210	2	A53183	epidermal growth f
230	455.5	8.1	1379	1	S01254	hepatocyte growth
231	455	8.1	467	2	I56579	protein-tyrosine k
232	455	8.1	505	1	S24550	protein-tyrosine k
233	454.5	8.0	483	2	T23634	hypothetical prote
234	454.5	8.0	557	1	TVFVS2	protein-tyrosine k
235	454.5	8.0	873	1	TVFVF	protein-tyrosine k
236	453.5	8.0	541	1	A43610	protein-tyrosine k
237	453.5	8.0	542	1	TVHUSC	protein-tyrosine k
238	453.5	8.0	873	1	TVFVFS	protein-tyrosine k
239	453.5	8.0	983	2	A45583	receptor tyrosine
240	453.5	8.0	1081	2	JC5494	protein-tyrosine k
241	453	8.0	1052	2	I53012	focal adhesion kin
242	452.5	8.0	496	2	T22405	protein-tyrosine k
243	452	8.0	496	2	A56040	protein-tyrosine k
244	452	8.0	537	1	A43806	protein-tyrosine k
245	452	8.0	1068	2	I51670	focal adhesion kin
246	451.5	8.0	465	2	I48926	protein-tyrosine k
247	451.5	8.0	505	2	I59296	protein-tyrosine k
248	451.5	8.0	532	1	B34104	protein-tyrosine k

249	451.5	8.0	532	1	A34104	protein-tyrosine k
250	451	8.0	1235	2	T13710	protein-tyrosine k
251	450.5	8.0	985	2	I51672	receptor tyrosine
252	450	8.0	952	2	I50612	protein-tyrosine k
253	450	8.0	1375	2	T30813	plasminogen relate
254	449.5	8.0	533	1	TVCHS	protein-tyrosine k
255	449	7.9	536	2	S33569	protein-tyrosine k
256	449	7.9	894	2	T20625	hypothetical prote
257	448.5	7.9	451	1	S49016	protein-tyrosine k
258	448.5	7.9	977	2	S49004	tyrosine kinase Mp
259	448	7.9	537	1	TVHUSY	protein-tyrosine k
260	448	7.9	542	2	A49114	protein-tyrosine k
261	448	7.9	975	2	I48974	receptor-protein t
262	447.5	7.9	1019	2	T13039	tyrosine kinase re
263	447	7.9	929	2	T32492	hypothetical prote
264	447	7.9	1846	2	T42047	insulin receptor h
265	446.5	7.9	308	1	TVFFS	protein-tyrosine k
266	446.5	7.9	362	2	S24551	protein-tyrosine k
267	446.5	7.9	450	1	S15094	protein-tyrosine k
268	446	7.9	533	1	TVFVFP	protein-tyrosine k
269	446	7.9	537	1	A45501	protein-tyrosine k
270	446	7.9	537	2	I51592	protein-tyrosine k
271	445.5	7.9	986	2	S78059	protein-tyrosine k
272	445.5	7.9	1308	2	A47253	epidermal growth f
273	445.5	7.9	1425	2	T30811	hepatocyte growth
274	445	7.9	984	2	A39753	protein-tyrosine k
275	444	7.9	507	2	A55625	protein-tyrosine k
276	444	7.9	526	2	S20808	protein-tyrosine k
277	444	7.9	544	2	I51593	protein-tyrosine k
278	443	7.8	499	1	A40092	protein-tyrosine k
279	443	7.8	523	1	TVFVMT	protein-tyrosine k
280	443	7.8	1028	2	A45388	protein-tyrosine k
281	442.5	7.8	984	1	A34076	protein-tyrosine k
282	442.5	7.8	1390	1	TVHUME	hepatocyte growth
283	442	7.8	464	2	A43625	protein-tyrosine k
284	441	7.8	534	1	S33568	protein-tyrosine k
285	440	7.8	526	2	S26420	protein-tyrosine k
286	440	7.8	1210	1	GQHUE	epidermal growth f
287	439	7.8	534	1	A44991	protein-tyrosine k
288	439	7.8	687	2	A49636	soluble vascular e
289	438	7.7	526	1	OKFVYR	protein-tyrosine k
290	438	7.7	539	2	B49114	protein-tyrosine k
291	438	7.7	995	2	A56599	embryo kinase 5 -
292	437.5	7.7	986	2	I78844	receptor protein-t
293	437	7.7	526	1	TVFVR	protein-tyrosine k
294	436.5	7.7	1009	2	S60248	protein-tyrosine k
295	436.5	7.7	1374	2	T30809	plasminogen relate
296	436	7.7	526	1	TVFV60	protein-tyrosine k
297	436	7.7	612	2	S33506	protein-tyrosine k
298	436	7.7	662	2	C40862	heparin-binding gr
299	436	7.7	723	2	I38412	receptor tyrosine
300	434.5	7.7	442	2	T20788	hypothetical prote
301	434.5	7.7	450	2	I48929	protein-tyrosine k
302	434.5	7.7	631	2	I56997	protein-tyrosine k
303	434.5	7.7	1166	1	S06142	protein-tyrosine k
304	434	7.7	879	2	PC1225	protein-tyrosine k
305	433	7.7	998	2	JC5672	receptor tyrosine
306	432.5	7.7	527	2	S13763	protein-tyrosine k
307	432.5	7.7	1223	1	TVCHLV	epidermal growth f
308	432	7.6	545	2	S52313	protein-tyrosine k
309	431	7.6	421	2	T19119	probable tyrosine
310	431	7.6	480	2	I48760	protein-tyrosine k
311	431	7.6	910	2	A53137	tyrosine kinase re
312	431	7.6	976	2	A36355	protein-tyrosine k
313	431	7.6	1033	2	S19247	cell adhesion prot
314	430	7.6	526	2	S15582	protein-tyrosine k
315	430	7.6	659	2	A45184	protein-tyrosine k
316	429.5	7.6	541	1	TVCHYS	protein-tyrosine k
317	429.5	7.6	541	2	S31645	protein-tyrosine k
318	429	7.6	546	2	S52314	protein-tyrosine k
319	429	7.6	659	2	I49553	protein-tyrosine k
320	428.5	7.6	543	1	TVHUYS	protein-tyrosine k
321	428	7.6	490	2	I50613	protein-tyrosine k
322	428	7.6	998	2	I58351	receptor protein-t
323	427.5	7.6	649	2	T33431	hypothetical prote
324	427	7.6	630	1	T01380	protein-tyrosine k
325	426.5	7.5	517	2	A43807	protein-tyrosine k
326	426.5	7.5	970	2	I78842	receptor protein-t
327	426	7.5	282	2	I51236	brain-derived neur
328	425.5	7.5	855	2	S42621	protein-tyrosine k
329	425	7.5	335	2	T37262	probable tyrosine
330	424.5	7.5	426	2	I48759	protein-tyrosine k
331	424.5	7.5	517	2	S24547	protein-tyrosine k
332	423.5	7.5	698	1	TVFVLV	protein-tyrosine k
333	423.5	7.5	1369	2	S70713	protein-tyrosine k
334	422.5	7.5	478	2	A57174	protein-tyrosine k
335	422.5	7.5	604	1	TVYUH	protein-tyrosine k
336	422.5	7.5	985	2	I51549	receptor tyrosine
337	422.5	7.5	1009	2	A57434	protein-tyrosine k
338	422.5	7.5	1323	2	E88257	protein let-23 [im
339	422.5	7.5	1374	2	S70712	protein-tyrosine k
340	422	7.5	527	2	I84483	protein-tyrosine k
341	421	7.4	392	2	S04205	protein-tyrosine k
342	421	7.4	849	2	I50617	protein-tyrosine k
343	420.5	7.4	528	1	TVFVG9	protein-tyrosine k
344	420	7.4	540	1	TVFVEB	protein-tyrosine k
345	420	7.4	544	2	S35745	protein-tyrosine k
346	420	7.4	545	2	S00727	kinase-related tra
347	419.5	7.4	448	2	T24082	hypothetical prote
348	419.5	7.4	993	2	I48653	mouse developmenta
349	418.5	7.4	988	2	I50611	protein-tyrosine k
350	417	7.4	419	2	T27938	hypothetical prote
351	417	7.4	998	2	S37627	protein-tyrosine k
352	416	7.4	540	2	B44776	protein-tyrosine k
353	414.5	7.3	663	1	TVMVRR	protein-tyrosine k
354	414.5	7.3	1260	1	TVRTNU	protein-tyrosine k
355	414	7.3	819	2	I48859	tyro 10 receptor k
356	414	7.3	1414	2	T33236	hypothetical prote
357	412.5	7.3	919	2	T29581	hypothetical prote
358	411.5	7.3	527	2	A49865	protein-tyrosine k
359	411	7.3	529	1	TVHUFR	protein-tyrosine k
360	410	7.3	987	2	A54092	protein-tyrosine k
361	408.5	7.2	1254	2	I48161	p-185 precursor -
362	408.5	7.2	1255	1	A24571	protein-tyrosine k
363	408	7.2	876	2	A49508	protein-tyrosine k
364	406.5	7.2	1717	1	A45558	epidermal growth f
365	406	7.2	620	1	S33253	protein-tyrosine k
366	405	7.2	913	2	A48280	receptor tyrosine
367	404	7.1	771	2	T26176	hypothetical prote
368	404	7.1	937	2	A45082	neurotrophic recep
369	403	7.1	987	2	I48953	eph-related recept
370	402	7.1	527	2	I49133	protein-tyrosine k
371	402	7.1	625	1	A43030	protein-tyrosine k
372	402	7.1	987	2	I48652	mouse developmenta
373	401	7.1	1400	1	I38185	protein-tyrosine k
374	400	7.1	1122	2	T42400	Eph receptor tyros
375	397.5	7.0	602	2	JU0215	protein-tyrosine k
376	396.5	7.0	938	2	I49071	protein kinase - m
377	396.5	7.0	1404	1	A48196	protein-tyrosine k
378	393	7.0	635	1	A53596	protein-tyrosine k
379	390.5	6.9	618	2	I48914	protein-tyrosine k
380	390	6.9	579	2	T15135	hypothetical prote
381	389	6.9	619	2	A44266	protein-tyrosine k
382	389	6.9	1378	1	I48751	protein-tyrosine k
383	388.5	6.9	364	2	T46926	hypothetical prote
384	387.5	6.9	1154	2	A39577	protein-tyrosine k
385	387	6.8	157	2	G00016	FGF-receptor - com
386	387	6.8	628	1	A40802	protein-tyrosine k
387	385	6.8	628	2	I48781	protein-tyrosine k
388	384.5	6.8	390	2	T24437	hypothetical prote
389	382	6.8	948	2	S51605	receptor-like tyro
390	381.5	6.7	433	2	T16817	hypothetical prote
391	380.5	6.7	628	1	A56707	protein-tyrosine k
392	378	6.7	1342	2	A36223	kinase-related tra
393	377.5	6.7	182	2	JC1189	tyrosine kinase re
394	375	6.6	596	1	TVFVSA	env-sea polyprotei

395	371.5	6.6	806	2	T18840	hypothetical prote
396	371	6.6	1091	2	S33596	protein-tyrosine k
397	369.5	6.5	497	1	S43532	protein-tyrosine k
398	369.5	6.5	1339	2	JC4387	epidermal growth f
399	369	6.5	600	4	A56379	ZP3 receptor precu
400	365.5	6.5	459	2	C88493	protein F57B9.8 [i
401	364.5	6.4	172	2	S27020	fibroblast growth
402	364.5	6.4	1177	2	A36984	protein-tyrosine k
403	364	6.4	1223	2	T15316	hypothetical prote
404	362	6.4	593	2	A47186	receptor protein t
405	361.5	6.4	241	2	PC4221	protein-tyrosine k
406	360.5	6.4	181	2	I50406	proto-fps protein
407	360	6.4	594	2	I58386	receptor tyrosine
408	360	6.4	2380	2	T29551	hypothetical prote
409	359.5	6.4	388	2	T24083	hypothetical prote
410	358	6.3	594	2	I56248	receptor tyrosine
411	356.5	6.3	546	2	D84555	probable protein k
412	356	6.3	293	2	T37261	probable tyrosine
413	356	6.3	791	2	T16031	hypothetical prote
414	354.5	6.3	1096	2	T16875	hypothetical prote
415	353	6.2	372	2	S23363	protein-tyrosine k
416	353	6.2	1330	1	GQFFE	epidermal growth f
417	350.5	6.2	430	2	T33070	hypothetical prote
418	350.5	6.2	1132	2	JW0091	Janus kinase (EC 2
419	350	6.2	172	2	S27019	fibroblast growth
420	348.5	6.2	248	2	A44547	receptor tyrosine
421	348.5	6.2	431	2	T29186	hypothetical prote
422	348.5	6.2	1132	2	JC4127	protein-tyrosine k
423	347.5	6.1	601	2	B39577	protein-tyrosine k
424	347.5	6.1	1072	2	T18802	hypothetical prote
425	347	6.1	607	2	I37560	protein-tyrosine k
426	346.5	6.1	1129	2	A47511	protein-tyrosine k
427	343.5	6.1	418	2	T21258	hypothetical prote
428	343.5	6.1	553	2	T04683	hypothetical prote
429	343	6.1	585	2	T29911	hypothetical prote
430	343	6.1	697	2	T26707	hypothetical prote
431	340.5	6.0	545	2	T33748	hypothetical prote
432	338.5	6.0	202	2	T33618	hypothetical prote
433	337.5	6.0	422	2	T48680	hypothetical prote
434	336.5	6.0	610	2	S58885	derailed receptor
435	334.5	5.9	172	2	S27022	fibroblast growth
436	334.5	5.9	1099	2	S48053	protein tyrosine k
437	333	5.9	407	2	G84635	probable protein k
438	332.5	5.9	172	2	S27021	fibroblast growth
439	332	5.9	414	2	T23940	hypothetical prote
440	331	5.9	1100	2	S43677	protein tyrosine k
441	330	5.8	412	2	T10671	protein kinase hom
442	329.5	5.8	354	2	JC1366	tyrosine kinase re
443	329	5.8	399	2	T20455	hypothetical prote
444	327	5.8	445	2	T33106	hypothetical prote
445	326	5.8	416	2	T29805	hypothetical prote
446	323	5.7	478	2	T23792	hypothetical prote
447	322.5	5.7	275	2	I48761	protein-tyrosine k
448	322.5	5.7	379	2	T21417	hypothetical prote
449	321.5	5.7	417	2	T33827	hypothetical prote
450	321.5	5.7	727	2	T15294	hypothetical prote
451	321	5.7	541	2	T25258	hypothetical prote
452	320.5	5.7	1124	2	A55747	L-JAK protein-tyro
453	317	5.6	1006	2	JC5526	kinase-defective E
454	316.5	5.6	311	2	S13808	protein-tyrosine k
455	316.5	5.6	605	2	S67815	protein-tyrosine k
456	316	5.6	328	2	T16747	hypothetical prote
457	313.5	5.5	563	2	T27313	hypothetical prote
458	313.5	5.5	821	2	T48400	serine/threonine-p
459	312.5	5.5	557	2	T16815	hypothetical prote
460	312	5.5	346	2	S13807	protein-tyrosine k
461	311.5	5.5	1030	2	F96763	hypothetical prote
462	310.5	5.5	829	2	T07406	probable protein k
463	309.5	5.5	553	2	T26036	hypothetical prote
464	306.5	5.4	534	2	T23425	hypothetical prote
465	306	5.4	602	1	TVRTRR	protein kinase (EC
466	303.5	5.4	567	2	JC5957	transforming growt
467	303.5	5.4	579	2	JC5955	transforming growt
468	303.5	5.4	606	2	JC5956	transforming growt
469	302.5	5.4	533	2	T20015	hypothetical prote
470	302	5.3	1187	1	TVHUY2	protein-tyrosine k
471	298.5	5.3	406	2	T52626	probable mitogen-a
472	296.5	5.2	363	1	S44734	probable protein-t
473	296.5	5.2	408	2	G88535	protein B0523.1 [i
474	294.5	5.2	548	2	T15523	hypothetical prote
475	293.5	5.2	462	2	S29851	protein kinase 6 (
476	293	5.2	517	2	T23413	hypothetical prote
477	292.5	5.2	349	2	T24308	hypothetical prote
478	292	5.2	1015	2	T00726	probable serine/th
479	290.5	5.1	390	2	T01451	protein kinase hom
480	289.5	5.1	493	2	T29030	hypothetical prote
481	289	5.1	417	2	T29770	hypothetical prote
482	288	5.1	357	2	C84856	probable protein k
483	288	5.1	546	2	T25257	hypothetical prote
484	286	5.1	394	2	JU0229	mixed-lineage prot
485	285.5	5.1	450	1	TVFVMR	protein kinase (EC
486	285.5	5.1	668	2	JC2363	protein kinase (EC
487	285.5	5.1	806	1	JN0612	protein kinase B-r
488	285.5	5.1	807	1	I51153	protein kinase B-r
489	285.5	5.1	888	2	A55318	serine/threonine p
490	285.5	5.1	1079	1	TVFVMI	gag-Rmil-env polyp
491	285	5.0	529	2	T27922	hypothetical prote
492	284	5.0	217	2	PC4173	insulin-like growt
493	284	5.0	545	2	T05675	hypothetical prote
494	283.5	5.0	888	2	JC5399	dual leucine zippe
495	282	5.0	1317	2	T03748	apoptosis associat
496	280.5	5.0	328	1	TVMSBF	protein kinase B-r
497	280.5	5.0	514	2	D88456	protein W03A5.1 [i
498	280.5	5.0	765	1	TVHUBF	protein kinase B-r
499	280.5	5.0	963	2	T09911	probable serine/th
500	279	4.9	816	2	T45684	hypothetical prote

ALIGNMENTS

RESULT 1
PFHUGA
platelet-derived growth factor receptor alpha precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Oct-2004
C;Accession: A40162; A32941
R;Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle, W.; Kraus, M.; Pierce, J
Science 243, 800-804, 1989
A;Title: Isolation of a novel receptor cDNA establishes the existence of two PDGF recepto
A;Reference number: A40162; MUID:89130149; PMID:2536956
A;Accession: A40162
A;Molecule type: mRNA
A;Residues: 1-1089 <MATS>
A;Cross-references: UNIPROT:P16234; UNIPARC:UPI0000131793; GB:M21574; NID:g189733; PIDN:A
R;Claesson-Welsh, L.; Eriksson, A.; Westermark, B.; Heldin, C.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 4917-4921, 1989
A;Title: cDNA cloning and expression of the human A-type platelet-derived growth factor
A;Reference number: A32941; MUID:89296915; PMID:2544881
A;Accession: A32941
A;Molecule type: mRNA
A;Residues: 1-1089 <CLA>
A;Cross-references: UNIPARC:UPI0000131793; GB:M22734; NID:g189725; PIDN:AAA60048.1; PID:g
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like doma
C;Genetics:
A;Gene: GDB:PDGFRA
A;Cross-references: GDB:120267; OMIM:173490
A;Map position: 4q11-4q12
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phospho
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1089/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>
F;25-524/Domain: extracellular #status predicted <EXT>
F;42-102/Domain: immunoglobulin homology <IMM1>
F;143-191/Domain: immunoglobulin homology <IMM2>

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F;228-292/Domain: immunoglobulin homology <IMM3>
F;428-503/Domain: immunoglobulin homology <IMM4>
F;525-548/Domain: transmembrane #status predicted <TMM>
F;549-1089/Domain: intracellular #status predicted <INT>
F;591-957/Domain: protein kinase homology <KIN>
F;599-607/Region: protein kinase ATP-binding motif
F;42,76,103,179,353,359,458,468/Binding site: carbohydrate (Asn) (covalent) #status pred
F;49-100,150-189,235-290,435-501/Disulfide bonds: #status predicted
F;627/Active site: Lys #status predicted
F;849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match            100.0%;  Score 5652;  DB 1;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-244;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 2
PFRTGA
platelet-derived growth factor receptor alpha precursor - rat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Oct-2004
C;Accession: A34710; S33767; S25100
R;Lee, K.H.; Bowen-Pope, D.F.; Reed, R.R.
Mol. Cell. Biol. 10, 2237-2246, 1990
A;Title: Isolation and characterization of the alpha platelet-derived growth factor recep
A;Reference number: A34710; MUID:90220609; PMID:2157969
A;Accession: A34710
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1088 <LEE>
A;Cross-references: UNIPROT:P20786; UNIPARC:UPI0000131794; GB:M63837; NID:g202929; PIDN:A
A;Note: in the authors' translation an additional residue, Val, is shown after position 8
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
Biochim. Biophys. Acta 1173, 294-302, 1993
A;Title: Conservation in sequence and affinity of human and rodent PDGF ligands and recep
A;Reference number: S33764; MUID:93305723; PMID:8318539
A;Accession: S33767
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 33-149,'R',151-518,'T',520-523 <HER1>
A;Cross-references: UNIPARC:UPI0000170AAE; EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID
A;Experimental source: strain Sprague Dawley
R;Herren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.
submitted to the EMBL Data Library, July 1992
A;Description: Cross-species conservation in sequence and function of PDGF ligands and r
A;Reference number: S25096
A;Accession: S25100
A;Molecule type: mRNA
A;Residues: 33-149,'R',151-518,'T',520-523 <HER2>
A;Cross-references: UNIPARC:UPI0000170AAE; EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; heterodimer; homodimer; phosphoprote
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-1088/Product: platelet-derived growth factor receptor alpha #status predicted <MAT>
F;24-523/Domain: extracellular #status predicted <EXT>
F;41-101/Domain: immunoglobulin homology <IMM1>
F;142-190/Domain: immunoglobulin homology <IMM2>
F;227-291/Domain: immunoglobulin homology <IMM3>
F;427-502/Domain: immunoglobulin homology <IMM4>
F;524-547/Domain: transmembrane #status predicted <TMM>
F;548-1088/Domain: intracellular #status predicted <INT>
F;590-956/Domain: protein kinase homology <KIN>
F;598-606/Region: protein kinase ATP-binding motif
F;48-99,149-188,234-289,434-500/Disulfide bonds: #status predicted
F;75,76,88,102,178,352,358,457,467/Binding site: carbohydrate (Asn) (covalent) #status pr
F;626/Active site: Lys #status predicted
F;848/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match            91.8%;  Score 5190.5;  DB 1;  Length 1088;
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  Matches  990;  Conservative   55;  Mismatches   43;  Indels    1;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db          1 MGTSQ-AFLVLSCLLTGPSLIVCQLLLPSILPNENEKIVPLSSSFSLRCFGESEVSWQHP 59

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db         60 MSEEEDPNVEIRTEENNSSLFVTVLEVVNASAAHTGWYTCYYNHTQTEESEIEGRHIYIY 119

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db        120 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCLTTDPDTEVTLHNNGRLVPASYDSRQGFNG 179

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db        180 TFSVGPYICEATVRGRTFKTSEFNVYALKATSELNLEMDTRQTVYKAGETIVVTCAVFNN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db        240 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGDYECAARQATKEVK 299

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db        300 EMKTVTISVHEKGFVQIRPTFGHLETVNLHQVREFVVEVQAYPTPRISWLKDNLTLIENL 359

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db        360 TEITTDVQRSQETRYQSKLKLIRAKEEDSGHYTIIVQNDDDMKSYTFELSTLVPASILEL 419

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db        420 VDDHHGSGGGQTVRCTAEGTPLPNIEWMICKDIKKCNNDTSWTVLASNVSNIITEFHQRG 479

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db        480 RSTVEGRVSFAKVEETIAVRCLAKNDLGIGNRELKLVAPSLRSELTVAAAVLVLLVIVIV 539

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db        540 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 599

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db        600 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 659

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db        660 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSRHPEKPKKDLDIFGLNPADESTRSY 719

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db        720 VILSFENNGDYVDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEAKN 779

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db        780 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 839

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db        840 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGVLLWEIFSLGGTPYPGMM 899

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Db        900 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 959

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db        960 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKEWEGGLDEQRLSADSGYII 1019

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db       1020 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1079

Qy       1081 SDLVEDSFL 1089
Db       1080 SDLVEDSFL 1088


RESULT 3
S33727
platelet-derived growth factor receptor alpha precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: I57511; S33727
R;Stiles, C.D.; Wang, C.
Mol. Cell. Biol. 10, 6781-6784, 1990
A;Title: Retinoic acid promotes transcription of the platelet-derived growth factor alpha
A;Reference number: I57511; MUID:91061789; PMID:2174116
A;Accession: I57511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1089 <RES>
A;Cross-references: UNIPROT:P26618; UNIPARC:UPI000016CF20; GB:M57683; NID:g199783; PIDN:
C;Genetics:
A;Gene: PDGF-alpha-R
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transmembrane
F;1-23/Domain: signal sequence #status predicted <SIG>
F;228-292/Domain: immunoglobulin homology <IMM>
F;591-957/Domain: protein kinase homology <KIN>
F;599-607/Region: protein kinase ATP-binding motif
F;42,76,89,103,179,353,359,458,468,506/Binding site: carbohydrate (Asn) (covalent) #statu

  Query Match             91.6%;  Score 5177;  DB 1;  Length 1089;
  Best Local Similarity   91.0%;  Pred. No. 1.7e-223;
  Matches  991;  Conservative   50;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db         61 MSEEEDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db        181 TFSVGPYICEAAVKGRTFKTSAFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

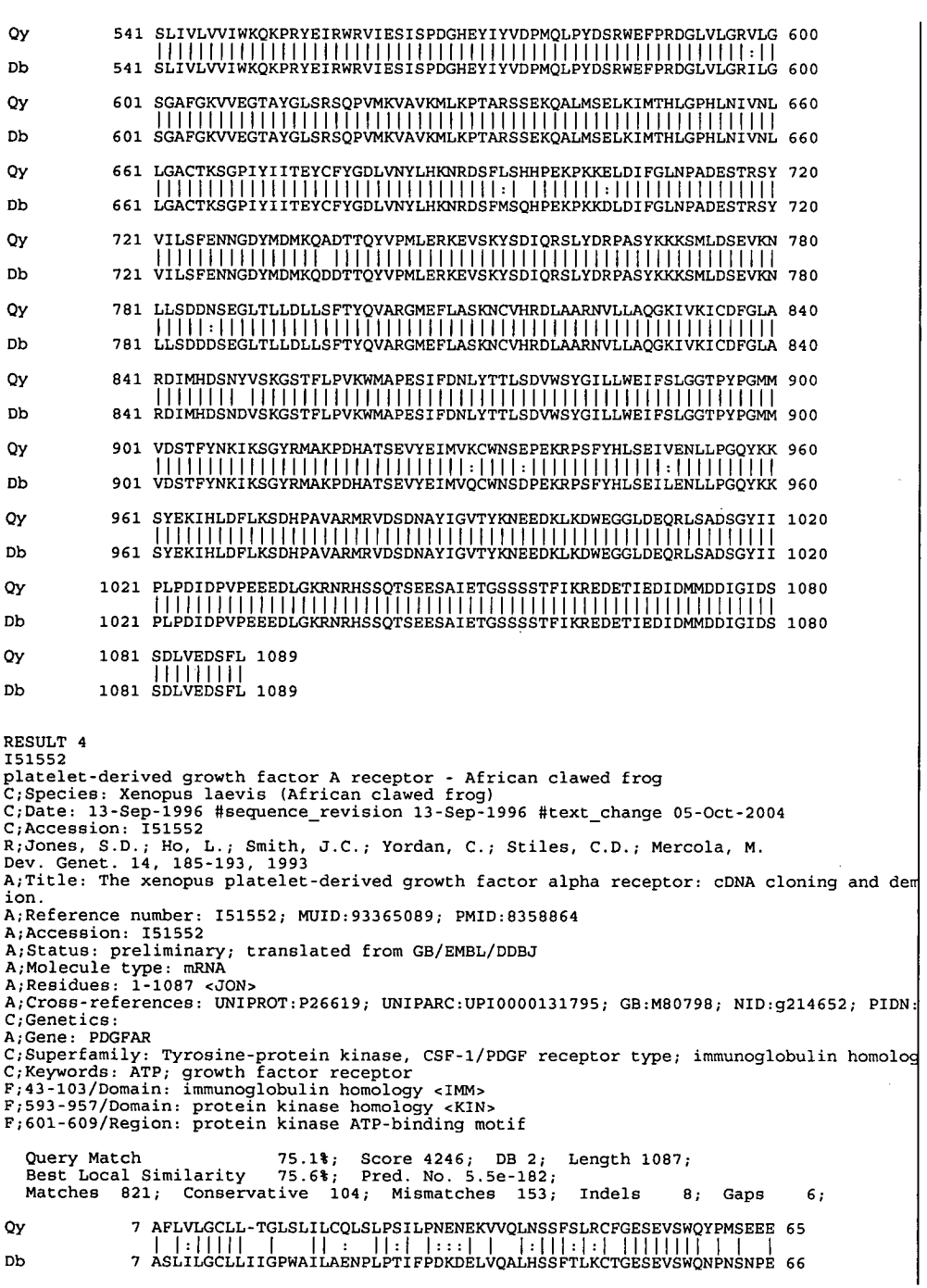
Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db        241 EVVDLQWTYPGGVRNKGITMLEEIKLPSIKVVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db        301 EMKRVTISVHEKGFVEIEPTFSQLEPVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db        421 VDDHHGSGGGQTVRCTAEEGPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db        481 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAEAVLVLLVIVIV 540
```

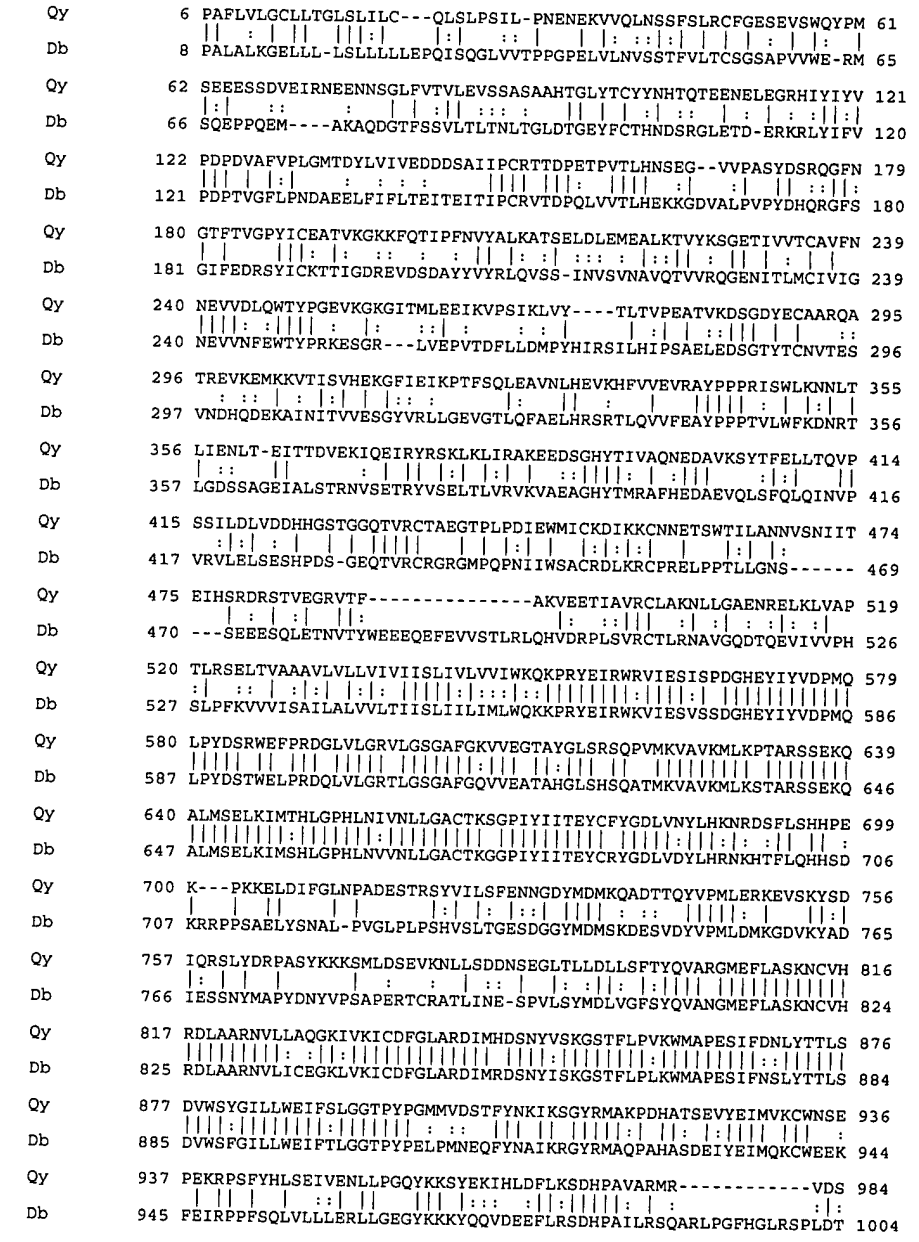


RESULT 4
I51552
platelet-derived growth factor A receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C;Accession: I51552
R;Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.
Dev. Genet. 14, 185-193, 1993
A;Title: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem
ion.
A;Reference number: I51552; MUID:93365089; PMID:8358864
A;Accession: I51552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1087 <JON>
A;Cross-references: UNIPROT:P26619; UNIPARC:UPI0000131795; GB:M80798; NID:g214652; PIDN:
C;Genetics:
A;Gene: PDGFAR
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; growth factor receptor
F;43-103/Domain: immunoglobulin homology <IMM>
F;593-957/Domain: protein kinase homology <KIN>
F;601-609/Region: protein kinase ATP-binding motif

Query Match 75.1%; Score 4246; DB 2; Length 1087;
Best Local Similarity 75.6%; Pred. No. 5.5e-182;
Matches 821; Conservative 104; Mismatches 153; Indels 8; Gaps 6;

RESULT 5
PFHUGB
platelet-derived growth factor receptor beta precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 05-Oct-2004
C;Accession: A28206; A31195; A38268; A31925; B31925; C31925
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f
A;Reference number: A28206; MUID:88217915; PMID:2835772
A;Accession: A28206
A;Molecule type: mRNA
A;Residues: 1-1106 <GRO>
A;Cross-references: UNIPROT:P09619; UNIPARC:UPI0000131791; GB:J03278; NID:g189731; PIDN:
R;Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet
Mol. Cell. Biol. 8, 3476-3486, 1988
A;Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re
A;Reference number: A31195; MUID:89096941; PMID:2850496
A;Accession: A31195
A;Molecule type: mRNA
A;Residues: 1-240,'D',242-1106 <CLA>
A;Cross-references: UNIPARC:UPI0000146F3C; GB:M21616; NID:g189729; PIDN:AAA36427.1; PID:
R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: A38268
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 828-884 <PAR>
A;Cross-references: UNIPARC:UPI00001725B5
R;Roberts, W.M.; Look, A.T.; Roussel, M.F.; Sherr, C.J.
Cell 55, 655-661, 1988
A;Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.
A;Reference number: A90908; MUID:89028677; PMID:2846185
A;Accession: A31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 676-727 <ROB>
A;Cross-references: UNIPARC:UPI00001725B6
A;Accession: B31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 901-932 <RO2>
A;Cross-references: UNIPARC:UPI00001725B6
A;Accession: C31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1047-1106 <RO3>
A;Cross-references: UNIPARC:UPI00001725B6
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C;Genetics:
A;Gene: GDB:PDGFRB
A;Cross-references: GDB:120710; OMIM:173410
A;Map position: 5q31-5q32
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
F;33-531/Domain: extracellular #status predicted <EXT>
F;47-102/Domain: immunoglobulin homology <IMM1>
F;142-192/Domain: immunoglobulin homology <IMM2>
F;228-293/Domain: immunoglobulin homology <IMM3>
F;429-510/Domain: immunoglobulin homology <IMM4>
F;532-555/Domain: transmembrane #status predicted <TMM>
F;556-1106/Domain: intracellular #status predicted <INT>
F;598-965/Domain: protein kinase homology <KIN>
F;606-614/Region: protein kinase ATP-binding motif
F;45,89,103,215,230,292,307,354,371,468,479/Binding site: carbohydrate (Asn) (covalent)
F;54-100,149-190,235-291,436-508/Disulfide bonds: #status predicted
F;634/Active site: Lys #status predicted
F;857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 41.7%; Score 2354.5; DB 1; Length 1106;
Best Local Similarity 44.1%; Pred. No. 1.2e-97;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;



```
Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106


RESULT 6
PFMSRB
platelet-derived growth factor receptor beta precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
C;Accession: A25742
R;Yarden, Y.; Escobedo, J.A.; Kuang, W.J.; Yang-Feng, T.L.; Daniel, T.O.; Tremble, P.M.;
Nature 323, 226-232, 1986
A;Title: Structure of the receptor for platelet-derived growth factor helps define a fam
A;Reference number: A25742; MUID:87014762; PMID:3020426
A;Accession: A25742
A;Molecule type: mRNA
A;Residues: 1-1098 <YAR>
A;Cross-references: UNIPROT:P05622; UNIPARC:UPI0000028828; EMBL:X04367; NID:g53618; PIDN
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C;Comment: The purified receptor was found be ubiquitinated.
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-1098/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
F;32-530/Domain: extracellular #status predicted <EXT>
F;46-101/Domain: immunoglobulin homology <IMM1>
F;141-191/Domain: immunoglobulin homology <IMM2>
F;227-292/Domain: immunoglobulin homology <IMM3>
F;428-509/Domain: immunoglobulin homology <IMM4>
F;531-554/Domain: transmembrane #status predicted <TMM>
F;555-1098/Domain: intracellular #status predicted <INT>
F;597-964/Domain: protein kinase homology <KIN>
F;605-613/Region: protein kinase ATP-binding motif
F;44,88,102,214,291,306,353,370,444,467,478/Binding site: carbohydrate (Asn) (covalent)
F;53-99,148-189,234-290,435-507/Disulfide bonds: #status predicted
F;633/Active site: Lys #status predicted
F;856/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             41.3%;  Score 2336.5;  DB 1;  Length 1098;
  Best Local Similarity   44.1%;  Pred. No. 7.8e-97;
  Matches  498;  Conservative  192;  Mismatches  356;  Indels   83;  Gaps   21;

Qy          6 PAFLVLG-CLLTGLSLILCQLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPMSE 63
Db          8 PALVLRGQLLLSVLWLLGPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPVMW------ 61

Qy         64 EESSDVEIRNEE-NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122
Db         62 EQMSQVPWQEAAMNQDGTFSSVLTLTNVTGGDTGEYFCVYNNSLGPELS-ERKRIYIFVP 120

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVP--ASYDSRQGFNG 180
Db        121 DPTMGFLPMDSEDLFIFVTDVTETTIPCRVTDPQLEVTLHEKKVDIPLHVPYDHQRGFTG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db        181 TFEDKTYICKTTIGDREVDSDTYYVYSLQVSS-INVSVNAVQTVVRQGESITIRCIVMGN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEE--IKVPSIKLVYTLTVPEATVKDSGDYECAARQATRE 298
Db        240 DVVNFQWTYPRMKSGRLVEPVTDYLFGVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

Qy        299 VKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIE 358
Db        299 HGDEKAINISVIENGYVRLLETLGDVEIAELHRSRTLRVVFEAYPMPSVLWLKDNRTLGD 358

Qy        359 N-LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSI 417
Db        359 SGAGELVLSTRNMSETRYVSELILVRVKVSEAGYYTMRAFHEDDEVQLSFKLQVNVPVRV 418

Qy        418 LDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIH 477
Db        419 LEL-SESHPANGEQTIRCRGRGMPQPNVTWSTCRDLKRCPRKLSPTPLGNS--------- 468

Qy        478 SRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAPTLR 522
Db        469 SKEESQLETNVTFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGGDSQEVTVVPHSLP 528

Qy        523 SELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPY 582
Db        529 FKVVVISAILALVVLTVISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPVQLPY 588

Qy        583 DSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALM 642
Db        589 DSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALM 648

Qy        643 SELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK-- 700
Db        649 SELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKHC 708

Qy        701 -PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
Db        709 PPSAELYSNAL-PVGFSLPSHLNLTGESDGGYMDMSKDESIDYVPMLDMKGDIKYADIES 767

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
Db        768 PSYMAPYDNYVPSAPERTYRATLIND-SPVLSYTDLVGFSYQVANGMDFLASKNCVHRDL 826

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
Db        827 AARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTYLPLKWMAPESIFNSLYTTLSDVW 886

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
Db        887 SFGILLWEIFTLGGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFET 946

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDSDNA 987
Db        947 RPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARFPGIHSLRSPLDTSSV 1006

Qy        988 YIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDL--GKRNRHSSQTS 1045
Db       1007 LYTAVQPNE----------------SDNDYIIPLPDPKPDVADEGLPEGSPSLASSTLN 1049

Qy       1046 EESAIETGSSSSTFIKRED----ETIEDIDMMDDIGIDSS-DLVEDSFL 1089
Db       1050 EVNTSSTISCDSPLELQEEPQQAEPEAQLEQPQDSGCPGPLAEAEDSFL 1098


RESULT 7
T30815
platelet-derived growth factor receptor beta - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: T30815
R;How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A;Title: Conserved linkage betwen the pufferfish (Fugu rubripes) and human genes for pla
A;Reference number: Z20882; MUID:97129405; PMID:8973913
A;Accession: T30815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1048 <HOW>
A;Cross-references: UNIPROT:P79749; UNIPARC:UPI00000FCCA5; EMBL:U63926; NID:g1752706; PI
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
```

Query Match 38.6%; Score 2182.5; DB 2; Length 1048;
Best Local Similarity 43.9%; Pred. No. 5.4e-90;
Matches 472; Conservative 175; Mismatches 334; Indels 93; Gaps 25;

```
Qy          9 LVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQ-------YPM 61
              :  |  ||:  : : |       |:| | : ::   || || | | || :|        :
Db         16 VALAALLSSCTTVSCL----KIVPEEKQLILAEGSSLSLTCAGSSETTWDLKSDDVPFFQ 71

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
               : ||||:  :  ::||    :|| :       :| :| |         |:   | : : ::|
Db         72 MKAESSDLNYKIVQSNS--TASVLTLWHVDWKNTAVYQC------REQLTGEIKEVAVFV 123

Qy        122 PDPDVAFVPLGM----TDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPAS--YDSR 175
              ||    | |  :    : : :: :    : :||  |:|   |||:: :  :| :  |
Db        124 PD---RFSPQTLRFIESSHGMVTKTSGESTVPCVVTNPNITVTLYDKDTDLPVNGVYVPS 180

Qy        176 QGFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTC 235
              :||         |:|   : |:  ::  ||||::    ::|  : | :|| | || : | |
Db        181 EGFKAYLDYRTYVCRGELNGEVKESQAFNVYSIHVPEDIDAYVNASQTVLKQGEPLTVNC 240

Qy        236 AVFNNEVVDLQWTYPGE--VKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
              |   |:|   |  |    || |      | : : :  :   |  | |||  || | | |
Db        241 TVQGVELVLFSWDIPNRDIVKHKP----ETVVLSATTMRSCLVFPHATVAHSGTYVCHAH 296

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNN 353
              ::|:: |    | |:| |:||: :| |  |     | |     ||: |||||:| | |:
Db        297 ESTQDQKAFASVNITVLERGFVAVKSTRKQNITAELQENVELRVEIEAYPPPQIRWKKDG 356

Qy        354 LTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQV 413
              :  : | |   : :  |||| : | |:| : |  | || :  ||| ||  || | | ||
Db        357 APVRGDKTII---IRQEHEIRYVTILTLVRVRTEQKGLYTALITNEDDVKEVTFALEVQV 413

Qy        414 PSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETS-WTILAN----- 467
              : | ||  |||      | | | ||| | | |:|  |  : ||||:|| | |
Db        414 LARIKDLT-DHHLPGKKQLVTCVAEGVPTPTIQWYSCDSMLKCNNQTSLWQQLKADPELL 472

Qy        468 NVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLG-AENRELKLVAPTLRSELT 526
              ::   :||  :|  : |  :||| | : |  |||   |  |  : |::|||: :| |::
Db        473 SIHTSVTE--ARQTNQVRSQVTFFKPQHT-TVRCETTNQEGLIDFRDVKLVSSSLFSQVV 529

Qy        527 VAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRW 586
              : | ||  |: |:|:|:|:|: :||||||||||:||||:| ||||||||||: ||||  |
Db        530 LLAVVLTLVPIIIMSIIILIAVWKKKPRYEIRWKVIESVSQDGHEYIYVDPIHLPYDLAW 589

Qy        587 EFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELK 646
              | ||| ||||| |||||||:||| ||:||| ||  :|||||||| ||| || ||||||||
Db        590 EMPRDNLVLGRTLGSGAFGRVVEATAHGLSHSQSSIKVAVKMLKATARRSETQALMSELK 649

Qy        647 IMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELD 706
              ||:|||||||||||| |||| ||:|:::|||| |||||:||||:|: :|| :: :| : :
Db        650 IMSHLGPHLNIVNLLAACTKHGPLYLVTEYCRYGDLVDYLHRNKHTFLQYYLDKNQDDGS 709

Qy        707 IF--GLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDR 764
              :   |  |  :  : ||    |::| |||| : :   |||| |: :  ||:||| | |:
Db        710 LISGGSTPLSQ-RKGYVSFGSESDGGYMDMSKDEPAVYVPMQEQMDTIKYADIQPSPYES 768

Qy        765 PAS---YKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAA 821
              |     |:::      |  ::||  |  ||  ||| |:||||:|||||||||||||||||
Db        769 PYQQDLYQEQG--GGRVDLVISD--SPALTYDDLLGFSYQVAKGMEFLASKNCVHRDLAA 824

Qy        822 RNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSY 881
              ||||: :||:|||||||||||||||:||||||||:|||||||| |||||||||||||||
Db        825 RNVLICEGKLVKICDFGLARDIMHDSNYISKGSTFLPLKWMAPESIFHNLYTTLSDVWSY 884

Qy        882 GILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRP 941
              ||||||||:|||||| : ::  ||: :| ||||||| ||: |||||| :||:   ||||
Db        885 GILLWEIFTLGGTPYPDLPMNELFYSPLKRGYRMAKPAHASDEVYEIMKRCWDETFEKRP 944

Qy        942 SFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAY-----------I 989
              |  |   | ::|   ||| | :::  ||||||||||| :    : :             :
Db        945 DFSFLVHCVGDMLTDSYKKKYSQVNETFLKSDHPAVARTKPRLSSPFPIANPAFGSPSLV 1004

Qy        990 GVT-----------YKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEE 1031
                 |::           ::|| :         :: ::: : ||||:|  || ||:
Db       1005 GLSDFPDPYNQNTRRFRNEAEV---------QEGVTSFNEYIIPIP--DPKPEK 1047
```

RESULT 8
S44269
platelet-derived growth factor receptor alpha - zebra fish (fragment)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 05-Oct-2004
C;Accession: S44269
R;Yu, W.; Richardson, W.D.
submitted to the EMBL Data Library, April 1994
A;Description: Zebrafish Platelet-derived Growth Factor Receptor (Alpha subunit), partial
A;Reference number: S44269
A;Accession: S44269
A;Molecule type: mRNA
A;Residues: 1-457 <YUW>
A;Cross-references: UNIPROT:Q90269; UNIPARC:UPI00000FB8B0; EMBL:Z32814; NID:g479105; PIDN
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; autophosphorylation; dimer; glycoprotein; growth factor receptor; phospho
F;1-327/Domain: protein kinase homology (fragment) <KIN>

Query Match 33.9%; Score 1914.5; DB 2; Length 457;
Best Local Similarity 79.2%; Pred. No. 1.7e-78;
Matches 365; Conservative 48; Mismatches 41; Indels 7; Gaps 5;

```
Qy        630 KPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKN 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKN 62

Qy        690 RDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERK 749
              || ||| | || ||:|||||:||||||:|||||||||  |||||||||||| |||||||
Db         63 RDGFLSRHTEKGKKDLDIFGINPADESSRSYVILSFEGKGDYMDMKQADTMQYVPMLEMN 122

Qy        750 EVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFL 809
              | |||| |||| || | |:::    : | ::|||||::|||| :|||||||||||||||
Db        123 EASKYSPIQRSDYDHPPSHRQ---FNDEAESLLSDDSAEGLTTMDLLSFTYQVARGMEFL 179

Qy        810 ASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFD 869
              |||||||||||||||:||||||||||||||||||:||||||||||||||||||||||||||
Db        180 ASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPVKWMAPESIFD 239

Qy        870 NLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIM 929
              |||||||||||||||||||||||||||||:|||:|||||||||| ||:||:|:|||:|
Db        240 NLYTTLSDVWSYGILLWEIFSLGGTPYPGMVVDSSFYNKIKSGYRMTKPEHASSDVYELM 299

Qy        930 VKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-VDSDNAY 988
              :|||||||||||: ||: | :|||  :|: ||::: |||||||| |:: :|:|:||
Db        300 MKCWNSEPEKRPSFHSLSDTVASLLPSGFKRCYERVNHDFLKSDHPAVTRVQCIDNDDAY 359

Qy        989 IGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEES 1048
              :|| ||| : |:|: | | |||||||:||||||||:||:   ||  ||||||||||||||
Db        360 MGVLYKN-QGKMKNRESGFDEQRLSSDSGYIIPLPDLDPL-SNEDYSKRNRHSSQTSEES 417

Qy       1049 AIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||:|||||||  ||| ||:||| ::|:: :|| ||||||||
Db        418 AIDTGSSSST-TKREGETLEDITLLDEMCLDSGDLVEDSFL 457
```

RESULT 9
I45877
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs
C;Species: Bos primigenius (aurochs)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 05-Oct-2004
C;Accession: I45877
R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.
Gene 141, 305-306, 1994
A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.
A;Reference number: I45877; MUID:94215924; PMID:7512939
A;Accession: I45877
A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Molecule type: mRNA
A;Residues: 1-977 <KUB>
A;Cross-references: UNIPARC:UPI000012DEB2; GB:D16680; NID:g516659; PIDN:BAA04084.1; PID:
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;329-395/Domain: immunoglobulin homology <IMM>
F;588-932/Domain: protein kinase homology <KIN>

  Query Match             26.2%;  Score 1481.5;  DB 2;  Length 977;
  Best Local Similarity   36.4%;  Pred. No. 9e-59;
  Matches  366;  Conservative  150;  Mismatches  368;  Indels  121;  Gaps   30;

Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
              :|||||| | ::| :| :     | |     | | : :  : |         |  :  ::|
Db         33 ELSLPSIHPAKSELIVSVGDEIRLLCTDPGFVKWTFEILGQLS--------EKTNPEWIT 84

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
              | | :|| |||      | :  |    ||::| ||:  |    : |  :  :::
Db         85 ----EKAEATNTGNYTC------TNKGGLSS-SIYVFVRDPEKLF----LIDLPLYGKEE 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
              :  :: |  |||| |  :|   ||  |   |       ||   |
Db        130 NDTLVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNV---YALKATSELDLEMEALKTVY--KSGETIVVTCAVFN- 239
                 | | :||   :  | :     |:||   : :     || |  : ||   ||| : :
Db        183 CLHCSANQRGKSMLSKKFTLKVRAAIKAVPVVSVS----KTSYLLREGEEFAVTCLIKDV 238

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLV--YTLTVPEATVKDSGDYECAARQATR 297
              :  ||  |      : | |           :    ||:  | | ||| : | |
Db        239 SSSVDSMWIKENSQQTKAQTKKNSWHQGDFSYLRQERLTISSARVNDSGVFMCYANNTFG 298

Qy        298 EVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPP-RISWLKNNLTL 356
                  |: | :|||| | |  :    ||  |    |||  ||| |    |:  | |
Db        299 SAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGENVDLVVEYEAYPKPVHRQWIYMNRTS 356

Qy        357 IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSS 416
              :   :    |   ||| ::| | | |  : | ||    | |    | || :
Db        357 TDKWDDYPKS-ENESNIRYVNELHLTRLKGTEGGTYTFHVSNSDVNSSVTFNVYVNTKPE 415

Qy        417 ILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTILANNVSNIITE 475
              ||     |      ::| | | | | |:|  |    ::|:                |  :
Db        416 ILT-----HDRLVNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP---------VGPVDVQ 461

Qy        476 IHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE----------NRELKLVAPT 520
              | :   |      | :: ::::       | | | | :|              | : :: | |
Db        462 IQNSSVSPFGKLVVYSTIDDSTFKHNGTVECRAYNDVGKSSASFNFAFKGNSKEQIHAHT 521

Qy        521 LRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQL 580
              | : | :   :   |: : :  ::|    : ||| ||::|:|:| |  :|: |:|:|| ||
Db        522 LFTPLLIGFVIAAGLMCIFV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQL 577

Qy        581 PYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQA 640
              ||| :|||||: |  |: ||:|||||||| |||||  :|   | ||||||||:|  .:|::|
Db        578 PYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREA 637

Qy        641 LMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK 700
              ||||||::::|| |:|||||||||||  ||  :|||||  ||||:|:| : ||||:    |
Db        638 LMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQED 697

Qy        701 PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRS 760
              :       |  : ||: :       ::  :|||||       ||       |   :| :||
Db        698 HAEVALYKNLLHSKESSCN------DSTNEYMDMKPG--VSYV-------VPTKADKRRS 742

Qy        761 LYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLA 820
              |  ||     :: :|   : :|:   | | |||||:||||:|| |||||||:|||||
Db        743 A--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLA 795

Qy        821 ARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWS 880
              |||:||  |:| ||||||||||| :||||| ||:  ||||||||||||: :||  |||||
Db        796 ARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWS 855

Qy        881 YGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKR 940
```

```
              ||| |||:|||| :|||||  ||| ||  || |:||  |:|| :|:|:||  ||:::| ||
Db        856 YGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKR 915

Qy        941 PSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
              |:|  : :::|  :       |  :       ::|||   :|::|
Db        916 PTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 960


RESULT 10
JN0677
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - chicken
N;Alternate names: tyrosine kinase receptor kit
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: JN0677
R;Sasaki, E.; Okamura, H.; Chikamune, T.; Kanai, Y.; Watanabe, M.; Naito, M.; Sakurai, M
Gene 128, 257-261, 1993
A;Title: Cloning and expression of the chicken c-kit proto-oncogene.
A;Reference number: JN0677; MUID:93292995; PMID:7685729
A;Accession: JN0677
A;Molecule type: mRNA
A;Residues: 1-960 <SAS>
A;Cross-references: UNIPROT:Q08156; UNIPARC:UPI000012DEB5; DDBJ:D13225; NID:g303532; PID:
A;Experimental source: brain
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
rotein kinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-960/Product: tyrosine kinase receptor #status predicted <MAT>
F;314-380/Domain: immunoglobulin homology <IMM>
F;573-916/Domain: protein kinase homology <KIN>
F;581-589/Region: protein kinase ATP-binding motif
F;76,135,149,269,286,306,318,338,356,453,469/Binding site: carbohydrate (Asn) (covalent)

  Query Match             25.9%;  Score 1461.5;  DB 1;  Length 960;
  Best Local Similarity   36.1%;  Pred. No. 6.9e-58;
  Matches  365;  Conservative  148;  Mismatches  359;  Indels  139;  Gaps   30;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |  :| |: :   :|  ||||    |:|     |:  ||       |:|  |  |:| :
Db          1 MEGAHLAWELAHAVLL-LSLIPAGGSVPH---EESSLVVNKGEELRLKCNEEGPVTWNF- 55

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEG---RHI 117
                : : |:   | ||:             :|:    | | |          : :|
Db         56 QNSDPSAKTRISNEKE--------WHTKNATIRDIGRYEC----------KSKGSIVNSF 97

Qy        118 YIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPET-PVTLHNSEG-VVPASYDSR 175
              |::| ||:| |    : | |:  ::|   :: |  |||:    ||   :|  :|
Db         98 YVFVKDPNVLF----LVDSLIYGKEDSDILLVCPLTDPDVLNFTLRKCDGKPLPK----- 148

Qy        176 QGFNGTFTVGP---------------YICEATVKG--KKFQTIPFNVYAL-KATSELDL 216
                 | ||   |               | | |   |  |  : |  ||  : ||   : |
Db        149 ---NMTFIPNPQKGIIIKNVQRSFKGCYQCLAKHNGVEKISEHIFLNVRPVHKALPVITL 205

Qy        217 EMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLV---- 272
                    : | ||   |||  : :   ||        ||   |:    |     : :
Db        206 SKS--YELLKEGEEFEVTCIITD---VD------SSVKASWISYKSAIVTSKSRNLGDYG 254

Qy        273 ----YTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVN 328
                  ||  :   | |||:: | |       |    ||:    |||: :  | :    :|
Db        255 YERKLTLNIRSVGVNDSGEFTCQAENPFG--KTNATVTLKALAKGFVRLFATMNTTIDIN 312

Qy        329 LHEVKHFVVEVRAYPPPRIS-WLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEE 387
                :  :  ||  ||| |:   |:  | || :| ::     : :    | |:| | | |
Db        313 AGQNGNLTVEYEAYPKPKEEVWMYMNETL-QNSSDHYVKFKTVGNNSYTSELHLTRLKGT 371

Qy        388 DSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEW 447
              : | ||    | ||  | || :  :    || |         |   ::| | | | | | |
Db        372 EGGIYTFFVSNSDASSSVTFNVYVKTKPEILTL-----DMLGNDILQCVATGFPAPTIYW 426

Qy        448 MICKDI-KKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNL 506
                |    ::| :  : : :   ||   : : | :|  ||  |  :  : |  : | |
Db        427 YFCPGTEQRCLDSPTISPMDVKVSYTNSSVPSFERILVESTVNASMFKSTGTICCEA--- 483
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Qy        507 LGAENRELKLV----------APTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRY 555
Db        484 --SSNGDKSSVFFNFAIKEQIRTHTLFTPLLIAFGVAAGLMCIIV--MILVYIYLQKPKY 539

Qy        556 EIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGL 615
Db        540 EVQWKVVEEI--NGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGL 597

Qy        616 SRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITE 675
Db        598 FKSDAAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHINIVNLLGACTIGGPTLVITE 657

Qy        676 YCFYGDLVNYLHKNRDSFL----SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDY 731
Db        658 YCCYGDLLNFLRRKRDSFICPKHEEHAEAAVYENLLHQAEPTADAV----------NEY 706

Qy        732 MDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLT 791
Db        707 MDMKPGVSYAVPPKADKK-------------RPV--KSGSYTDQDVTLSMLEDDELALD 750

Qy        792 LLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVS 851
Db        751 VEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNYVV 810

Qy        852 KGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKS 911
Db        811 KGNARLPVKWMAPESIFNCVYTFESDVWSYGILLWELFSLGSSPYPGMPVDSKFYKMIKE 870

Qy        912 GYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962
Db        871 GYRMFSPECSPPEMYDIMKSCWDADPLQRPTFKQIVQLIEQQLSDNAPRVY 921
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RESULT 11
A49814
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A49814; S49088
R;Tsujimura, T.; Hirota, S.; Nomura, S.; Niwa, Y.; Yamazaki, M.; Tono, T.; Morii, E.; Ki
Blood 78, 1942-1946, 1991
A;Title: Characterization of Ws mutant allele of rats: a 12-base deletion in tyrosine ki
A;Reference number: A49814; MUID:92003944; PMID:1912577
A;Accession: A49814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-978 <TSU>
A;Cross-references: UNIPROT:Q63116; UNIPARC:UPI00000E6323; GB:D12524; NID:g220707; PIDN:
R;Tsujimura, T.; Tono, T.; Yamazaki, M.; Nomura, S.; Kitamura, Y.
submitted to the EMBL Data Library, October 1991
A;Description: Two isoforms of rat c-kit receptor tyrosine kinase.
A;Reference number: S49088
A;Accession: S49088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511,516-978 <TS2>
A;Cross-references: UNIPARC:UPI00000E7246; EMBL:X62491; NID:g509135; PIDN:CAA44354.1; PI
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; phosphotransferase; tyrosine-specific protein kina
F;129-188/Domain: immunoglobulin homology <IMM>
F;589-932/Domain: protein kinase homology <KIN>
F;597-605/Region: protein kinase ATP-binding motif

  Query Match   25.8%; Score 1458; DB 1; Length 978;
  Best Local Similarity   35.9%; Pred. No. 1e-57;
  Matches 365; Conservative 152; Mismatches 353; Indels 146; Gaps   30;

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Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIQPAQSELIVEAGDTIRLTCTDPAFVKWTF-----EILDVRIENKQSE-----WIR 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEG----RHIYIYVPDPDVAFVPLGMTDYLVIVE 141
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Db         85 E--KAEATHTGKYTC----------VSGSGLRSSIYVFVRDPAVLFL-VGLP---LFGK 127

Qy        142 DDDSAIIPCRTTDPE-TPVTLHNSEG--------VVPASYDSRQGFNGTFTVGPY----- 187
Db        128 EDNDALVRCPLTDPQVSNYSLIECDGKSLPTDLKFVP---NPKAGITIKNVKRAYHRLCI 184

Qy        188 ICEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVDL 245
Db        185 RCAAQREGKWMRSDKFTLKVRAAIKAIPVVSVPETSHLLKEGDTFTVICTIKDVSTSVDS 244

Qy        246 QWTYPGEVKGKGITMLEEIKV---PSIKLVY---------------TLTVPEATVKDSG 286
Db        245 MW---------------IKLNPQPQSKAQVKRNSWHQGDFNYERQETLTISSARVNDSG 288

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
Db        289 VFMCYANNTFGSAN--VTTTLKVVEKGFINIFPVKNTTVFVTDGENVDLVVEFEAYPKPE 346

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
Db        347 HQQWIYMNRT-PTNRGEDYVKSDNQSNIRYVNELRLTRLKGTEGGTYTFLVSNSDVSASV 405

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTIL 465
Db        406 TFDVYVNTKPEILTYDRLMNG-----RLQCVAAGFPEPTIDWYFC-----TGAEQRCTV- 454

Qy        466 ANNVSNIITEIHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE---------- 510
Db        455 --PVPPVDVQIQNASVSPFGKLVVQSSIDSSVFRHNGTVECKASNAVGKSSAFFNFAFKG 512

Qy        511 NRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGH 570
Db        513 NSKEQIQPHTLFTPLLIGFVVTAGLMGIIV--MVLAYKYLQKPMYEVQWKVVEEI--NGN 568

Qy        571 EYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLK 630
Db        569 NYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLK 628

Qy        631 PTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNR 690
Db        629 PSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKR 688

Qy        691 DSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKE 750
Db        689 DSFIFSKQEEQADAALYKNLLHSKES-------SCDSSNEYMDMKPG-VSYVVP------ 734

Qy        751 VSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLA 810
Db        735 ---------TKTDKRRSARIDSYIERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLA 785

Qy        811 SKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDN 870
Db        786 SKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFNC 845

Qy        871 LYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMV 930
Db        846 VYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAAMYEVMK 905

Qy        931 KCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984
Db        906 TCWDADPLKRPTFKQVVQLIEKQISDSSKHIYSNLANCNPNPENPVVVDHSVRVNS 961
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RESULT 12
TVHUKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - human
N;Alternate names: mast/stem cell growth factor receptor; tyrosine kinase receptor c-kit
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-Oct-2004
C;Accession: S01426; PC1015; A41815; B41815; C41815; I37948; I56954; I54336
R;Yarden, Y.; Kuang, W.J.; Yang-Feng, T.; Coussens, L.; Munemitsu, S.; Dull, T.J.; Chen,
EMBO J. 6, 3341-3351, 1987

```
A;Title: Human proto-oncogene c-kit: a new cell surface receptor tyrosine kinase for an
A;Reference number: S01426; MUID:88111521; PMID:2448137
A;Accession: S01426
A;Molecule type: mRNA
A;Residues: 1-976 <YAR>
A;Cross-references: UNIPROT:P10721; UNIPARC:UPI000003F17D; GB:X06182; NID:g34084; PIDN:C
R;Hu, W.X.; Cornu, F.; Andre, C.; Galibert, F.
Chinese Biochem. J. 7, 618-629, 1991
A;Title: Nucleotide sequece of two neighbouring fragments of human c-kit proto-oncogene
A;Reference number: PC1015
A;Accession: PC1015
A;Molecule type: DNA
A;Residues: 412-713 <HUW>
A;Cross-references: UNIPARC:UPI00001725B3
A;Note: article in Chinese with English abstract
R;Spritz, R.A.; Giebel, L.B.; Holmes, S.A.
Am. J. Hum. Genet. 50, 261-269, 1992
A;Title: Dominant negative and loss of function mutations of the c-kit (mast/stem cell g
A;Reference number: A41815; MUID:92133600; PMID:1370874
A;Accession: A41815
A;Molecule type: DNA
A;Residues: 579-583,'L',585-589 <SPR>
A;Cross-references: UNIPARC:UPI000011F7BF; GB:S78839; NID:g244084; PIDN:AAB21234.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78839, NCBIP:78842)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: B41815
A;Molecule type: DNA
A;Residues: 637-641,'SPELPW' <SP2>
A;Cross-references: UNIPARC:UPI000011F7C0; GB:S78843; NID:g244086; PIDN:AAB21235.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78843, NCBIP:78844)
A;Note: disease-related mutant from patient with piebaldism
A;Accession: C41815
A;Molecule type: DNA
A;Residues: 556-560,'GGDKWK' <SP3>
A;Cross-references: UNIPARC:UPI000011F7C1; GB:S78845; NID:g244088; PIDN:AAB21236.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:78845, NCBIP:78846)
A;Note: disease-related mutant from patient with piebaldism
R;Giebel, L.B.; Strunk, K.M.; Holmes, S.A.; Spritz, R.A.
Oncogene 7, 2207-2217, 1992
A;Title: Organization and nucleotide sequence of the human KIT (mast/stem cell growth fa
A;Reference number: I37948; MUID:93064697; PMID:1279499
A;Accession: I37948
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-976 <RES>
A;Cross-references: UNIPARC:UPI000003F17D; EMBL:X69301; NID:g34089; PIDN:CAA49159.1; PID
A;Note: an alternative splice form omitting residues 510-513 is described
R;Yamamoto, K.; Tojo, A.; Aoki, N.; Shibuya, M.
Jpn. J. Cancer Res. 84, 1136-1144, 1993
A;Title: Characterization of the promoter region of the human c-kit proto-oncogene.
A;Reference number: I56954; MUID:94103107; PMID:7506248
A;Accession: I56954
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RE2>
A;Cross-references: UNIPARC:UPI00000737F3; GB:S67773; NID:g459358; PIDN:AAB29529.1; PID:
R;Spritz, R.A.; Holmes, S.A.; Berg, S.Z.; Nordlund, J.J.; Fukai, K.
Hum. Mol. Genet. 2, 1499-1500, 1993
A;Title: A recurrent deletion in the KIT (mast/stem cell growth factor receptor) proto-c
A;Reference number: I54336; MUID:94061059; PMID:7694728
A;Accession: I54336
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 242-250 <RE3>
A;Cross-references: UNIPARC:UPI0000072C21; GB:S67686; NID:g460545; PIDN:AAD13996.1; PID:
C;Genetics:
A;Gene: GDB:KIT
A;Cross-references: GDB:120117; OMIM:164920
A;Map position: 4q12-4q12
A;Introns: 23/1; 113/1; 207/1; 252/3; 309/1; 372/2; 411/1; 449/2; 514/1; 549/3; 592/1; 6
A;Note: defects in this gene may result in piebaldism
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related
rotein; tyrosine-specific protein kinase
F;1-976/Product: protein-tyrosine kinase kit precursor, long form #status predicted <MAT
F;1-509,514-976/Product: protein-tyrosine kinase kit precursor, short form #status predi
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-976/Product: protein-tyrosine kinase kit #status predicted <MAT>
F;23-520/Domain: extracellular #status predicted <EXT>
F;51-99/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;226-292/Domain: immunoglobulin homology <IMM3>
F;328-394/Domain: immunoglobulin homology <IMM4>
F;423-493/Domain: immunoglobulin homology <IMM5>
F;521-543/Domain: transmembrane #status predicted <TMM>
F;544-976/Domain: intracellular #status predicted <INT>
F;587-931/Domain: protein kinase homology <KIN>
F;595-603/Region: protein kinase ATP-binding motif
F;58-97,136-186,233-290,428-491/Disulfide bonds: #status predicted
F;130,145,283,293,300,320,352,367,463,486/Binding site: carbohydrate (Asn) (covalent) #s
F;623,640,792/Active site: Lys, Glu, Asp #status predicted
F;797,810/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             25.7%;  Score 1454.5;  DB 1;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-57;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::: :|::     | |     | | : : :|          ||    ::|
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                | | :|| |||   | :          ||::| ||    |    : | :  ::|:
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               :: |  |||| |  :|   :|  |   | |       |   |
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
               |    :||   :  | :    | ||   : :   :   : : ||   ||| : :
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
                    |   ||  |      |             : :   |||:  | | ||| : | |
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
                       |: | :|||| | |  :    ||  |    :||  |:| |    |:
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
               | | :   :     |    ||| |:| | | |  : | || :  | |   :  | :
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
                 ||    ||:          ::| | | | | |:|  |   ::     | ::|  :
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
               |  : :     :  |:  :  :  :    | | | | :|           | : ::
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
               || : | :   ::  :: :|:  ::|   : ||| ||::|:|:| |  :|: |:|:||
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
               ||||| :|||||: |  |: ||:|||||||| ||||| :|   | ||||||||:|  :|:
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
               :|||||||::::|| |:|||||||||||  ||  :|||| ||||:|:| : ||||:
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694
```

```
Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939
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RESULT 13
TVMSKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N;Alternate names: tyrosine kinase receptor c-kit
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-Oct-2004
C;Accession: S00474; B44876; I49596
R;Qiu, F.; Ray, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Besmer, P.
EMBO J. 7, 1003-1011, 1988
A;Title: Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase fa
A;Reference number: S00474; MUID:88296403; PMID:2456920
A;Accession: S00474
A;Molecule type: mRNA
A;Residues: 1-975 <QIU>
A;Cross-references: UNIPROT:P05532; UNIPARC:UPI000002852E; GB:Y00864; NID:g50423; PIDN:C
R;Rossi, P.; Marziali, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A;Title: A novel c-kit transcript, potentially encoding a truncated receptor, originates
A;Reference number: A44876; MUID:92331813; PMID:1378413
A;Accession: B44876
A;Molecule type: DNA
A;Residues: 771-814 <ROS>
A;Cross-references: UNIPARC:UPI00001725B4
A;Note: sequence extracted from NCBI backbone (NCBIN:108837, NCBIP:108840)
R;Yasuda, H.; Galli, S.J.; Geissler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A;Title: Cloning and functional analysis of the mouse c-kit promoter.
A;Reference number: I49596; MUID:93221533; PMID:7682073
A;Accession: I49596
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: UNIPARC:UPI00000003B6; GB:L11358; NID:g293325; PIDN:AAA37420.1; PID:
C;Genetics:
A;Gene: kit; c-kit
A;Map position: 5
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-975/Product: protein-tyrosine kinase kit #status predicted <KTC>
F;23-519/Domain: extracellular #status predicted <EXT>
F;51-100/Domain: immunoglobulin homology <IMM1>
F;130-189/Domain: immunoglobulin homology <IMM2>
F;227-295/Domain: immunoglobulin homology <IMM3>
F;331-397/Domain: immunoglobulin homology <IMM4>
F;426-496/Domain: immunoglobulin homology <IMM5>
F;520-542/Domain: transmembrane #status predicted <TMM>
F;543-975/Domain: intracellular #status predicted <INT>
F;586-929/Domain: protein kinase homology <KIN>
F;594-602/Region: protein kinase ATP-binding motif

F;58-98,137-187,234-293,431-494/Disulfide bonds: #status predicted
F;146,296,303,323,355,370,466,489/Binding site: carbohydrate (Asn) (covalent) #status pre
F;622,639,790/Active site: Lys, Glu, Asp #status predicted
F;795,808/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.6%; Score 1446.5; DB 1; Length 975;
Best Local Similarity 35.7%; Pred. No. 3.3e-57;
Matches 357; Conservative 152; Mismatches 374; Indels 117; Gaps 29;

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Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPAQSELIVEAGDTLSLTCIDPDFVRWTFKTYFNEM----VENKKNE-----WIQ 85

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         86 E--KAEATRTGTYTCSNSNGLTSS-------IYVFVRDPAKLFL-VGLP---LFGKEDSD 132

Qy        146 AIIPCRTTDPE-TPVTLHNSEG-VVPASYDSRQGFNGTFTVGPYI--------------- 188
Db        133 ALVRCPLTDPQVSNYSLIECDGKSLPTDL--------TFVPNPKAGITIKNVKRAYHRLC 184

Qy        189 --CEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVD 244
Db        185 VRCAAQRDGTWLHSDKFTLKVREAIKAIPVVSVPETSHLLKKGDTFTVVCTIKDVSTSVN 244

Qy        245 LQW-------TYPGEVK----GKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
Db        245 SMWLKMNPQPQHIAQVKHNSWHRGDFNYERQE--------TLTISSARVDDSGVFMCYAN 296

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKN 352
Db        297 NTFGSAN--VTTTLKVVEKGFINISPVKNTTVFVTDGENVDLVVEYEAYPKPEHQQWIYM 354

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412
Db        355 NRTSANKGKDYVKSDNK-SNIRYVNQLRLTRLKGTEGGTYTFLVSNSDASASVTFNVYVN 413

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETS-WTILANNVS 470
Db        414 TKPEILTYDRLING-----MLQCVAEGFPEPTIDWYFCTGAEQRCTTPVSPVDVQVQNVS 468

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
Db        469 -----VSPFGKLVVQSSIDSSVFRHNGTVECKASNDVGKSSAFFNFAFKEQIQAHTLFTP 523

Qy        531 VLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRW 586
Db        524 LLIGFVVAAGAMGIIVMVLTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDHKW 581

Qy        587 EFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELK 646
Db        582 EFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELK 641

Qy        647 IMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELD 706
Db        642 VLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFISFSKQEEQAEAAL 701

Qy        707 IFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPA 766
Db        702 YKNLLHSTEP-------SCDSSNEYMDMKPG-VSYVVP--------------TKTDKRR 738

Qy        767 SYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLL 826
Db        739 SARIDSYIERDVTPAIMEDDELALDLDDLLSFSYQVAKAMAFLASKNCIHRDLAARNILL 798

Qy        827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLW 886
Db        799 THGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFSCVYTFESDVWSYGIFLW 858

Qy        887 EIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHL 946
Db        859 ELFSLGSSPYPGMPVDSKFYKMIKEGFRMVSPEHAPAEMYDVMKTCWDADPLKRPTFKQV 918
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Qy        947 SEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984
Db        919 VQLIEKQISDSTKHIYSNLANCNPNPENPVVVDHSVRVNS 958


RESULT 14
I51703
c-kit-related kinase 1 (XKrk1) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004
C;Accession: I51703
R;Baker, C.V.; Sharpe, C.R.; Torpey, N.P.; Heasman, J.; Wylie, C.C.
Mech. Dev. 50, 217-228, 1995
A;Title: A Xenopus c-kit-related receptor tyrosine kinase expressed in migrating stem ce
A;Reference number: I51703; MUID:95344996; PMID:7619732
A;Accession: I51703
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-954 <BAK>
A;Cross-references: UNIPROT:Q91909; UNIPARC:UPI00000FB397; EMBL:Z48770; NID:g763033; PID
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP
F;575-915/Domain: protein kinase homology <KIN>
F;583-591/Region: protein kinase ATP-binding motif

  Query Match             25.1%;  Score 1416.5;  DB 2;  Length 954;
  Best Local Similarity   36.4%;  Pred. No. 6.9e-56;
  Matches  361;  Conservative  157;  Mismatches  368;  Indels  107;  Gaps   32;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMS--EEESSDVEIR--NEENNSGLF 81
Db         19 AVPKINDGEDRVTVNVGDKVSLECRDAHLVTLAFQKSGLMKKPRDLKSRPLNNSETDQFF 78

Qy         82 VTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVE 141
Db         79 VII----KADLRHIGRYIC--TNTETQEN----TSVSLFVKDPARPFLDIPFID----VT 124

Qy        142 DDDSAIIPCRTTDPETPVTLHNSEG-VVPASYDSRQGFNGTFTV--------GPYICEAT 192
Db        125 EGADTVGMCFPTDPDMDIAIEKCDGSPLPENFTFTTDIEAGITIKTVQLAFDSCYVCSGN 184

Qy        193 VKGKKFQTIPFNVYALKATSEL-DLEMEALKTVYKSGETIVVTCAVFN-NEVVDLQWTYP 250
Db        185 KSGTVKKSSTFSIHVKPVPKKVPTVFLSKSRQLVKTGEPFEVTCAVLDVFSTVKAQWL-- 242

Qy        251 GEVKGKGITMLEEIKVPSIKLVYTLTVPEATV--KDSGDYECAARQATREVKEMKKVTIS 308
Db        243 -DVK-EGVTKQANFRSSNV-FSYNLTLKSDGVPYSESRTFTCQAENAIGQVN--ATFTLD 297

Qy        309 VHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRIS-WLKNNLTLIENLTEITTDV 367
Db        298 VIDVGYVNLTVLENTTISVNAGDNLVLKVYIDAYPHPDDGVWTYFNETLL-NTSDHYVAT 356

Qy        368 EKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGS 427
Db        357 KDEGNNRYVSELHLIRLKGTEKGVYTFYTTNSDDDASVSFNIQVKTRPEILIAERTSEG- 415

Qy        428 TGGQTVRCTAEGTPLPDIEWMICK-DIKKCNNETSWTILANNVSNIITEIHSRDRSTVEG 486
Db        416 ----TLQCVATGFPVPAIQWYFCPGSEQRC---TDYPPLSPVNEKFIQENSSLGRIVVES 468

Qy        487 RVTFAKVEETIAVRCLAKNLLGAENR------ELKLVAPTLRSELT---VAAAVLVLLVI 537
Db        469 TIDVNDLKKNGTVQCVASNEVESAYSVFSFAIKEKLRTHTLFTPLLIGFIAAAGL----- 523

Qy        538 VIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGR 597
Db        524 MCIAVAVLMYKYLQKPKYEIQWKVVEEI--NGNNYVYIDPTQLPYDNKWEFPRDRLCFGK 581

Qy        598 VLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNI 657
Db        582 ILGAGAFGKVVEATAYGLLKEDSRLTVAVKMLKPSAHSTEREALMSELKVLSYLGHHKNI 641

Qy        658 VNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPK----KELDIFG--LN 711
Db        642 VNLLGACTVGGPTLVITEYCCYGDLLNYLRRKRDSFIC-----PKFEDNSEAALYKNLLN 696

Qy        712 PADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKK 771
Db        697 TRD--------MGCEGMSEYIDMKPA--VSYV-------VPTKTDKRRS----------G 729

Qy        772 SMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKI 831
Db        730 SFGDQDVSVSIPEEDDLALDTEDLINFSYQVAQGMNFLASKNCIHRDLAARNILLTHGRI 789

Qy        832 VKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSL 891
Db        790 TKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFHCVYTFESDVWSYGILLWEIFSL 849

Qy        892 GGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVE 951
Db        850 GSSPYPRIPVDSKFYKMIKDGYRMMSPECAPLEMYEIMRSCWNSDPLKRPTFKQIVQMVE 909

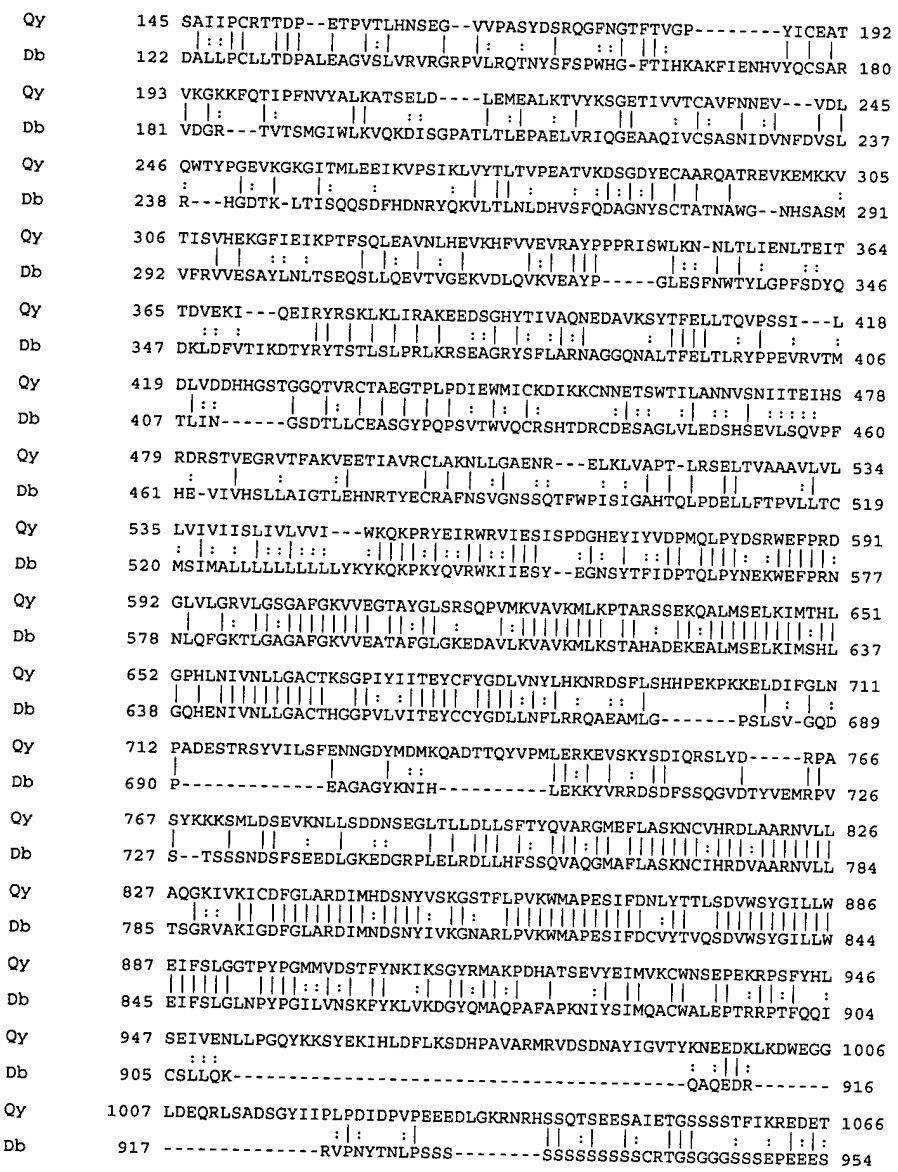
Qy        952 NLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDS 984
Db        910 Q----QLSDSKGNTPLPYPVSHVPLDHAVRINS 938


RESULT 15
TVCTMD
macrophage colony-stimulating factor 1 receptor precursor - cat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Felis silvestris catus (domestic cat)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 05-Oct-2004
C;Accession: A31636
R;Woolford, J.; McAuliffe, A.; Rohrschneider, L.R.
Cell 55, 965-977, 1988
A;Title: Activation of the feline c-fms proto-oncogene: multiple alterations are require
A;Reference number: A31636; MUID:89077553; PMID:2849512
A;Accession: A31636
A;Molecule type: mRNA
A;Residues: 1-980 <WOO>
A;Cross-references: UNIPROT:P13369; UNIPARC:UPI000012DDB9; EMBL:X03663
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-980/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;24-509/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TMM>
F;535-980/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase homology <KIN>
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F;45,73,94,153,275,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #statu
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             25.0%;  Score 1412.5;  DB 1;  Length 980;
  Best Local Similarity   33.2%;  Pred. No. 1.1e-55;
  Matches  359;  Conservative  180;  Mismatches  356;  Indels  185;  Gaps   33;

Qy         27 LPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLE 86
Db         20 VPVIQPSGPELVVEPGTTVTLRCVGNGSVEWDGPISPHWNLDLDPPS---------SILT 70

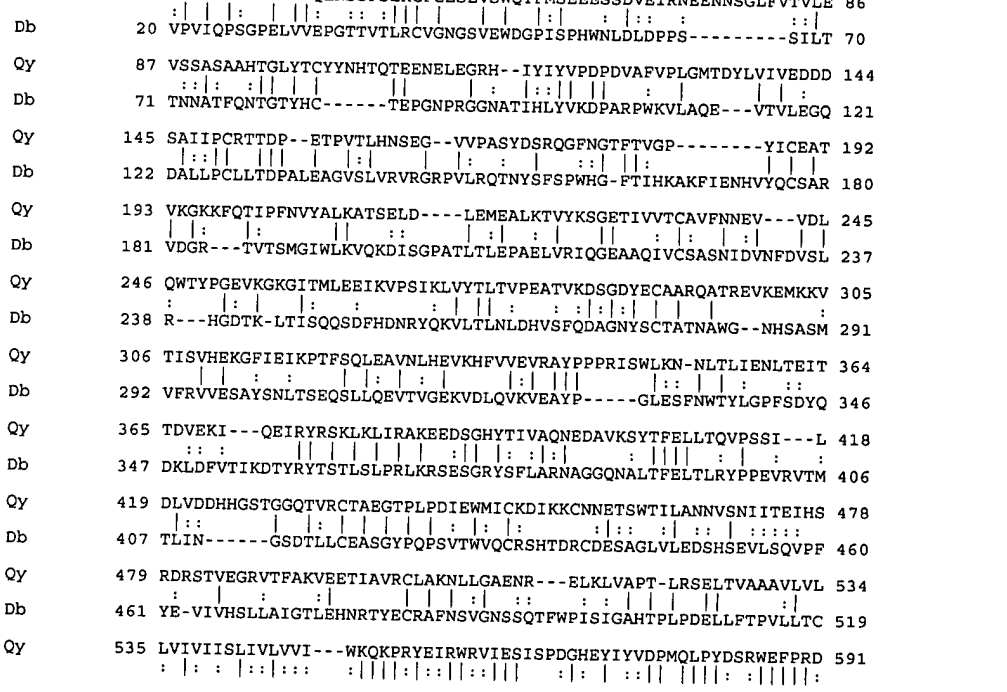
Qy         87 VSSASAAHTGLYTCYYNHTQTEENELEGRH--IYIYVPDPDVAFVPLGMTDYLVIVEDDD 144
Db         71 TNNATFQNTGTYHC------TEPGNPQGGNATIHLYVKDPARPWKVLAQE---VTVLEGQ 121
```



RESULT 16
TVMVMD
protein-tyrosine kinase (EC 2.7.1.112) fms precursor - feline sarcoma virus (strain McDo
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: A00654

R;Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 85-89, 1984
A;Title: Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected ho
A;Reference number: A00654; MUID:84119469; PMID:6582485
A;Accession: A00654
A;Molecule type: DNA
A;Residues: 1-941 <HAM>
A;Cross-references: UNIPROT:P00545; UNIPARC:UPI00001725B1
C;Comment: This protein is synthesized as a gag-fms polyprotein.
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein,
otein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-941/Product: protein-tyrosine kinase fms #status predicted <MAT>
F;24-509/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-484/Domain: immunoglobulin homology <IMM5>
F;510-534/Domain: transmembrane #status predicted <TMM>
F;535-941/Domain: intracellular #status predicted <INT>
F;577-915/Domain: protein kinase homology <KIN>
F;585-593/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-482/Disulfide bonds: #status predicted
F;45,73,94,153,275,286,302,335,410,477,490/Binding site: carbohydrate (Asn) (covalent) #s
F;613,630,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 24.8%; Score 1400.5; DB 1; Length 941;
Best Local Similarity 35.9%; Pred. No. 3.5e-55;
Matches 346; Conservative 165; Mismatches 339; Indels 115; Gaps 30;



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Db        520 MSIMALLLLLLLLLLYKYKQKPKYQVRWKIIESY--EGNSYTFIDPTQLPYNEKWEFPRN 577

Qy        592 GLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHL 651

Db        578 NLQFGKTLGTGAFGKVVEATAFGLGKEDAVLKVAVKMLKSTAHADEKEALMSELKIMSHL 637

Qy        652 GPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLN 711

Db        638 GQHENIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRQAEAM-------PGPSLSV-GQD 689

Qy        712 PADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYD-----RPA 766

Db        690 P-------------EAGAGYKNIH----------LEKKYVRRDSGFSSQGVDTYVEMRPV 726

Qy        767 SYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLL 826

Db        727 S--TSSSNDSFSEEDLGKEDGRPLELRDLLHFSSQVAQGMAFLASKNCIHRDVAARNVLL 784

Qy        827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLW 886

Db        785 TSGRVAKIGDFGLARDIMNDSNYIVKGNARLPVKWMAPESIFDCVYTVQSDVWSYGILLW 844

Qy        887 EIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHL 946

Db        845 EIFSLGLNPYPGILVNSKFYKLVKDGYQMAQPAFAPKNIYSIMQACWALEPTRRPTFQQI 904

Qy        947 SEIVE 951

Db        905 CSLLQ 909


RESULT 17
T30816
macrophage colony-stimulating factor receptor - Japanese pufferfish
C;Species: Fugu rubripes (Japanese pufferfish)
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: T30816
R;How, G.F.; Venkatesh, B.; Brenner, S.
Genome Res. 6, 1185-1191, 1996
A;Title: Conserved linkage betwen the pufferfish (Fugu rubripes) and human genes for pla
A;Reference number: Z20882; MUID:97129405; PMID:8973913
A;Accession: T30816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-975 <HOW>
A;Cross-references: UNIPROT:P79750; UNIPARC:UPI00000FB6C2; EMBL:U63926; NID:g1752706; PI
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog

  Query Match           24.7%;  Score 1395;  DB 2;  Length 975;
  Best Local Similarity  35.6%;  Pred. No. 6.5e-55;
  Matches  346;  Conservative  170;  Mismatches  321;  Indels  136;  Gaps   34;

Qy         35 NEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEVSSASAAH 94

Db         35 SEVVVKPGTSLELKCGGDGPVNWQTRLPKHK------RYMSRSPGNLRTI-RVARPTAEF 87

Qy         95 TGLYTCYYNHTQTEENELEGRH----IYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPC 150

Db         88 TGTYKCFYSAW------AQHRHLTSSVHVYVKDPNRVFW-TSSTSLRVVRKEGEDYLLPC 140

Qy        151 RTTDPETP----------------VTLHNSEGVVPASYDSRQGFNGTFTVGPYICEATV 193

Db        141 LLTDPEATDLGLRMDNGTTVPPEMNYTVYRHRGILIRSL--QPSFN-----ADYVCTAKV 193

Qy        194 KG--KKFQTIPFNV-YALKATSELDLEMEALKTVYKSGETIVVTCAVFN-NEVVDLQWTY 249

Db        194 KGVEKTSKTFSINVIQKLRFPPYVFLEMDEYVRIV--GEELQIRCMTHNPNFNYNVTWNY 251

Qy        250 PGEVKGKGITMLEEIKVPS---IKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVT 306

Db        252 TTKSR---VTIEERVRSSGENRLDIQSILTISAVDLADTGNISCI---GTNEAGVNSSNT 305

Qy        307 -ISVHEKGFIEIKPTF-----SQLEAVNLHEVK--HFVVEVRAYPPPRISWLKNNLTLIE 358

Db        306 YLLVVEKPYIRLWPQLIPKLASQGLSVEVNEGEDLELGVMVEAYP---------------- 350

Qy        359 NLTE-----ITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFEL-LTQ 412

Db        351 QITDHRWHTPTSPSTSMQEHIYHARLQLKRMNAQEQGQYTFYAKSNLANGSISFHVKMYQ 410

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIK-KCNNETSWTILANNVSN 471

Db        411 KPIAVVRWENI-------TTLTCTSFGYPAPQIIWYQCSGIRPTCNGNNTGLPKQNHPQA 463

Qy        472 IITEIHSRDRSTVEGRVTF--AKVEETIAVRCLAKNLLGAENRELKL-VAPTLRSELTVA 528

Db        464 LTVEVQREEYGAVEVESVFTVGLSNHRMTVECVAFNLVGVSSSDTFTVEVSDKLFTSTLIG 523

Qy        529 AAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEF 588

Db        524 AA--GVLAIFLLLLVFLLYKYKQKPRFEIRWKIIE--AREGNNYTFIDPTQLPYNEKWEF 579

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP-VMKVAVKMLKPTARSSEKQALMSELKI 647

Db        580 PRDKLKLGKVLGAGAFGKVVEATAFGLGEDKDNTLRVAVKMLKANAHSDEREALMSELKI 639

Qy        648 MTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDI 707

Db        640 LSHLGHHQNIVNLLGACTYGGPVLVITEYCSLGDLLNFLRQKAETFVNLVMNIPE----- 694

Qy        708 FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLY--DRP 765

Db        695 ---------------IMENSNDYKNI--CNQKWYI-----RSDSGISSTSSSTYLEMRP 731

Qy        766 ASYKKKSMLDSEVKNLLSDDNSE-GLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNV 824

Db        732 S---QQSHIEASGRKSLCEDNGDWPLDIDDLLRFSLQVAQGLDFLASRNCIHRDVAARNV 788

Qy        825 LLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGIL 884

Db        789 LLTDKRVAKICDFGLARDIMNDSNYVVKGNARLPVKWMAPESIFDCVYTVQSDVWSYGIL 848

Qy        885 LWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFY 944

Db        849 LWEIFSLGKSPYPSMAVDSRFYKMVKRGYQMSQPDFALPEIYMIMKMCWNLEPTERPTFS 908

Qy        945 HLSEIVENLLPGQ 957

Db        909 MISQMINRLLGGQ 921


RESULT 18
S16385
macrophage colony-stimulating factor 1 receptor precursor - rat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) CSF-1R
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004
C;Accession: I60321; S16385
R;Borycki, A.G.; Guillier, M.; Leibovitch, M.P.; Leibovitch, S.A.
Growth Factors 6, 209-218, 1992
A;Title: Molecular cloning of CSF-1 receptor from rat myoblasts. Sequence analysis and r
A;Reference number: I60321; MUID:93001225; PMID:1389227
A;Accession: I60321
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-978 <RES>
A;Cross-references: UNIPROT:Q00495; UNIPARC:UPI000012DDBB; EMBL:X61479; NID:g57543; PIDN
A;Note: in Genbank entry RRCSF1, release 113.0, the source is designated as Rattus rattus
A;Note: submitted to the EMBL Data Library, August 1991
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; kinase-relate
 protein; tyrosine-specific protein kinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-978/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;20-515/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
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F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-485/Domain: immunoglobulin homology <IMM5>
F;516-535/Domain: transmembrane #status predicted <TMM>
F;536-978/Domain: intracellular #status predicted <INT>
F;578-915/Domain: protein kinase homology <KIN>
F;586-594/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
F;614,631,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             23.9%;  Score 1352.5;  DB 2;  Length 978;
  Best Local Similarity   34.8%;  Pred. No. 5.1e-53;
  Matches  336;  Conservative  162;  Mismatches  349;  Indels  119;  Gaps   26;

Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEV 87
Db         21 PVIEPSGPELVVEPGETVTLRCVSNGSVEWDGPISPYWTLDPE------SPG---STLTT 71

Qy         88 SSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAI 147
Db         72 RNATFKNTGTYRC----TELEDPMAGSTTIHLYVKDPAHSWNLLAQE---VTVVEGQEAV 124

Qy        148 IPCRTTDP--ETPVTLHNSEG--VVPAS---YDSRQGF----NGTFTVGPYICEATVKGK 196
Db        125 LPCLITDPALKDSVSLMREGGRQVLRKTVYFFSAWRGFIIRKAKVLDSNTYVCKTMVNGR 184

Qy        197 KFQTIPFNVYALKATSE-LDLEMEALKTVYKSGETIVVTCAVFNNEV---VDLQWTYPGE 252
Db        185 ESTSTGIWLKVNRVHPEPPQIKLEPSKLVRIRGEAAQIVCSATNAEVGFNVILK------ 238

Qy        253 VKGKGITMLE-----EIKVPSIKLVYTLTVPEATVKDSGDYECAA------RQATREVKE 301
Db        239 ---RGDTKLEIPLNSDFQDNYYKKVRALSLNAVDFQDAGIYSCVASNDVGTRTAT----- 290

Qy        302 MKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLT 361
Db        291 ---MNFQVVESAYLNLTSEQSLLQEVSVGDSLILTVHADAYP----SIQHYNWTYLGPFF 343

Qy        362 EITTDVEKIQE---IRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSIL 418
Db        344 EDQRKLEFITQRAIYRYTFKLFLNRVKASEAGQYFLMAQNKAGWNNLTFELTLRYPPEVS 403

Qy        419 DLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICK-DIKKCNNETSWTILANNVSNIITEIH 477
Db        404 VTWMPVNGS---DVLFCDVSGYPQPSVTWMECRGHTDRCDEAQALQVWNDTHPEVLSQ-K 459

Qy        478 SRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSEL-------TVAAA 530
Db        460 PFDKVIIQSQLPIGTLKHNMTYFCKTHNSVGNSSQYFRAVSLGQSKQLPDESLFTPVVVA 519

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
Db        520 CMSVMSLLVLLLLLLLYKYKQKPKYQVRWKIIERY--EGNSYTFIDPTQLPYNEKWEFPR 577

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
Db        578 NNLQFGKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLKSTAHADEKEALMSELKIMSH 637

Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
Db        638 LGQHENIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRKAEAMLGP-----------SL 685

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYD-----RP 765
Db        686 SPGQDS---------EGDSSYKNIH----------LEKKYVRRDSGFSSQGVDTYVEMRP 726

Qy        766 ASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVL 825
Db        727 VS---TSSSDSFFKQDLDKEPSRPLELWDLLHFSSQVAQGMAFLASKNCIHRDVAARNVL 783

Qy        826 LAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILL 885
Db        784 LTSGHVAKIGDFGLARDIMNDSNYVVKGNARLPVKWMAPESILYCVYTVQSDVWSYGILL 843

Qy        886 WEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYH 945
Db        844 WEIFSLGLNPYPGILVNNKFYKLVKDGYQMAQPVFAPKNIYSIMQSCWDLEPTRRPTFQQ 903

Qy        946 LSEIVE 951
Db        904 ICFLLQ 909


RESULT 19
TVHUMD
macrophage colony-stimulating factor 1 receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S08123; A24533; I56672; I57648; I59083; I52772
R;Hampe, A.; Shamoon, B.M.; Gobet, M.; Sherr, C.J.; Galibert, F.
Oncogene Res. 4, 9-17, 1989
A;Title: Nucleotide sequence and structural organization of the human FMS proto-oncogene
A;Reference number: S08123; MUID:89239490; PMID:2524025
A;Accession: S08123
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-972 <HAM>
A;Cross-references: UNIPROT:P07333; UNIPARC:UPI000004984A; GB:U63963; EMBL:X14720; NID:g1
A;Note: this sequence was submitted to the EMBL Data Library, March 1989
R;Coussens, L.; Van Beveren, C.; Smith, D.; Chen, E.; Mitchell, R.L.; Isacke, C.M.; Verma
Nature 320, 277-280, 1986
A;Title: Structural alteration of viral homologue of receptor proto-oncogene fms at carbo
A;Reference number: A24533; MUID:86175013; PMID:2421165
A;Accession: A24533
A;Molecule type: mRNA
A;Residues: 1-53,'A',55-972 <COU>
A;Cross-references: UNIPARC:UPI000016A6AB; GB:J03149
A;Note: the authors translated the codon GCA for residue 54 as Pro
R;Wheeler, E.F.; Roussel, M.F.; Hampe, A.; Walker, M.H.; Fried, V.A.; Look, A.T.; Rettenm
J. Virol. 59, 224-233, 1986
A;Title: The amino-terminal domain of the v-fms oncogene product includes a functional si
 sequences.
A;Reference number: I56672; MUID:86281820; PMID:3525854
A;Accession: I56672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: UNIPARC:UPI000000060C; GB:M14002; NID:g182676; PIDN:AAA35849.1; PID:g
R;Visvader, J.; Verma, I.M.
Mol. Cell. Biol. 9, 1336-1341, 1989
A;Title: Differential transcription of exon 1 of the human c-fms gene in placental troph
A;Reference number: I57648; MUID:89261741; PMID:2524648
A;Accession: I57648
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-16 <RE2>
A;Cross-references: UNIPARC:UPI000000060C; GB:M25786; NID:g349454; PIDN:AAA58421.1; PID:g
R;Browning, P.J.; Bunn, H.F.; Cline, A.; Shuman, M.; Nienhuis, A.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 7800-7804, 1986
A;Title: Replacement' of COOH-terminal truncation of v-fms with c-fms sequences markedly
A;Reference number: I59083; MUID:87017034; PMID:3532121
A;Accession: I59083
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 874-972 <RE3>
A;Cross-references: UNIPARC:UPI0000000418; GB:M14193; NID:g182521; PIDN:AAA35834.1; PID:g
R;Nienhuis, A.W.; Bunn, H.F.; Turner, P.H.; Gopal, T.V.; Nash, W.G.; O'Brien, S.
Cell 42, 421-428, 1985
A;Title: Expression of the human c-fms proto-oncogene in hematopoietic cells and its dele
A;Reference number: I52772; MUID:85282599; PMID:4028159
A;Accession: I52772
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: 244-295 <RE4>
A;Cross-references: UNIPARC:UPI0000000409; GB:M11067; NID:g182674; PIDN:AAA35848.1; PID:
C;Genetics:
A;Gene: GDB:CSF1R; FMS
A;Cross-references: GDB:120600; OMIM:164770
A;Map position: 5q33.2-5q33.3
A;Introns: 17/1; 103/1; 198/1; 243/3; 297/1; 361/2; 400/1; 440/2; 504/1; 542/3; 585/1; 6
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-972/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;24-512/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-383/Domain: immunoglobulin homology <IMM4>
F;412-487/Domain: immunoglobulin homology <IMM5>
F;513-537/Domain: transmembrane #status predicted <TMM>
F;538-972/Domain: intracellular #status predicted <INT>
F;580-917/Domain: protein kinase homology <KIN>
F;588-596/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,419-485/Disulfide bonds: #status predicted
F;45,73,153,240,275,302,335,353,412,428,480/Binding site: carbohydrate (Asn) (covalent)
F;616,633,778/Active site: Lys, Glu, Asp #status predicted
F;783,796/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             23.8%;  Score 1346.5;  DB 1;  Length 972;
  Best Local Similarity   34.0%;  Pred. No. 9.4e-53;
  Matches  335;  Conservative  164;  Mismatches  334;  Indels  151;  Gaps   31;

Qy         27 LPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLE 86
              :| | |:  | ||:  :: :||| |   | |  | |   :    : :: ::|     :|
Db         20 IPVIEPSVPELVVKPGATVTLRCVGNGSVEWDGPPSPHWT----LYSDGSSS-----ILS 70

Qy         87 VSSASAAHTGLYTCYYNHTQTEENELEG--RHIYIYVPDPDVAFVPLGMTDYLVIVEDDD 144
              ::|:  :|| | |      ||  :  |    |::|| ||     |  :    |:| :|
Db         71 TNNATFQNTGTYRC------TEPGDPLGGSAAIHLYVKDP---ARPWNVLAQEVVVFEDQ 121

Qy        145 SAIIPCRTTDP--ETPVTLHNSEGVVPASYDSRQGFN--GTFTV--------GPYICEAT 192
              |::||  |||  |  |:|    |  |    :   |:    ||:          | | |
Db        122 DALLPCLLTDPVLEAGVSLVRVRG-RPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSAL 180

Qy        193 VKGKKFQTIPFNVYALK------ATSELDLEMEALKTVYKSGETIVVTCAVFNNEV---V 243
              : |:|  :|   :   |      | : :  |:  ::    ||   : |:  : :|   |
Db        181 MGGRKVMSISIRLKVQKVIPGPPALTLVPAELVRIR-----GEAAQIVCSASSVDVNFDV 235

Qy        244 DLQWTYPGEVKGKGITMLEEIKVPS--------IKLVYTLTVPEATVKDSGDYECAARQA 295
              ||                 :: :|          : | || : :   : :|:| | |
Db        236 FLQHNN------------TKLAIPQQSDFHNNRYQKVLTLNLDQVDFQHAGNYSCVASNV 283

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPR-ISWLKNNL 354
              : |   :   | |  :: :   : :: | : |  :  | | |||  :  :|
Db        284 --QGKHSTSMFFRVVESAYLNLSSEQNLIQEVTVGEGLNLKVMVEAYPGLQGFNW----- 336

Qy        355 TLI---------ENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
              | :         |   ||        |:   | | | |  ::| |: :|:|    ::
Db        337 TYLGPFSDHQPEPKLANATTK----DTYRHTFTLSLPRLKPSEAGRYSFLARNPGGWRAL 392

Qy        406 TFELLTQVP---SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICK-DIKKCNNETS 461
              ||||  : |   | |   ::       |  |: | | | | |:: |: |     :|:
Db        393 TFELTLRYPPEVSVIWTFIN------GSGTLLCAASGYPQPNVTWLQCSGHTDRCDEAQV 446

Qy        462 WTILANNVSNIITE--IHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAP 519
              :  :    ::::   |   : ||:  :|   :|       | | | :|: :     ::
Db        447 LQVWDDPYPEVLSQEPFH---KVTVQSLLTVETLEHNQTYECRAHNSVGSGSWAFIPISA 503

Qy        520 TLRSE-------LTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEY 572
              :         |  | : :: :::: |::|:  :||||:|::||::|||   :|: |
Db        504 GAHTHPPDEFLFTPVVVACMSIMALLLLLLLLLLYKYKQKPKYQVRWKIIESY--EGNSY 561

Qy        573 IYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPT 632
              ::|| ||||: :|||||: |  |: ||:|||||||| ||:|| :   |:|||||||| |
Db        562 TFIDPTQLPYNEKWEFPRNNLQFGKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLKST 621

Qy        633 ARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDS 692
              | : ||:|||||||||:||| | |||||||||   ||: :|||| ||||:|:| :  ::
Db        622 AHADEKEALMSELKIMSHLGQHENIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRKAEA 681

Qy        693 FLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVS 752
              |                |:|  :          |   || ::           ||:| |
Db        682 MLGP------------SLSPGQDP---------EGGVDYKNIH----------LEKKYVR 710

Qy        753 KYSDIQRSLYD-----RPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGME 807
              : |      |     || |    |  ||  :  |  ::   | | ||| |: |||:||
Db        711 RDSGFSSQGVDTYVEMRPVS---TSSNDSFSEQDLDKEDGRPLELRDLLHFSSQVAQGMA 767

Qy        808 FLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESI 867
              |||||||:|||:|||||||  | : || |||||||||:||||: ||:  ||||||||||
Db        768 FLASKNCIHRDVAARNVLLTNGHVAKIGDFGLARDIMNDSNYIVKGNARLPVKWMAPESI 827

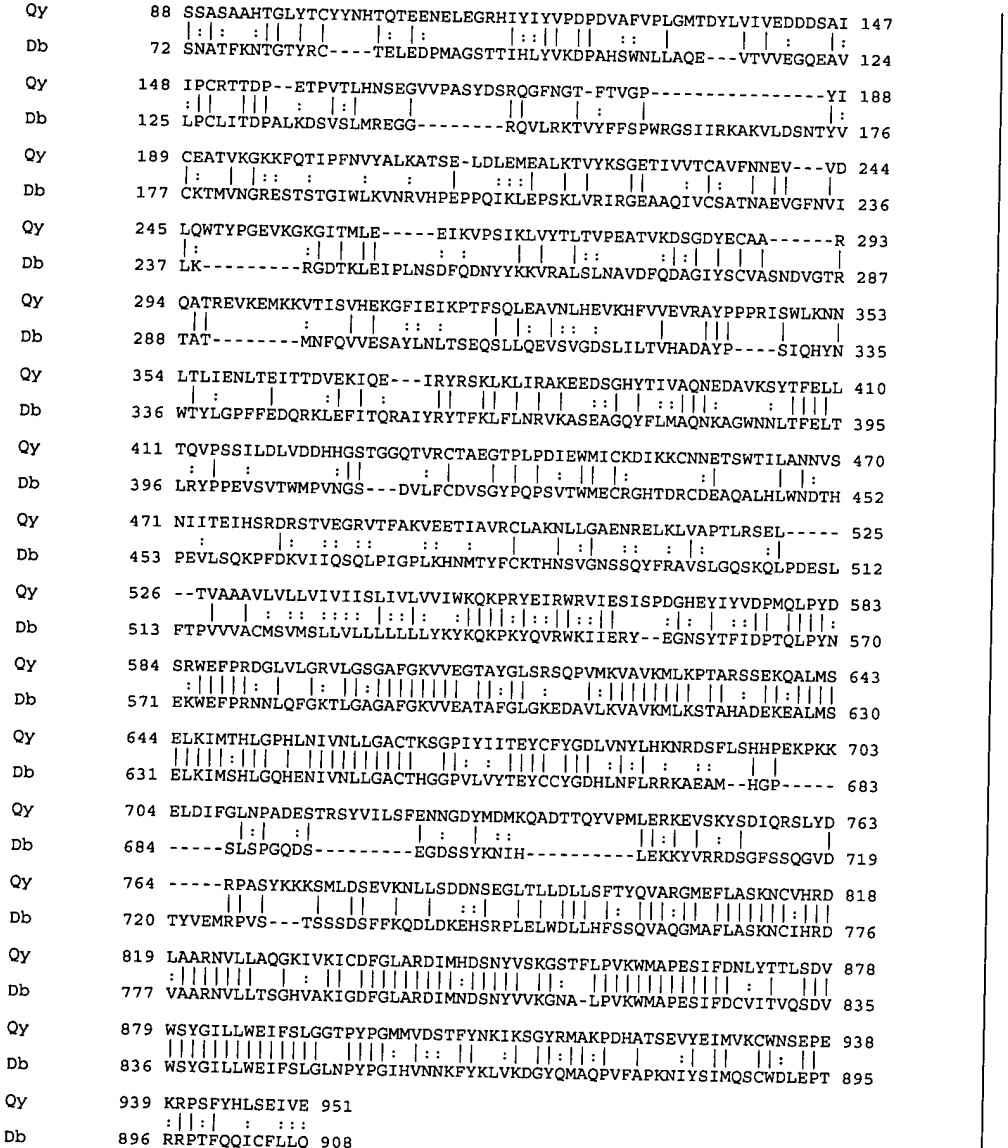
Qy        868 FDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYE 927
              || :||  |||||||||||||||  ||||::|:|  ||  :| ||:||:|  |   :|
Db        828 FDCVYTVQSDVWSYGILLWEIFSLGLNPYPGILVNSKFYKLVKDGYQMAQPAFAPKNIYS 887

Qy        928 IMVKCWNSEPEKRPSFYHLSEIVE 951
              ||  ||  ||  ||:|  :   ::
Db        888 IMQACWALEPTHRPTFQQICSFLQ 911

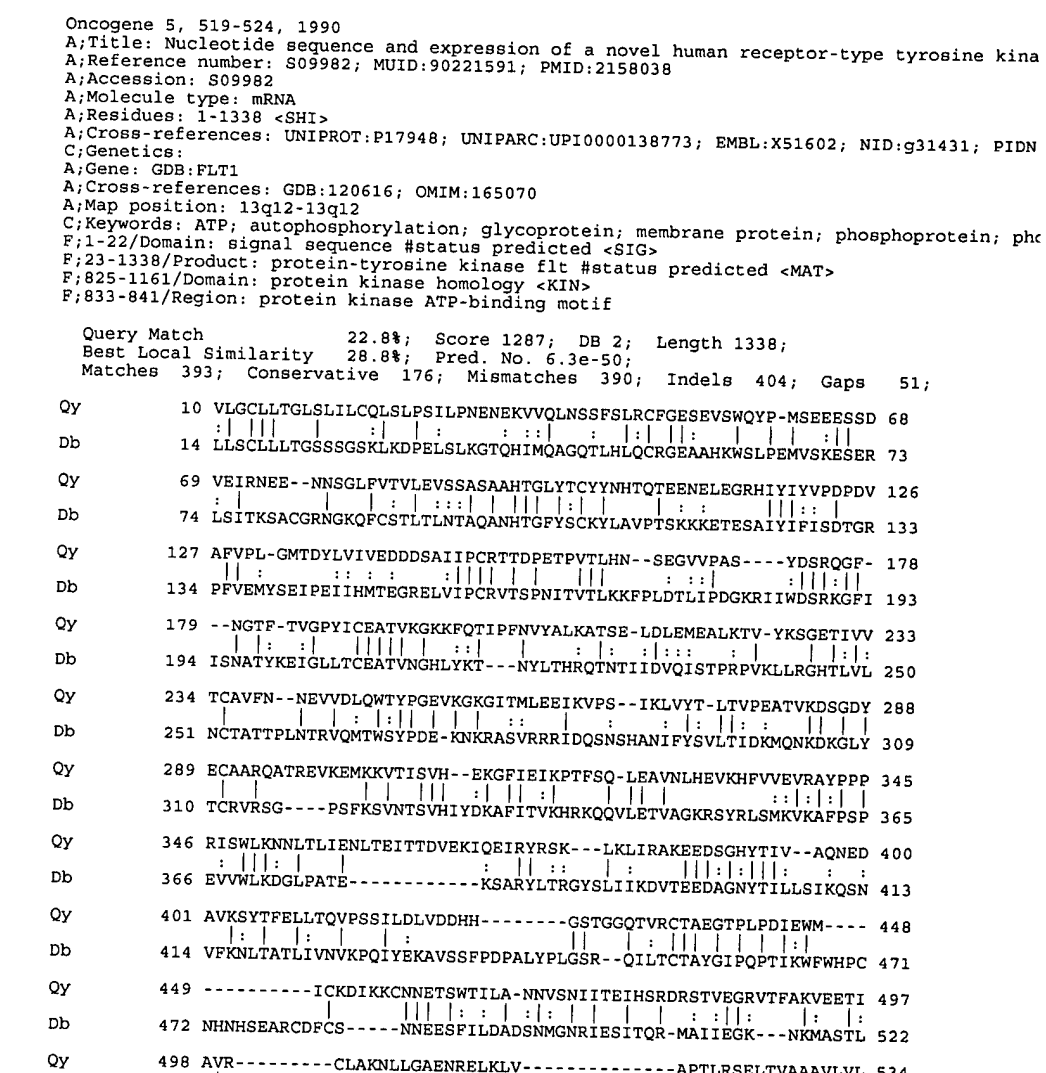

RESULT 20
TVMSMD
macrophage colony-stimulating factor 1 receptor precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csf1r/fms
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: S01880
R;Rothwell, V.M.; Rohrschneider, L.R.
Oncogene Res. 1, 311-324, 1987
A;Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.
A;Reference number: S01880; MUID:88217329; PMID:2966922
A;Accession: S01880
A;Molecule type: mRNA
A;Residues: 1-976 <ROT>
A;Cross-references: UNIPARC:UPI00001725B2; EMBL:X06368
C;Genetics:
A;Gene: fms
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT
F;20-515/Domain: extracellular #status predicted <EXT>
F;35-86/Domain: immunoglobulin homology <IMM1>
F;120-179/Domain: immunoglobulin homology <IMM2>
F;217-280/Domain: immunoglobulin homology <IMM3>
F;316-381/Domain: immunoglobulin homology <IMM4>
F;410-485/Domain: immunoglobulin homology <IMM5>
F;516-535/Domain: transmembrane #status predicted <TMM>
F;536-976/Domain: intracellular #status predicted <INT>
F;578-914/Domain: protein kinase homology <KIN>
F;586-594/Region: protein kinase ATP-binding motif
F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status
F;614,631,776/Active site: Lys, Glu, Asp #status predicted
F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

  Query Match             23.8%;  Score 1344;  DB 1;  Length 976;
  Best Local Similarity   34.9%;  Pred. No. 1.2e-52;
  Matches  340;  Conservative  152;  Mismatches  347;  Indels  134;  Gaps   26;

Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEV 87
              | | |:  | ||:   : :|||     | |  |:|   : | |      : |  : |
Db         21 PVIEPSGPELVVEPGETVTLRCVSNGSVEWDGPISPIWTLDPE------SPG---STLTT 71
```



RESULT 21
S09982
protein-tyrosine kinase (EC 2.7.1.112) flt1 precursor - human
N;Alternate names: receptor-type tyrosine kinase flt
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Oct-2004
C;Accession: S09982
R;Shibuya, M.; Yamaguchi, S.; Yamane, A.; Ikeda, T.; Tojo, A.; Matsushime, H.; Sato, M.



Oncogene 5, 519-524, 1990
A;Title: Nucleotide sequence and expression of a novel human receptor-type tyrosine kina
A;Reference number: S09982; MUID:90221591; PMID:2158038
A;Accession: S09982
A;Molecule type: mRNA
A;Residues: 1-1338 <SHI>
A;Cross-references: UNIPROT:P17948; UNIPARC:UPI0000138773; EMBL:X51602; NID:g31431; PIDN
C;Genetics:
A;Gene: GDB:FLT1
A;Cross-references: GDB:120616; OMIM:165070
A;Map position: 13q12-13q12
C;Keywords: ATP; autophosphorylation; glycoprotein; membrane protein; phosphoprotein; phc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1338/Product: protein-tyrosine kinase flt #status predicted <MAT>
F;825-1161/Domain: protein kinase homology <KIN>
F;833-841/Region: protein kinase ATP-binding motif

Query Match 22.8%; Score 1287; DB 2; Length 1338;
Best Local Similarity 28.8%; Pred. No. 6.3e-50;
Matches 393; Conservative 176; Mismatches 390; Indels 404; Gaps 51;

```
Qy        564 ----------------------SISPDGHEY--IYVDP---------MQLPYD-SRWEF 588
Db        763 TCTCVAATLFWLLLTLLIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEF 822

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
Db        823 ARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKIL 882

Qy        649 THLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF-------LSHHPEK 700
Db        883 THIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKK 942

Qy        701 PKKELDI-FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
Db        943 EKMEPGLEQGKKPRLDSVTSSE--SFASSGFQEDKSLSD-------VEEEE--------- 984

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
Db        985 ---DSDGFYK-----------------EPITMEDLISYSFQVARGMEFLSSRKCIHRDL 1023

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
Db       1024 AARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVW 1083

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
Db       1084 SYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKE 1143

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDK 999
Db       1144 RPRFAELVEKLGDLLQ----------------------ANVQQDGKD-YIPI-------- 1172

Qy       1000 LKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSST- 1058
Db       1173 ---------NAILTGNSGFTYSTPAF-----SEDFFK------ESISAPKFNSGSSDDVR 1212

Qy       1059 ------FIKRED-ETIEDI-----DMMDDIGIDSSDLVEDSFL 1089
Db       1213 YVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPML 1255


RESULT 22
I78875
receptor tyrosine kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: I78875
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J
Oncogene 8, 2293-2298, 1993
A;Title: Molecular cloning of murine FLT and FLT4.
A;Reference number: I58375; MUID:93330572; PMID:8393164
A;Accession: I78875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1333 <RES>
A;Cross-references: UNIPROT:P35969; UNIPARC:UPI0000028DE1; GB:L07297; NID:g293782; PIDN:
C;Genetics:
A;Gene: FLT
C;Keywords: ATP
F;826-1161/Domain: protein kinase homology <KIN>
F;834-842/Region: protein kinase ATP-binding motif

  Query Match             22.6%;  Score 1280;  DB 2;  Length 1333;
  Best Local Similarity   28.8%;  Pred. No. 1.3e-49;
  Matches  398;  Conservative  189;  Mismatches  394;  Indels  400;  Gaps   54;

Qy          8 FLVLGCLL-----TGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMS 62
Db         12 YALLGCLLLTGYGSGSKLKVPELSLKG-----TQHVMQAGQTLFLKCRGEAAHSWSLPTT 66

Qy         63 -EEESSDVEIR-----NEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRH 116
Db         67 VSQEDKRLSITPPSACGRDNRQ--FCSTLTLDTAQANHTGLYTCRYLPTSTSKKKKAESS 124

Qy        117 IYIYVPDPDVAFVPLGMTDY--LVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVP--- 169
Db        125 IYIFVSDAGSPFIEM-HTDIPKLVHMTEGRQLIIPCRVTSPNVTVTLKKFPFDTLTPDGQ 183

Qy        170 -ASYDSRQGF---NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKT 223
Db        184 RITWDSRRGFIIANATYKEIGLLNCEATVNGHLYQT---NYLTHRQTNTILDVQIRPPSP 240

Qy        224 V-YKSGETIVVTCAVFN--NEVVDLQWTYPGEV---------------------------- 253
Db        241 VRLLHGQTLVLNCTATTELNTRVQMSWNYPGKATKRASIRQRIDRSHSHNNVFHSVLKIN 300

Qy        254 ------KG-----------------------KGITMLEEIK------------------- 265
Db        301 NVESRDKGLYTCRVKSGSSFQSFNTSVHVYEKGFISVKHRKQPVQETTAGRRSYRLSMKV 360

Qy        266 --VPSIKLV-------------------YTLTVPEATVKDSGDYECAARQATREVKEMKK 304
Db        361 KAFPSPEIVWLKDGSPATLKSARYLVHGYSLIIKDVTTEDAGDYTILL--GIKQSRLFKN 418

Qy        305 VTISVHEKGFIEIKP-----TFSQLEAVNLHEV---KHFVVEVRAYPPPRISWL------ 350
Db        419 LTATL----IVNVKPQIYEKSVSSLPSPPLYPLGSRQVLTCTVYGIPRPTITWLWHPCHH 474

Qy        351 ---------------------------------KNNLTLIE------------------- 358
Db        475 NHSKERYDFCTENEESFILDPSSNLGNRIESISQRMTVIEGTNKTVSTLVVADSQTPGIY 534

Qy        359 -------------NLTEITTDV--------EK-------------IQEIRYR-------- 376
Db        535 SCRAFNKIGTVERNIKFYVTDVPNGFHVSLEKMPAEGEDLKLSCVVNKFLYRDITWILLR 594

Qy        377 -----------SKLKLIRAKE--------------EDSGHYTIVAQN----EDAVKSYTF 407
Db        595 TVNNRTMHHSISKQKMATTQDYSITLNLVIKNVSLEDSGTYACRARNIYTGEDILRK--T 652

Qy        408 ELL---TQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTI 464
Db        653 EVLVRDSEAPHLLQNLSDYEVSISGSTTLDCQARGVPAPQITWF--KNNHKIQQEPG-II 709

Qy        465 LANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRE--LKLVAPTLR 522
Db        710 LGPGNSTLFIE-----------RVT---EEDEGVYRCRATNQKGAVESAAYLTVQGTSDK 755

Qy        523 SELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDP----- 577
Db        756 SNLELITLTCTCVAATLFWLLLTLFIRKLK-------RSSSEVKTD-YLSIIMDPDEVPL 807

Qy        578 ----MQLPYD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPT 632
Db        808 DEQCERLPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEG 867

Qy        633 ARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRD 691
Db        868 ATASEYKALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRD 927

Qy        692 SFLSH-----HPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPML 746
Db        928 LFCLNKDAALHMELKKESLE----------------------------------PGL 950

Qy        747 ERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGM 806
Db        951 EQGQKPRLDSVSSSSVTSSSFPEDRSVSDVEGDEDYSEISKQPLTMEDLISYSFQVARGM 1010

Qy        807 EFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPES 866
Db       1011 EFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRRGDTRLPLKWMAPES 1070

Qy        867 IFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVY 926
Db       1071 IFDKVYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMRTPEYATPEIY 1130
```

```
Qy       927 EIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDN 986
Db      1131 QIMLDCWHKDPKERPRFAELVEKLGDLLQANVQQDGK----DYI----PLNAILTRNSSF 1182

Qy       987 AYIGVTYKNEEDKLKD-------WEGGLDEQRLSADSGYI--IPLPDIDPVPEEEDLGKR 1037
Db      1183 TYSTPTF--SEDLFKDGFADPHFHSGSSDDVR------YVNAFKFMSLERIKTFEEL--- 1231

Qy      1038 NRHSSQTSEESAIETGS-SSSTFIKR--EDETIEDIDMMDDIGIDS-------SDLVEDS 1087
Db      1232 SPNSTSMFEDYQLDTSTLLGSPLLKRFTWTETKPKASMKIDLRIASKSKEAGLSDLPRPS 1291

Qy      1088 F 1088
Db      1292 F 1292
```

RESULT 23
I60598
Fit-1 tyrosine kinase receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
C;Accession: I60598
R;Yamane, A.; Seetharam, L.; Yamaguchi, S.; Gotoh, N.; Takahashi, T.; Neufeld, G.; Shibu
Oncogene 9, 2683-2690, 1994
A;Title: A new communication system between hepatocytes and sinusoidal endothelial cells
A;Reference number: I60598; MUID:94336223; PMID:8058332
A;Accession: I60598
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1336 <RES>
A;Cross-references: UNIPROT:P53767; UNIPARC:UPI0000138774; GB:D28498; NID:g511662; PIDN:
C;Keywords: ATP
F;825-1161/Domain: protein kinase homology <KIN>
F;833-841/Region: protein kinase ATP-binding motif

Query Match 22.6%; Score 1278; DB 2; Length 1336;
Best Local Similarity 29.0%; Pred. No. 1.6e-49;
Matches 398; Conservative 187; Mismatches 400; Indels 388; Gaps 53;

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Qy         10 VLGC-LLTGLSLILC---QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP--MSE 63
Db         14 LLGCLLLTG----YCSGSKLKGPELSLKGTQHVMQAGQTLFLKCRGEAAHSWSLPTTVSQ 69

Qy         64 EESSDVEIRNE-ENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122
Db         70 EDKKLSVTRSACGRNNRQFCSTLTLNMAQANHTGLYSCRYLPKSTSKEKKMESAIYIFVS 129

Qy        123 DPDVAFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVP----ASYDSR 175
Db        130 DAGSPFIEMHSDIPKLVHMTEGRELIIPCRVTSPNITVTLKKFPFDALTPDGQRIAWDSR 189

Qy        176 QGF---NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKTV-YKSGE 229
Db        190 RGFIIANATYKEIGLLTCEATVNGHLYQT---SYLTHRQTNTILDVQISPPSPVRFLRGQ 246

Qy        230 TIVVTCAVFN--NEVVDLQWTYPGE-VKGKGITMLEEIKVPSIKLVYT-LTVPEATVKDS 285
Db        247 TLVLNCTVTTDLNTRVQMSWNYPGKATKRASIRQRIDQSNPHSNVFHSVLKINNVESRDK 306

Qy        286 GDYECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQLEAVNLHEVKH-FVVEVRAY 342
Db        307 GLYTCRVKSGS----SFRTFNTSVHVYEKGFISVKHRKQQVQETIAGKRSHRLSMKVKAF 362

Qy        343 PPPRISWLKN----------------------------------------------NLTL-- 356
Db        363 PSPEVVWLKDGVPATEKSARYSVHGYSLIIKDVTAEDAGDYTILLGIKQSKLFRNLTATL 422

Qy        357 ------------------------------------------------------------ 356
Db        423 IVNVKPQIYEKSVSSLPSPPLYPLGSRQVLTCTVYGIPQPTIKWLWHPCHYNHSKERNDF 482

Qy        357 ------------------IENLTE---------------------------------- 362
```

```
Db        483 CFGSEESFILDSSSNIGNRIEGITQRMMVIEGTNKTVSTLVVADSRTPGSYSCKAFNKIG 542

Qy        363 --------ITTDV--------EKI-------------QEIRYR---------------- 376
Db        543 TVERDIRFYVTDVPNGFHVSLEKIPTEGEDLKLSCVVSKFLYRDITWILLRTVNNRTMHH 602

Qy        377 --SKLKLIRAKE--------------EDSGHYTIVAQNEDAVKSYT-FELLTQVPSSILD 419
Db        603 SISKQKMATTQDYSITLNLVIKNVSLEDSGTYACRARN-----IYTGEEILRKTEVLVRD 657

Qy        420 L--------VDDHHGS-TGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVS 470
Db        658 LEAPLLLQNLSDHEVSISGSTTLDCQARGVPAPQITWF--KNNHKIQQEPG-IILGPGNS 714

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGA--ENRELKLVAPTLRSELTVA 528
Db        715 TLFIE----------RVT---EEDEGVYRCRATNQKGVVESSAYLTVQGTSDKSNLELI 760

Qy        529 AAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDP---------MQ 579
Db        761 TLTCTCVAATLFWLLLTLFIRKLK-------RSSSEVKTD-YLSIIMDPDEVPLDEQCER 812

Qy        580 LPYD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        813 LPYDASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEY 872

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSFLSH- 696
Db        873 KALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDFFCLNK 932

Qy        697 ----HPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVS 752
Db        933 DAALHMEPKKEKLE-----------------------------------PDLEQDQKP 955

Qy        753 KYSDIQRSLYDRPASYKK-KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLAS 811
Db        956 RLDSVSSSESFTSSGFQEDKSVSDVEGGEDYSEISKQPLTMEDLISYSFQVARGMEFLSS 1015

Qy        812 KNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNL 871
Db       1016 RKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRRGDTRLPLKWMAPESIFDKV 1075

Qy        872 YTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVK 931
Db       1076 YSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMRTPEYATPEIYQIMLD 1135

Qy        932 CWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGV 991
Db       1136 CWHKDPKERPRFAELVEKLGDLLQANVQQDGK----DYI----PLNAILTRNSGFTYSVP 1187

Qy        992 TYKNEEDKLKDWEGGLDEQRL----SADSGYI--IPLPDIDPVPEEEDLGKRNRHSSQTS 1045
Db       1188 TF--SEDFFKD---GFTDPKFHSGSSDDVRYVNAFKFMSLERIKTFEEL---SPNATSMF 1239

Qy       1046 EESAIETGS-SSSTFIKR--EDETIEDIDMMDDIGIDS-------SDLVEDSF 1088
Db       1240 EDYHLDTSSLLTSPLLKRFTWTETKPKASMKIDLRITSKSKEAGLSDLPGPSF 1292
```

RESULT 24
S49010
embryonic receptor kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
C;Accession: S49010
R;Choi, K.; Wall, C.; Hanratty, R.; Keller, G.
Oncogene 9, 1261-1266, 1994
A;Title: Isolation of a gene encoding a novel receptor tyrosine kinase from differentiate
A;Reference number: S49010; MUID:94181281; PMID:8134130
A;Accession: S49010
A;Status: preliminary
A;Molecule type: mRNA

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A;Residues: 1-1330 <CHO>
A;Cross-references: UNIPROT:P35969; UNIPARC:UPI000016CD30; EMBL:X78568; NID:g510664; PID
C;Keywords: ATP
F;823-1158/Domain: protein kinase homology <KIN>
F;831-839/Region: protein kinase ATP-binding motif

  Query Match           21.8%;  Score 1231.5;  DB 2;  Length 1330;
  Best Local Similarity  28.3%;  Pred. No. 1.9e-47;
  Matches  390;  Conservative  191;  Mismatches  399;  Indels  399;  Gaps   54;

Qy          8 FLVLGCLL-----TGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMS 62
              : :|||||     :|  | : :|||        : |:|   :  |:| ||:  ||  | :
Db         12 YALLGCLLLTGYGSGSKLKVPELSLKG-----TQHVMQAGQTLFLKCRGEAAHSWSLPTT 66

Qy         63 -EEESSDVEIR-----NEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRH 116
               :|   : |         :|    | : | : :| | ||||||| |  | | : :
Db         67 VSQEDKRLSITPPSACGRDNRQ--FCSTLTLDTAQANHTGLYTCRYLPTSTSKKKKAESS 124

Qy        117 IYIYVPDPDVAFVPLGMTDYLVIVE-DDDSAIIPCRTTDPETPVTLHN--SEGVVP---- 169
              |||:| |    |: :  ||   :|   :   :| || | |   |||     : : |
Db        125 IYIFVSDAGSPPIEM-HTDIPKLVHMTEGRQLIICRVTSPNVTVTLKKFPFDTLTPDGQR 183

Qy        170 ASYDSRQGF---NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKTV 224
              ::|||:||   | |:  :|   ||| | |  :||   |    : |:  ||:::     |
Db        184 ITWDSRRGFIIANATYKEIGLLNCEA-VNGHLYQT---NYLTHRQTNTILDVQIRPPSPV 239

Qy        225 -YKSGETIVVTCAVFN--NEVVDLQWTYPGEV---------------------------- 253
                |:|:|: |      |  | : | |||:
Db        240 RLLLGQTLVLNCTATTELNTRVQMSWNYPGKATKRASIRQRIDRSHSHNNVFHSVLKINN 299

Qy        254 -----KG-----------------------KGITMLEEIK--------------------- 265
                  ||                       ||   ::  |
Db        300 VESRDKGLYTCRVKSGSSFQSFNTSVHVYEKGFISVKHRKQPVQETTAGRRSYRLSMKVK 359

Qy        266 -VPSIKLV-------------------YTLTVPEATVKDSGDYECAARQATREVKEMKKV 305
               || ::|                    |:| : : | :|:|||        :: :  | :
Db        360 AFPSPEIVWLKDGSPATLKSARYLVHGYSLIIKDVTTEDAGDYTILL--GIKQSRLFKNL 417

Qy        306 TISVHEKGFIEIKP-----TFSQLEAVNLHEV---KHFVVEVRAYPPPRISWL------- 350
              | ::     : :||     : | | :  |: :   :     |   | | |:||
Db        418 TATL----IVNVKPQIYEKSVSSLPSPPLYPLGSRQVLTCTVYGIPRPTITWLWHPCHHN 473

Qy        351 -------------------------------KNNLTLIE--------------------- 358
                                            :|:||
Db        474 HSKERYDFCTENEESFILDPSSNLGNRIESISQRMTVIEGTNKTVSTLVVADSQTPGIYS 533

Qy        359 ------------NLTEITTDV--------EK-------------IQEIRYRS-------- 377
                         |:   |||         ||              : :  ||
Db        534 CRAFNKIGTVERNIKFYVTDVPNGFHVSLEKMPAEGEDLKLSCVVNKFLYRDITWILLRT 593

Qy        378 ------------------------KLKLIRAKEEDSGHYTIVAQN----EDAVKSYTFEL 409
                                     | :     ||||  |   |:|    || ::    |:
Db        594 VNNRTMHNSISKQNGHHSSYSITLNLVIKNVSLEDSGTYACRARNIYTGEDILRK--TEV 651

Qy        410 L---TQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILA 466
              |   :: |  : :| |      :|  |: | | | | | | |:  |:  |   |    ||
Db        652 LVRDSEAPHLLQNLSDYEVSISGSTTLDCQARGVPAPQITWL--KNNHKIQQEPG-IILG 708

Qy        467 NNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRE--LKLVAPTLRSE 524
                | :  |          |||    |:    || : |  ||       | :   : :|
Db        709 PGNSTLFIE----------RVT---EEDEGVYRCRSTNQKGAVESAAYLTVQGTSDKSN 754

Qy        525 LTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDP------- 577
              | :       :   :  |:: : | | |       |    :  | :  | :||
Db        755 LELITLTYTCVAATLFWLLLTLFIRKLK-------RSSSEVKTD-YLSIIMDPDEVPLDE 806

Qy        578 --MQLPYD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTAR 634
                :|||| | ||| |: | ||: || ||||||: :|:|: :|     |||||||  |
Db        807 QCERLPYDASNWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGAT 866

Qy        635 SSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF 693
              :|| :|||:||||:||:| |||:|||||||||  ||: :| ||| ||:| |||   || |
Db        867 ASEYKALMTELKILTHIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLF 926

Qy        694 LSH-----HPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLER 748
                    :     | |  |: |:                                  | ||:
Db        927 CLNKDAALHMELKKESLE-----------------------------------PGLEQ 949

Qy        749 KEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEF 808
                :  :   :  |     :  : :|: | |     |: : : ||: ||:|:::|||| |||
Db        950 GQKPRLDSVSSSSVTSSSFPEDRSVSDVEGDEDYSEISKQPLTMEDLISYSFQVARRMEF 1009

Qy        809 LASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIF 868
              |:|: |:|||||||:||::  :|||||||||||  : :|| :| | ||:|||||||||
Db       1010 LSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRRGDTRLPLKWMAPESIF 1069

Qy        869 DNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEI 928
              | :|:| |||||||:||||||||||:||||: :|  | :::| | ||  |::|| |:|:|
Db       1070 DKVYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLKEGMRMRTPEYATPEIYQI 1129

Qy        929 MVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAY 988
              |: ||: :|::|| |  | | : :||    ::  :    |::    |  | :  :|:  |
Db       1130 MLDCWHKDPKERPRFAELVEKLGDLLQANVQQDGK----DYI----PLNAILTRNSNFTY 1181

Qy        989 IGVTYKNEEDKLKD-------WEGGLDEQRLSADSGYI--IPLPDIDPVPEEEDLGKRNR 1039
                |:   ||: ||          |  |: |      |:       :: :   |:|   :
Db       1182 STPTF--SEDRGKDGFADPHFHSGSSDDVR------YVNAFKFMSLERIKTFEEL---SP 1230

Qy       1040 HSSQTSEESAIETGS-SSSTFIKR--EDETIEDIDMMDDIGIDS-------SDLVEDSF 1088
              :|:   |:  ::| :   |  :||    ||      |  |: | |       |||   ||
Db       1231 NSTSMFEDYQLDTSTLLGSPLLKRFTWTETKPKASMKIDLRIASPRKEAGLSDLPRPSF 1289
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RESULT 25
S51656
vascular endothelial growth factor receptor 1 precursor - Japanese quail
N;Alternate names: quail endothelial kinase 1 (Quek 1); vascular endothelial growth fact
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
C;Accession: JC4953; A56598; I51162; S51656
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A;Reference number: JC4953; MUID:97017121; PMID:8863722
A;Accession: JC4953
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1348 <EIC1>
A;Cross-references: UNIPROT:P52583; UNIPARC:UPI0000138775; EMBL:X83288; NID:g603523; PID
A;Note: submitted to the EMBL Data Library, December 1994
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Mech. Dev. 42, 33-48, 1993
A;Title: Two molecules related to the VEGF receptor are expressed in early endothelial c
A;Reference number: A56598; MUID:93378866; PMID:8396413
A;Contents: E16 spinal cord
A;Accession: A56598
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 910-1348 <EIC2>
A;Cross-references: UNIPARC:UPI0000171474; GB:S65205; NID:g410680; PIDN:AAB28127.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:137162, NCBIP:137163)
R;Marcelle, C.; Eichmann, A.
Oncogene 7, 2479-2487, 1992
A;Title: Molecular cloning of a family of protein kinase genes expressed in the avian em
A;Reference number: I50595; MUID:93096482; PMID:1281306
A;Accession: I51162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1023-1079 <MAR>
A;Cross-references: UNIPARC:UPI00000FB4F0; EMBL:X69694; NID:g395226; PIDN:CAA49364.1; PI
A;Note: the species is not identified by the authors; the most probable species is shown
C;Comment: This protein is an endothelial-specific receptor and binds vascular endotheli
C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1348/Product: vascular endothelial growth factor receptor 1 #status predicted <MAT>
F;756-777/Domain: transmembrane #status predicted <TMM>
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F;823-1160/Domain: protein kinase homology <KIN>
F;831-839/Region: protein kinase ATP-binding motif

Query Match 21.7%; Score 1226; DB 2; Length 1348;
Best Local Similarity 27.2%; Pred. No. 3.3e-47;
Matches 372; Conservative 177; Mismatches 402; Indels 418; Gaps 46;

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Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDV 69
Db         11 VLLCLAPVFAGLFISMDQPTLSIQKSVLTITTNDTLNITCSGQRAVYWSWPNNQ---SSV 67

Qy         70 EIRNEEN--NSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVA 127
Db         68 EKRLAVTGCSEGPFCKTLTLLRVIGNDTGDYRCLYGDSQAATT------IYVYVQDYRSP 121

Qy        128 FV-PLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLH---NSEGVVP----ASYDSRQGFN 179
Db        122 FVTSVGDQLGIVYITKNKTVVVPCLGTVSNLNVSLHAKYPEKVFVPDGKSISWDNKKG-- 179

Qy        180 GTFTV--------GPYICEATVKGKKFQT-------IPFNVYALKATSELDLEMEALKTV 224
Db        180 --FTIPSHLINYAGMVFCEAKIDNESYQSVIYIVAVVGYRIYDLTMNPHYQVELAV---- 233

Qy        225 YKSGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLE------EIKVPSIKLVYTLT 276
Db        234 ---GEKLVLNCTVRTELNVGIDFRWDYP-SIKERRATIRDLKTTAGEIKT----FVSTLT 285

Qy        277 VPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFV 336
Db        286 IESVNLSDKGRYTCAASSGRMNMKNSSYFII--HESPFIHLEKMENVVE-MKLGDTVSIP 342

Qy        337 VEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVA 396
Db        343 VKFKGYPPPEAKWYKNGKVINANHT-----------VKLGYALVITEATEKDAGNYTVVL 391

Qy        397 QN--EDAVKSYTFELLTQVP-----SSILDLVDDH-HGST-------------------- 428
Db        392 TNPTNKMQKRHTFTLLVNVPPQIGENALMAPVDSYKYGSTQALTCTIYAVPPPAAVLWYW 451

Qy        429 --------------------------------GGQTV---------------------- 433
Db        452 QLEEECTFSPQKVRLGANPYACRKWKVISERKGGNQVEIKQRVVTIAGKTKTVSTLVIQA 511

Qy        434 ------------------------------------------------RCTAE------- 438
Db        512 ANVSALYRCMATNRAGSSERVISFHVTRGLEINLQPRSQLTEKDNTSLQCTADKFTFEKL 571

Qy        439 ---------------GTPLPDIEWMICKD---IKKCN---------NETSWTILAN---- 467
Db        572 SWYKLSTHVSQTPFGGLPMP-----VCKNLDALQKLNATVSNVNGENVTLELILRNISLQ 626

Qy        468 ----------------------------------NVSNIITEIHSRDR--STVEG--- 486
Db        627 DGGDYVCIAQDKKAKTQHCLVKHLTVQEPLHPRLVGNLENQTTNIGETIEVLCTVNGVPP 686

Qy        487 -RVTFAKVEETI-----------------AVR--------CLAKNLLGAENRELKLVAP 519
Db        687 PNITWFKNSETLFEDSGIVLKDGNKTLTIRRVRKEDGGLYTCLACNILGCKKAEAFFSVQ 746

Qy        520 TLRSELTVAAAVLV-LLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDP- 577
Db        747 GAEEKTNLELIILVGTAVIAMFFWLLLVIILRTVKRAN------GGDMKTGYLSIIMDPD 800

Qy        578 --------MQLPYD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKM 628
Db        801 EVPIDEHCERLPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKM 860

Qy        629 LKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLH 687
Db        861 LKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEYCKFGNLSAYLR 920

Qy        688 KNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLE 747
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Db        921 SKRSEFI---PYKMKSA----RFRQGKENYTGDISTDLKQRLDSITSSQSSTSS------ 967

Qy        748 RKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEG-LTLLDLLSFTYQVARGM 806
Db        968 ------------------GFVEERSLSDVEEEDAGSEDLCKNPLTMEDLICYSFQVARGM 1009

Qy        807 EFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPES 866
Db       1010 EFLASRKCIHRDLAARNILLSDNNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPET 1069

Qy        867 IFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVY 926
Db       1070 IFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMY 1129

Qy        927 EIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDN 986
Db       1130 QTMLDCWHGDPKQRPTFSELVEHLGNLLQ----------------------ANVRQDGKD 1167

Qy        987 AYI---GVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQ 1043
Db       1168 YVVLPLSVSLNMEE----------------DSGLSLPTSPAS-CKEEEEVCDPKFHYDN 1209

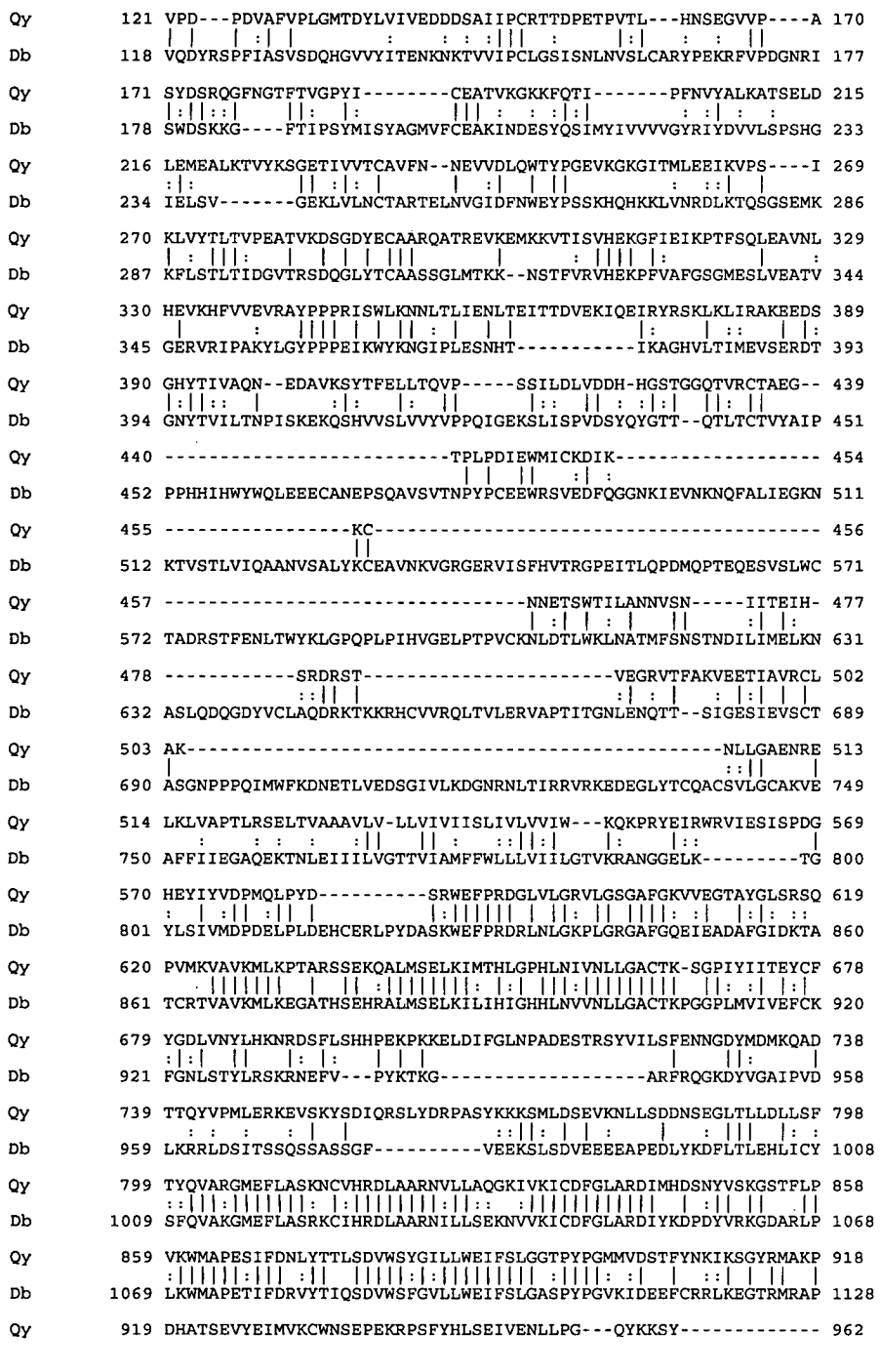
Qy       1044 TSEESAIETGSSSSTFIKRED-----ETIEDIDMMDDIGIDSSDLVEDS 1087
Db       1210 TAGISQYRQGS------KRKSRPVSVKTFEDIPLVTTVKVVQEENQTDS 1252
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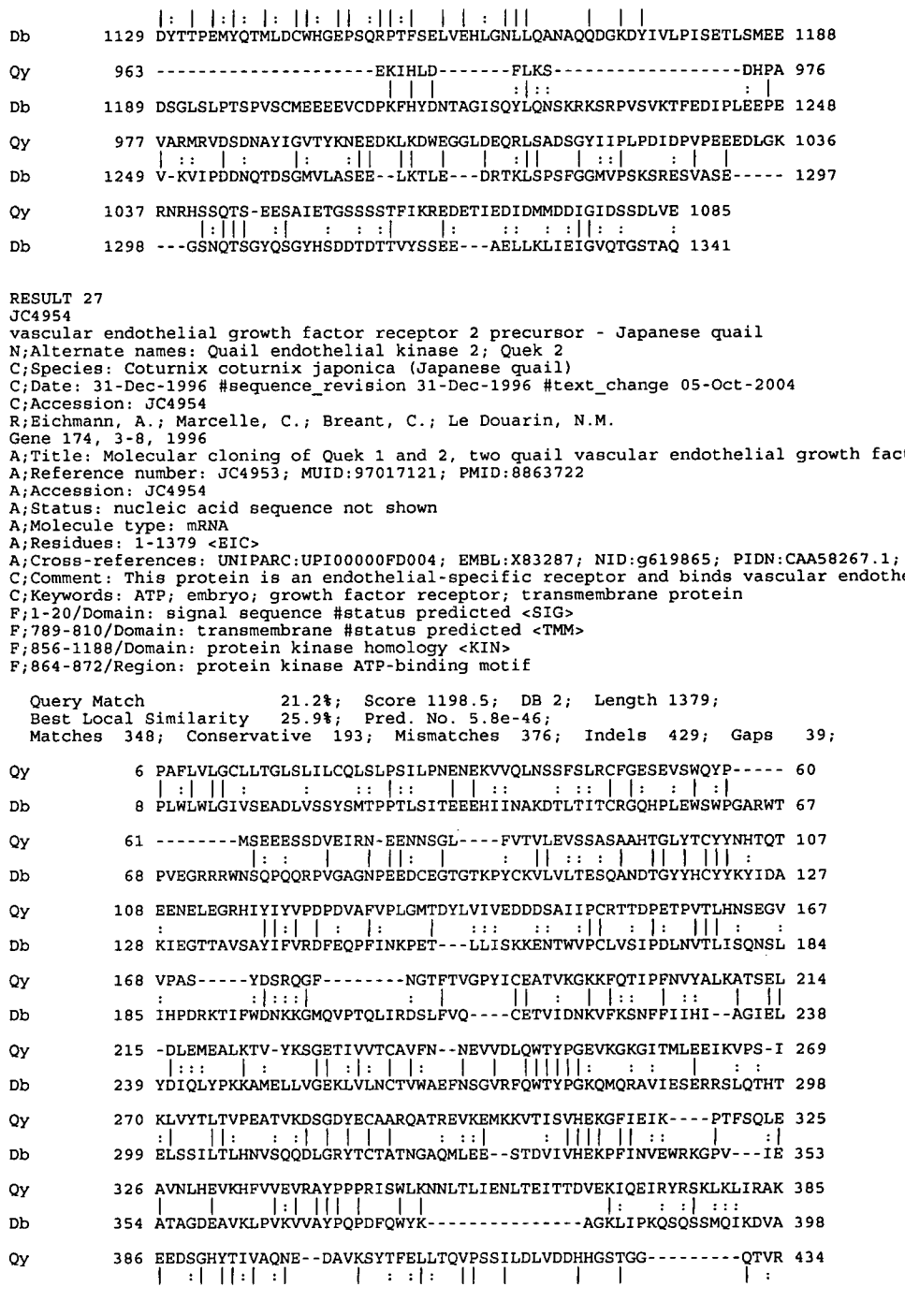
RESULT 26
JC1402
protein-tyrosine kinase (EC 2.7.1.112) KDR - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 05-Oct-2004
C;Accession: JC1402; I58357
R;Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gospc
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A;Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelial
A;Reference number: JC1402; MUID:93038639; PMID:1417831
A;Accession: JC1402
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-48,'I',50-616,'E',618-700,'E',702-748,'F',750-1263,'I',1265-1290,'P',1292-1
A;Cross-references: UNIPROT:P35968; UNIPARC:UPI000017A3C3; EMBL:X61656; NID:g31717
R;Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.; Shows, T.B.
Oncogene 6, 1677-1683, 1991
A;Title: Identification of a new endothelial cell growth factor receptor tyrosine kinase
A;Reference number: I58357; MUID:92019839; PMID:1656371
A;Accession: I58357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 3-1356 <TER2>
A;Cross-references: UNIPARC:UPI000016A991; GB:L04947; NID:g186674; PIDN:AAA59459.1; PID:g
C;Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.
C;Genetics:
A;Gene: GDB:KDR
A;Cross-references: GDB:127921; OMIM:191306
A;Map position: 4q12-4q12
C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kir
F;766-790/Domain: transmembrane #status predicted <TMM>
F;832-1167/Domain: protein kinase homology <KIN>
F;840-848/Region: protein kinase ATP-binding motif

Query Match 21.3%; Score 1206.5; DB 2; Length 1356;
Best Local Similarity 25.5%; Pred. No. 2.5e-46;
Matches 365; Conservative 190; Mismatches 424; Indels 451; Gaps 44;

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Qy         14 LLTGLSLILC-------------QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db          5 VLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWP 64

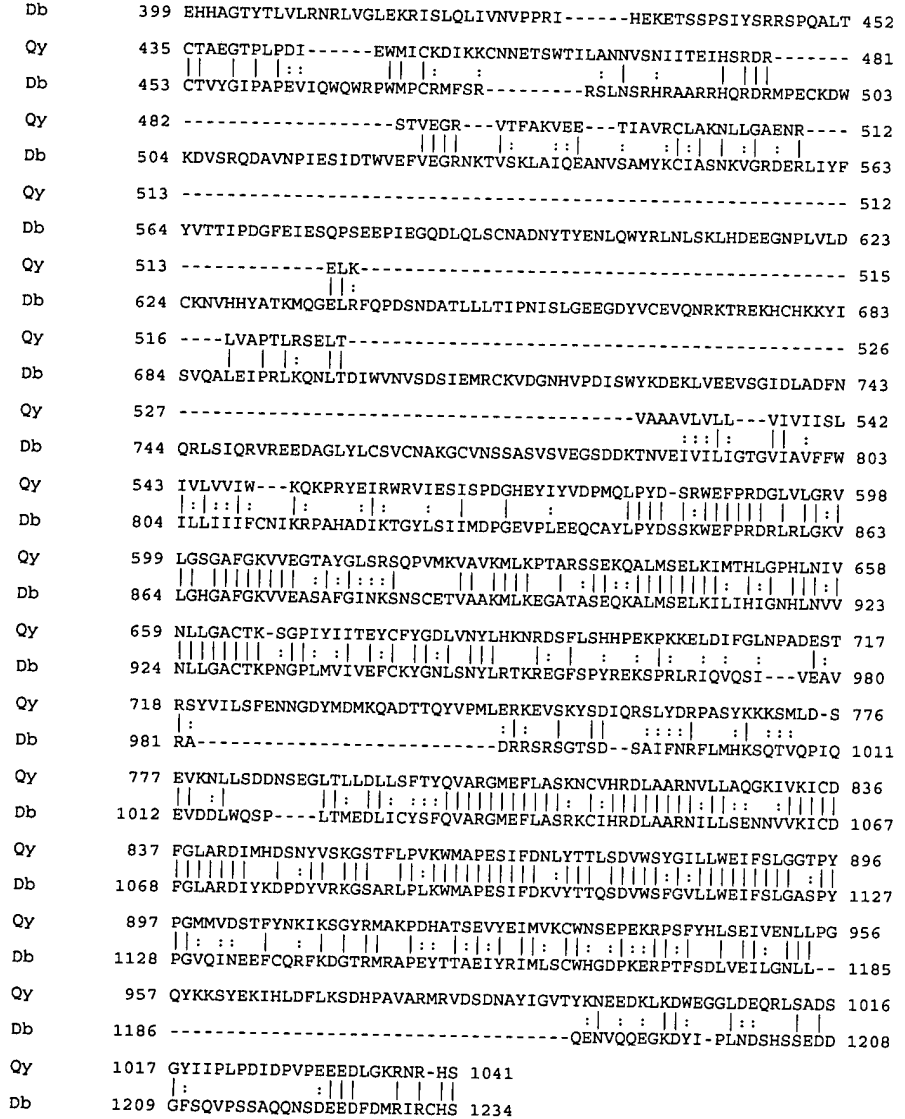
Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db         65 -NNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDL------ASVIYVY 117
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RESULT 27
JC4954
vascular endothelial growth factor receptor 2 precursor - Japanese quail
N;Alternate names: Quail endothelial kinase 2; Quek 2
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Oct-2004
C;Accession: JC4954
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A;Reference number: JC4953; MUID:97017121; PMID:8863722
A;Accession: JC4954
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1379 <EIC>
A;Cross-references: UNIPARC:UPI00000FD004; EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PI
C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelia
C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;789-810/Domain: transmembrane #status predicted <TMM>
F;856-1188/Domain: protein kinase homology <KIN>
F;864-872/Region: protein kinase ATP-binding motif

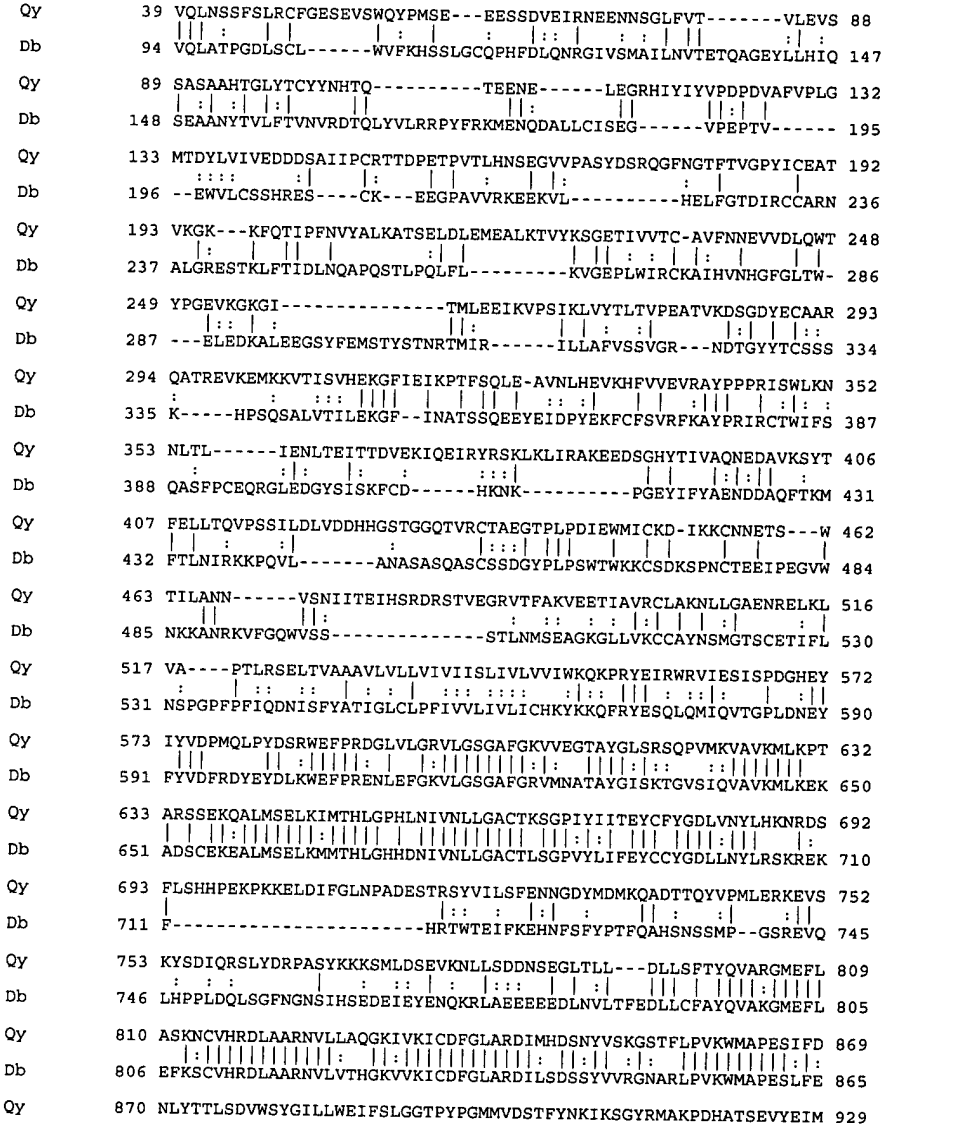
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Best Local Similarity 25.9%; Pred. No. 5.8e-46;
Matches 348; Conservative 193; Mismatches 376; Indels 429; Gaps 39;



RESULT 28
S18827
Flt3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: S18827
R;Rosnet, O.; Marchetto, S.; deLapeyriere, O.; Birnbaum, D.
Oncogene 6, 1641-1650, 1991
A;Title: Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSF1
A;Reference number: S18827; MUID:92019834; PMID:1656368

A;Accession: S18827
A;Molecule type: mRNA
A;Residues: 1-1000 <ROS>
A;Cross-references: UNIPROT:Q00342; UNIPARC:UPI0000145A53; EMBL:X59398; NID:g50978; PIDN
C;Keywords: ATP
F;609-953/Domain: protein kinase homology <KIN>
F;617-625/Region: protein kinase ATP-binding motif

Query Match 20.6%; Score 1164.5; DB 2; Length 1000;
Best Local Similarity 31.5%; Pred. No. 1.3e-44;
Matches 319; Conservative 164; Mismatches 330; Indels 199; Gaps 33;



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Db        866 GIYTIKSDVWSYGILLWEIFSLGVNPYPGIPVDANFYKLIQSGFKMEQPFYATEGIYFVM 925

Qy        930 VKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR 981
              ||  :  ||||| :|:  :   |    :  |: :  :    :||:: : |
Db        926 QSCWAFDSRKRPSFPNLTSFLGCQLAEAEEAMYQNMGGNV--PEHPSIYQNR 975


RESULT 29
A48999
protein-tyrosine kinase (EC 2.7.1.112) flt4 precursor - human
N;Alternate names: class III receptor tyrosine kinase FLT4; fms-like tyrosine kinase 4
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: A48999; A44930; G02316; S36130; A42010
R;Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara, L.; Alitalo, R.
Cancer Res. 52, 5738-5743, 1992
A;Title: FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and is e
A;Reference number: A48999; MUID:93007958; PMID:1327515
A;Accession: A48999
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1298 <PAJ>
A;Cross-references: UNIPROT:P35916; UNIPARC:UPI0000138777; PIDN:AAB23636.1; PID:g257352
A;Experimental source: HEL erythroleukemia cells
A;Note: sequence extracted from NCBI backbone (NCBIP:115335)
R;Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo, R.; Bailey, S.K.;
Cancer Res. 52, 746-748, 1992
A;Title: FLT4, a novel class III receptor tyrosine kinase in chromosome 5q33-qter.
A;Reference number: A44930; MUID:92119639; PMID:1310071
A;Accession: A44930
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 761-1190 <APR>
A;Cross-references: UNIPARC:UPI000017A3EA; GB:X68203; NID:g31433
A;Note: sequence extracted from NCBI backbone (NCBIP:78155)
R;Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01039
A;Accession: G02316
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1298 <WOO>
A;Cross-references: UNIPARC:UPI0000138777; EMBL:U43143; NID:g1150990; PIDN:AAA85215.1; P
R;Galland, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S36130
A;Accession: S36130
A;Molecule type: mRNA
A;Residues: 1-23,'D',25-744,'P',746-751,'RP',754-889,'Q',891-1127,'V',1129-1145,'H',1147
A;Cross-references: UNIPARC:UPI000003CA99; EMBL:X69878; NID:g297049; PIDN:CAA49505.1; PI
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.
Genomics 13, 475-478, 1992
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.
A;Reference number: A42010; MUID:92307693; PMID:1319394
A;Accession: A42010
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 776-889,'Q',891-1127,'V',1129-1145,'H',1147-1163,'D',1165-1200 <GAL2>
A;Cross-references: UNIPARC:UPI000017A3EB
C;Genetics:
A;Gene: GDB:FLT4
A;Cross-references: GDB:128732; OMIM:136352
A;Map position: 5q34-5q35
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-1298/Product: protein-tyrosine kinase FLT4 #status predicted <MAT>
F;843-1176/Domain: protein kinase homology <KIN>
F;851-859/Region: protein kinase ATP-binding motif

  Query Match             20.6%;  Score 1163.5;  DB 2;  Length 1298;
  Best Local Similarity   26.6%;  Pred. No. 1.9e-44;
  Matches  365;  Conservative  190;  Mismatches  393;  Indels  423;  Gaps   48;
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Qy          8 FLVLGC---LLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEE 64
              :| ||    |::| |     :: |::   |   |:    | |: | |:  : | :| ::|
Db         12 WLCLGLLDGLVSGYS-----MTPPTLNITEESHVIDTGDSLSISCRGQHPLEWAWPGAQE 66

Qy         65 -------ESSDVEIRN--EENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGR 115
                    :| |  :    |  ::  :  || :    |  || | ||| : :
Db         67 APATGDKDSEDTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARIEGTTAA 126

Qy        116 HIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVV-----PA 170
                |::| | :  |:    |  ::|   |:  :||  : |   ||| :   |:
Db        127 SSYVFVRDFEQPFINKPDT---LLVNRKDAMWVPCLVSIPGLNVTLRSQSSVLWPDGQEV 183

Qy        171 SYDSRQGFNGTFTVGPYI-------CEATVKGKKFQTIPFNVYALKATSELDLEMEALKT 223
              :| |:|       | :       || |   : | : || |: :       |:::   |:
Db        184 VWDDRRGM---LVSTPLLHDALYLQCETTWGDQDFLSNPFLVH-ITGNELYDIQLLPRKS 239

Qy        224 V-YKSGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLE-EIKVPSIKLVYTLTVPE 279
              :   || :|: | |:   |  |   | |||:   :|  : |   :    :|  ||:
Db        240 LELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHN 299

Qy        280 ATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIK----PTFSQLEAVNLHEVKHF 335
              :  | | | | |    :  :|  :|   |||  || ::    |    |||    |:
Db        300 VSQHDLGSYVCKANNGIQRFRESTEVI--VHENPFISVEWLKGPI---LEATAGDELVKL 354

Qy        336 VVEVRAYPPPRISWLKNNLTLIEN-------LTEITTDVEKIQEIRYRSKLKLIRAKEED 388
              |:: |||||   | |:   |           | |:|                |
Db        355 PVKLAAYPPPEFQWYKDGKALSGRHSPHALVLKEVT--------------------EAS 393

Qy        389 SGHYTIVAQNEDA--VKSYTFELLTQVPSSILD------LVDDHHGSTGGQTVRCTAEGT 440
              :| ||:   |  |   :: : ||:  ||  | :       :   |      | : ||| |
Db        394 TGTYTLALWNSAAGLRRNISLELVVNVPPQIHEKEASSPSIYSRHSR---QALTCTAYGV 450

Qy        441 PLP-DIEW-------------------------MICKD---------IKKCNNETSWT-- 463
              |||  |:|                        |:|         :    :  :||
Db        451 PLPLSIQWHWRPWTPCKMFAQRSLRRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEF 510

Qy        464 ------------------------ILANNVSN-------IITEIHSRDRSTVEGRVTFAK 492
                                       :::| |          :| |    |  |:| : :
Db        511 VEGKNKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYFYVTTI--PDGFTIESKPSEEL 568

Qy        493 VE-ETIAVRCLA-----------------------------KNL--------------- 506
              :| : : : | |                            ||:
Db        569 LEGQPVLLSCQADSYKYEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATPLAASLEEVA 628

Qy        507 LGAENRELKLVAPTLRSE----------------------LTVAAAVLVLLVIVIISLI 543
              || :  | |  | : |                      |:| |      |  :  |:
Db        629 PGARHATLSLSIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLL 688

Qy        544 VLV-----------------VIWK----------------------QKPRYEIRWRVIE 563
              | |                 ::|                      |: | |   | :
Db        689 VNVSDSLEMQCLVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLC 748

Qy        564 SI-----------------SPD------------------------------------ 568
              |:                | |
Db        749 SVCNAKGCVNSSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADI 808

Qy        569 --GHEYIYVDPMQLP---------YD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLS 616
                |:  | :|| ::|          || |:|||||: | ||||||  |||||||| :|:|:
Db        809 KTGYLSIIMDPGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIH 868

Qy        617 RSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITE 675
              :      |||||||  | :|| :||||||||: |:| |||:|||||||||  ||: :| |
Db        869 KGSSCDTVAVKMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPQGPLMVIVE 928

Qy        676 YCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMK 735
              :| ||:| |:|   ||:|                  :|  |         | |  | :  |
Db        929 FCKYGNLSNFLRAKRDAF----------------SPCAEK-------SPEQRGRFRAMV 964

Qy        736 QADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNL-LSDDNSEGLTLLD 794
              :      :  |:|:       :  : : :     :::  | | ::| ||      ||: |
Db        965 E------LARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSP-----LTMED 1013
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Qy        795 LLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGS 854
Db       1014 LVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGS 1073

Qy        855 TFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYR 914
Db       1074 ARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTR 1133

Qy        915 MAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHL------- 967
Db       1134 MRAPELATPAIRRIMLNCWSGDPKARPAFSELVEILGDLLQGRGLQEEEEVCMAPRSSQS 1193

Qy        968 ----DFLKSDHPAVARMRVDSDNA-------YIGVTYKN--------------EEDKLK 1001
Db       1194 SEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMK 1253

Qy       1002 DWE----------GGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSS 1042
Db       1254 TFEEFPMTPTTYKGSVDNQ---TDSGMVL------ASEEFEQIESRHRQES 1295


RESULT 30
A39931
protein-tyrosine kinase (EC 2.7.1.112) flk-2, hematopoietic - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 31-Dec-2004
C;Accession: A39931
R;Matthews, W.; Jordan, C.T.; Wiegand, G.W.; Pardoll, D.; Lemischka, I.R.
Cell 65, 1143-1152, 1991
A;Title: A receptor tyrosine kinase specific to hematopoietic stem and progenitor cell-e
A;Reference number: A39931; MUID:91292518; PMID:1648448
A;Accession: A39931
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-992 <MAT>
A;Cross-references: UNIPROT:Q00342; UNIPARC:UPI0000027EC0; GB:M64689; NID:g193327; PIDN:
C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
F;609-953/Domain: protein kinase homology <KIN>
F;617-625/Region: protein kinase ATP-binding motif

  Query Match           20.4%;  Score 1152.5;  DB 2;  Length 992;
  Best Local Similarity  32.0%;  Pred. No. 4.3e-44;
  Matches  314;  Conservative  154;  Mismatches  316;  Indels  197;  Gaps   32;

Qy         39 VQLNSSFSLRCFGESEVSWQYPMSE---EESSDVEIRNEENNSGLFVT-------VLEVS 88
Db         94 VQLATPGDLSCL------WVFKHSSLGCQPHFDLQNRGIVSMAILNVTETQAGEYLLHIQ 147

Qy         89 SASAAHTGLYTCYYNHTQ----------TEENE------LEGRHIYIYVPDPDVAFVPLG 132
Db        148 SERANYTVLFTVNVRDTQLYVLRRPYFRKMENQDALLCISEG------VPEPTV------ 195

Qy        133 MTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNGTFTVGPYICEAT 192
Db        196 --EWVLCSSHRES----CK---EEGPAVVRKEEKVL----------HELFGTDIRCCARN 236

Qy        193 VKGK---KFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTC-AVFNNEVVDLQWT 248
Db        237 ALGRECTKLFTIDLNQAPQSTLPQLFL---------KVGEPLWIRCKAIHVNHGFGLTW- 286

Qy        249 YPGEVKGKGI--------------TMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
Db        287 ---ELEDKALEEGSYFEMSTYSTNRTMIR------ILLAFVSSVGR---NDTGYYTCSSS 334

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLE-AVNLHEVKHFVVEVRAYPPPRISWLKN 352
Db        335 K-----HPSQSALVTILEKGF--INATSSQEEYEIDPYEKFCFSVRFKAYPRIRCTWIFS 387

Qy        353 NLTL------IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYT 406
Db        388 QASFPCEQRGLEDGYSISKFCD------HKNK----------PGEYIFYAENDDAQFTKM 431

Qy        407 FELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKD-IKKCNNETS---W 462

Db        432 FTLNIRKKPQVL-------ANASASQASCSSDGYPLPSWTWKKCSDKSPNCTEEIPEGVW 484

Qy        463 TILANN------VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKL 516
Db        485 NKKANRKVFGQWVSS--------------STLNMSEAGKGLLVKCCAYNSMGTSCETIFL 530

Qy        517 VA----PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEY 572
Db        531 NSPGPFPFIQDNISFYATIGLCLPFIVVLIVLICHKYKKQFRYESQLQMIQVTGPLDNEY 590

Qy        573 IYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPT 632
Db        591 FYVDFRDYEYDLKWEFPRENLEFGKVLGSGAFGRVMNATAYGISKTGVSIQVAVKMLKEK 650

Qy        633 ARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDS 692
Db        651 ADSCEKEALMSELKMMTHLGHHDNIVNLLGACTLSGPVYLIFEYCCYGDLLNYLRSKREK 710

Qy        693 FLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVS 752
Db        711 F----------------------HRTWTEIFKEHNFSSYPTFQAHSNSSMP--GSREVQ 745

Qy        753 KYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLL---DLLSFTYQVARGMEFL 809
Db        746 LHPPLDQLSGFNGNSIHSEDEIEYENQKRLAEEEEEDLNVLTFEDLLCFAYQVAKGMEFL 805

Qy        810 ASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFD 869
Db        806 EFKSCVHRDLAARNVLVTHGKVVKICDFGLARDILSDSSYVVRGNARLPVKWMAPESLFE 865

Qy        870 NLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIM 929
Db        866 GIYTIKSDVWSYGILLWEIFSLGVNPYPGIPVDANFYKLIQSGFKMEQPFYATEGIYFVM 925

Qy        930 VKCWNSEPEKRPSFYHLSEIV 950
Db        926 QSCWAFDSRKRPSFPNLTSFL 946


RESULT 31
I58375
protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004
C;Accession: I58375; B42010
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J
Oncogene 8, 2293-2298, 1993
A;Title: Molecular cloning of murine FLT and FLT4.
A;Reference number: I58375; MUID:93330572; PMID:8393164
A;Accession: I58375
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1363 <RES>
A;Cross-references: UNIPROT:P35917; UNIPARC:UPI0000028D92; GB:L07296; NID:g293780; PIDN:I
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.
Genomics 13, 475-478, 1992
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.
A;Reference number: A42010; MUID:92307693; PMID:1319394
A;Accession: B42010
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar
A;Molecule type: DNA
A;Residues: 1033-1072 <GAL>
A;Cross-references: UNIPARC:UPI000017A423
C;Genetics:
A;Gene: FTL4
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;843-1176/Domain: protein kinase homology <KIN>
F;851-859/Region: protein kinase ATP-binding motif

  Query Match           20.4%;  Score 1152.5;  DB 2;  Length 1363;
  Best Local Similarity  26.6%;  Pred. No. 6.4e-44;
  Matches  361;  Conservative  182;  Mismatches  358;  Indels  457;  Gaps   47;
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Qy          8 FLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEE--- 64
Db         12 WLCLG-LLQGLANGY-SMTPPTLNITEDSYVIDTGDSLSISCRGQHPLEWTWPGAQEVLT 69

Qy         65 ----ESSDVEIRN--EENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIY 118
Db         70 TGGKDSEDTRVVHDCEGTEARPYCKVLLLAQTHANNTGSYHCYYKYIKARIEGTTAASTY 129

Qy        119 IYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVV-----PASYD 173
Db        130 VFVRDFKHPFINKPDT---LLVNRKDSMWVPCLVSIPGLNITLRSQSSALHPDGQEVLWD 186

Qy        174 SRQGFNGTFTV---GPYI-CEATVKGKKFQTIPFNVYALKAT-SEL-DLEMEALKTV-YK 226
Db        187 DRRGMRVPTQLLRDALYLQCETTWGDQNFLS---NLFVVHITGNELYDIQLYPKKSMELL 243

Qy        227 SGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIK-VPS-------IKLVYTLT 276
Db        244 VGEKLVLNCTVWAEFDSGVTFDWDYPGK-------QAERAKWVPERRSQQTHTELSSILT 296

Qy        277 VPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIK----PTFSQLEAVNLHEV 332
Db        297 IHNVSQNDLGPYVCEANNGIQRFRESTEVI--VHEKPFISVEWLKGPV---LEATAGDEL 351

Qy        333 KHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHY 392
Db        352 VKLPVKLAAYPPPEFQWYK--------------DRKAVTGRHNPHALVLKEVTEASAGVY 397

Qy        393 TIVAQNEDA--VKSYTFELLTQVPSSILD------LVDDHHGSTGGQTVRCTAEGTPLP- 443
Db        398 TLALWNSAAGLRQNISLELVVNVPPHIHEKEASSPSIYSRHSR---QTLTCTAYGVPQPL 454

Qy        444 DIEW-------------------------MICKDIKKCNNE---------TSWTILANNV 469
Db        455 SVQWHWRPWTPCKTFAQRSLRRRQQRDGMPQCRDWKEVTTQDAVNPIESLDSWTEFVEGK 514

Qy        470 SNIITEIHSRDRS-----------------------------TVEGRVTFAKVE-ETI 497
Db        515 NKTVSKLVIQDANVSAMYKCVVVNKVGQDERLIYFYVTTIPDGFSIESEPSEDPLEGQSV 574

Qy        498 AVRCLAKN-------------------------LLGAENREL------------------ 514
Db        575 RLSCRADNYTYEHLRWYRLNLSTLHDAQGNPLLLDCKNVHLFATPLEANLEEAEPGARHA 634

Qy        515 ----------------------------------------KLVAPTLRSELT--------- 526
Db        635 TLSLNIPRVAPEDEGDYVCEVQDRRSQDKHCHKKYLSVQALEAPRLTQNLTDLLVNVSDS 694

Qy        527 ------VAAA-------------------------------------------------- 530
Db        695 LEMRCPVAGAHVPSIVWYKDERLLEKESGIDLADSNQRLSIQRVREEDAGRYLCSVCNAK 754

Qy        531 ---------------------VLVLL---VIVIISLIVLVVIW---KQKPRYEIRWRVIE 563
Db        755 GCVNSSASVAVEGSEDKGSMEIVILIGTGVIAVFFWVLLLLIFCNMKRPAHADIK----- 809

Qy        564 SISPDGHEYIYVDPMQLP---------YD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAY 613
Db        810 ----TGYLSIIMDPGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGHGAFGKVVEASAF 865

Qy        614 GLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYI 672
Db        866 GINKGSSCDTVAVKMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPNGPLMV 925

Qy        673 ITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYM 732
Db        926 IVEFCKYGNLSNFLRVKRDTF----------------NP------------------YA 950

Qy        733 DMKQADTTQYVPMLE--RKEVSKYSDIQRSLYDRPASYK---KKSMLDSEVKNL-LSDDN 786
Db        951 EKSPEQRRRFRAMVEGAKADRRRPGSSDRALFTRFLMGKGSARRAPLVQEAEDLWLSP-- 1008

Qy        787 SEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHD 846
Db       1009 ---LTMEDLVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDIVKICDFGLARDIYKD 1065

Qy        847 SNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFY 906
Db       1066 PDYVRKGSARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFC 1125

Qy        907 NKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIH 966
Db       1126 QRLKDGTRMRAPELATPAIRHIMQSCWSGDPKARPAFSDLVEILGDLLQG---------- 1175

Qy        967 LDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDID 1026
Db       1176 ------------------------------------GGWQEE---------------- 1181

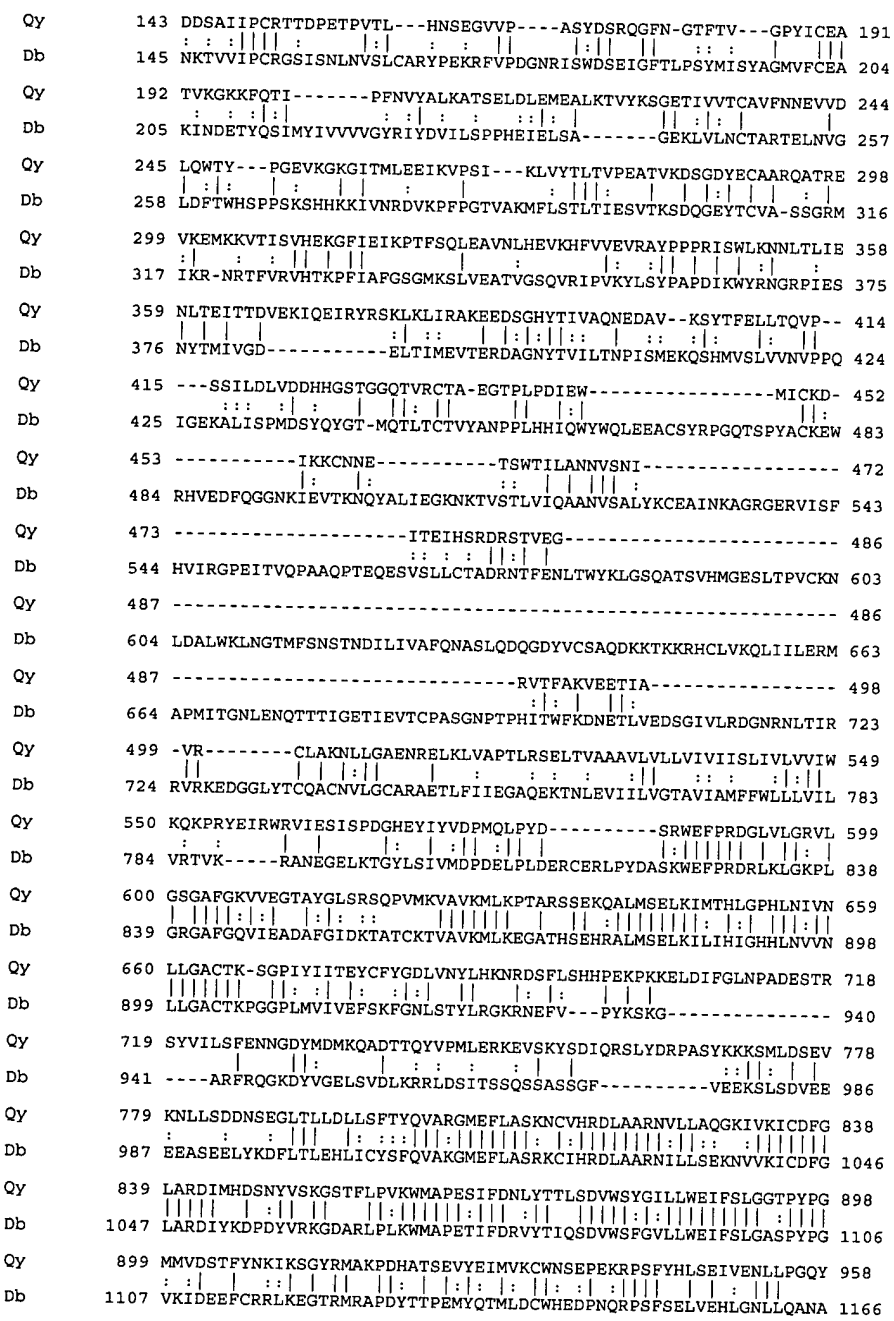
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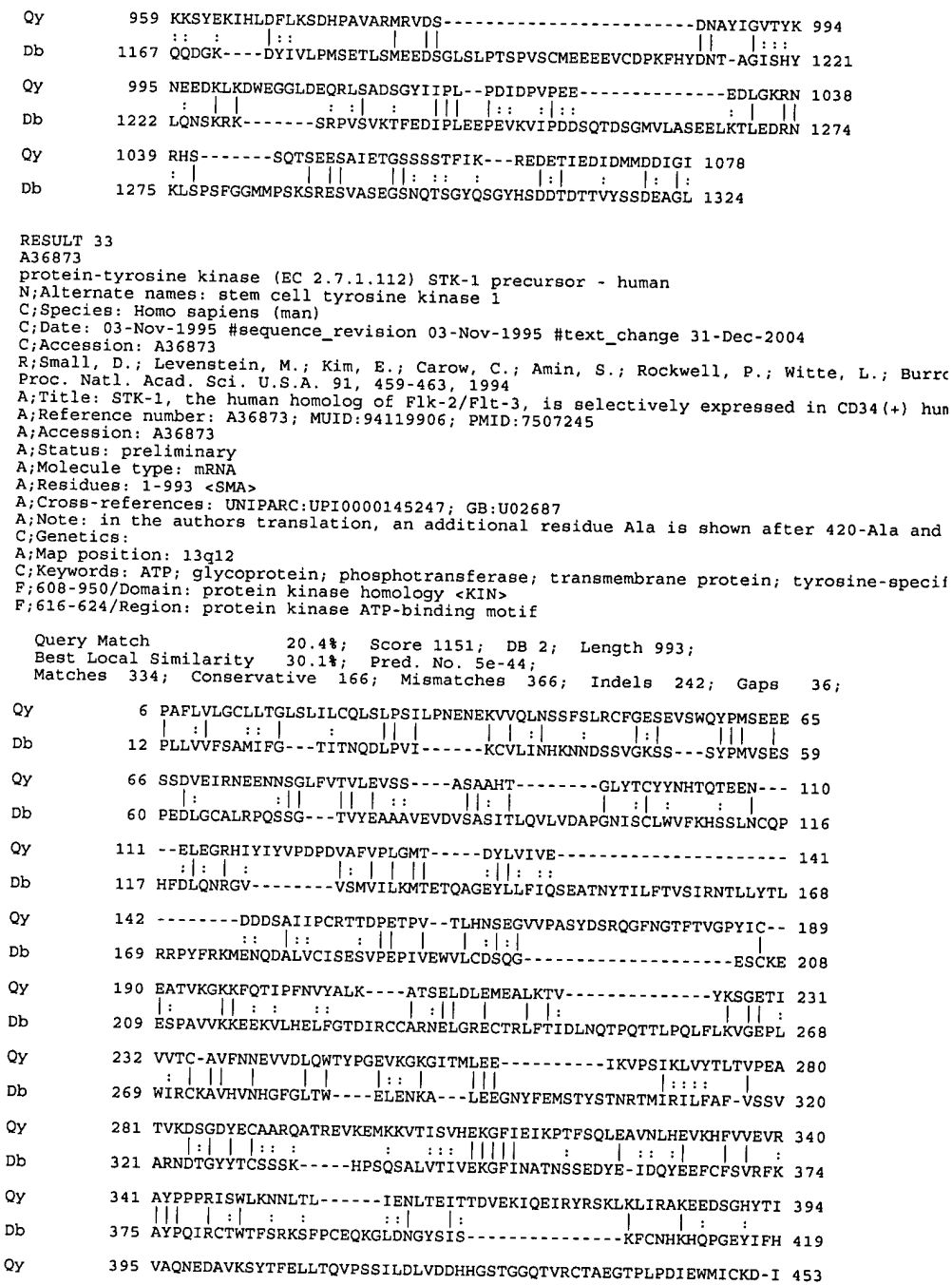
RESULT 32
A41228
protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C;Species: Mus musculus (house mouse)
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 31-Dec-2004
C;Accession: A41228; A46065; I58365; S18832; S29991
R;Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A;Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitiv
A;Reference number: A41228; MUID:92020984; PMID:1717995
A;Accession: A41228
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1367 <MAT>
A;Cross-references: UNIPROT:P35918; UNIPARC:UPI0000028D93; GB:X59397; NID:g50976; PIDN:C
R;Millauer, B.; Wizigmann-Voos, S.; Schnurch, H.; Martinez, R.; Moller, N.P.; Risau, W.;
Cell 72, 835-846, 1993
A;Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a majo
A;Reference number: A46065; MUID:93208880; PMID:7681362
A;Accession: A46065
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-24,'T',26-782,'VL',785-916,'C',918-1367 <MIL>
A;Cross-references: UNIPARC:UPI000003CA97; GB:X70842; NID:g57923; PIDN:CAA50192.1; PID:g
A;Note: submitted to the EMBL Data Library, January 1993
A;Note: sequence extracted from NCBI backbone (NCBIP:128064)
R;Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemiecki, A.; Wilks, A.F.
Oncogene 8, 11-18, 1993
A;Title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embryo
A;Reference number: I58365; MUID:93141255; PMID:8423988
A;Accession: I58365
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-678,'D',680-1340,'RSPPV' <OEL>
A;Cross-references: UNIPARC:UPI0000170C47; GB:S53103; NID:g264004; PIDN:AAB25043.1; PID:
C;Genetics:
A;Gene: FLK-1; NYK
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F;830-1165/Domain: protein kinase homology <KIN>
F;838-846/Region: protein kinase ATP-binding motif

  Query Match   20.4%; Score 1152; DB 2; Length 1367;
  Best Local Similarity   25.2%; Pred. No. 6.8e-44;
  Matches 345; Conservative 199; Mismatches 430; Indels 396; Gaps   40;

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Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSD-VEIRNEENNSGLFVTVLE 86
Db         32 PKLSTQKDILTILANTTLQITCRGQRDLDWLWPNAQRDSEERVLVTECGGGDSIFCKTLT 91

Qy         87 VSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIV----ED 142
Db         92 IPRVVGNDTGAYKCSYRDVDIAST------VYVYVRDYRSPFI-ASVSDQHGIVYITENK 144
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RESULT 33
A36873
protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human
N;Alternate names: stem cell tyrosine kinase 1
C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 31-Dec-2004
C;Accession: A36873
R;Small, D.; Levenstein, M.; Kim, E.; Carow, C.; Amin, S.; Rockwell, P.; Witte, L.; Burrc
Proc. Natl. Acad. Sci. U.S.A. 91, 459-463, 1994
A;Title: STK-1, the human homolog of Flk-2/Flt-3, is selectively expressed in CD34(+) hun
A;Reference number: A36873; MUID:94119906; PMID:7507245
A;Accession: A36873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-993 <SMA>
A;Cross-references: UNIPARC:UPI0000145247; GB:U02687
A;Note: in the authors translation, an additional residue Ala is shown after 420-Ala and
C;Genetics:
A;Map position: 13q12
C;Keywords: ATP; glycoprotein; phosphotransferase; transmembrane protein; tyrosine-specif
F;608-950/Domain: protein kinase homology <KIN>
F;616-624/Region: protein kinase ATP-binding motif

Query Match 20.4%; Score 1151; DB 2; Length 993;
Best Local Similarity 30.1%; Pred. No. 5e-44;
Matches 334; Conservative 166; Mismatches 366; Indels 242; Gaps 36;

```
                 |:|:||  :  | |  :    :|                | ::| ||    |  | |
Db        420 AAENDDAQFTKMFTLNIRRKPQVL-------AEASASQASCFSDGYPL-SWTWKKCSDKS 471

Qy        454 KKCNNETS---WTILANN------VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAK 504
                |  | :   |   ||       ||:              :  ::  :   |:| |
Db        472 PNCTEEITEGVWNRKANRKVFGQWVSS-------------STLNMSEAIKGFLVKCCAY 517

Qy        505 NLLGAENRELKLVA----PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWR 560
                | ||     : | :    | ::  ::  | : | |: :::  :::   :|:: ||| : :
Db        518 NSLGTSCETILLNSPGPFPFIQDNISFYATIGVCLLFIVVLTLLICHKYKKQFRYESQLQ 577

Qy        561 VIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP 620
                :::      :|| |||  :  || :|||||: |  |:||||||||||:  ||||:|::
Db        578 MVQVTGSSDNEYFYVDFREYEYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGV 637

Qy        621 VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYG 680
                 ::|||||||  | |||::|||||||:|| || | ||||||||||| |||||:| ||| ||
Db        638 SIQVAVKMLKEKADSSEREALMSELKMMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYG 697

Qy        681 DLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTT 740
                ||:|||   |: |                        |::  :  |:|  :    |:
Db        698 DLLNYLRSKREKF----------------------HRTWTEIFKEHNFSFYPTFQSHPN 734

Qy        741 QYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSE-VKNLLSDDNSEGLTLLDLLSFT 799
                  :|     ::   ||    |:   |: :  :: |  | |  :::   ||  ||| |
Db        735 SSMPGSREVQIHPDSDQISGLHGN--SFHSEDEIEYENQKRLEEEEDLNVLTFEDLLCFA 792

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
                ||||:|||||  |:||||||||||||:  ||:|||||||||||||| ||||| :|:  |||
Db        793 YQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNYVVRGNARLPV 852

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
                |||||||:|: :||  |||||||||||||||  ||||: ||: ||  |::|::| :|
Db        853 KWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPYPGIPVDANFYKLIQNGFKMDQPF 912

Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
                :|| |:| ||  ||  :  |||||  :|:  :   |    :  |: :  |   |: |
Db        913 YATEEIYIIMQSCWAFDSRKRPSFPNLTSFLGCQLADAEEAMYQNV--DGRVSECPH--- 967

Qy        980 MRVDSDNAYIGVTYKNEEDKLKDWEGGL 1007
                        ||:|    :: : ||
Db        968 ------------TYQNRRPFSREMDLGL 983


RESULT 34
FOMVHZ
gag-kit polyprotein precursor - feline sarcoma virus (strain Hardy-Zuckerman 4)
N;Contains: amino end of core protein p30; core protein p12; core protein p15; protein-t
C;Species: feline sarcoma virus
A;Note: host Felis sp. (cat)
C;Date: 04-Dec-1986 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A03936; A00655
R;Besmer, P.; Murphy, J.E.; George, P.C.; Qiu, F.; Bergold, P.J.; Lederman, L.; Snyder J
Nature 320, 415-421, 1986
A;Title: A new acute transforming feline retrovirus and relationship of its oncogene v-k
A;Reference number: A00655; MUID:86175044; PMID:3007997
A;Accession: A03936
A;Molecule type: DNA
A;Residues: 1-790 <BES>
A;Cross-references: UNIPROT:P04322; UNIPARC:UPI000017101D; GB:X03711; NID:g61535; PIDN:C
C;Genetics:
A;Gene: gag-kit
C;Superfamily: feline sarcoma virus gag-kit polyprotein; protein kinase homology
C;Keywords: ATP; core protein; oncogene; phosphotransferase; polyprotein; transforming p
F;1-74/Domain: leader peptide #status predicted <LDP>
F;75-781/Product: gag-kit polyprotein #status predicted <MAT>
F;75-201/Product: core protein p15 #status predicted <C15>
F;202-271/Product: core protein p12 #status predicted <C12>
F;272-414/Product: core protein p30 (fragment) #status predicted <P30>
F;439-783/Domain: protein kinase homology <KIN>
F;447-455/Region: protein kinase ATP-binding motif
F;475/Active site: Lys #status predicted

  Query Match           18.9%;  Score 1067;  DB 1;  Length 790;
  Best Local Similarity   53.8%;  Pred. No. 2.1e-40;
  Matches  211;  Conservative   62;  Mismatches   93;  Indels   26;  Gaps    6;

Qy        560 RVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 619
                :|:| |: :     |:|| ||||| :|||||: |  |: ||:|||||||| ||||| :|
Db        412 QVVEEINGNN----YIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSD 467

Qy        620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFY 679
                  |||||||:|  :|::|||||||::::|| |:|||||||||  ||  :||||| |
Db        468 AAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCY 527

Qy        680 GDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADT 739
                |||:|:| : ||||:    |   :      |  : ||: :      ::  :|||||
Db        528 GDLLNFLRRKRDSFICSKQEDHAEVALYKNLLQSKESSCN------DSTNEYMDMKPG-- 579

Qy        740 TQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFT 799
                  ||       |   :| :||   |  ||     :: :|   : :|    | | |||||:
Db        580 VSYV-------VPTKADKRRSA--RIGSY-----IERDVTPAIMEDGELALDLEDLLSFS 625

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
                ||||:|| |||||||:||||||||:||  |:| |||||||||| :||||| ||:  |||
Db        626 YQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPV 685

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
                |||||||||: :||  |||||||| |||:|||| :||||| ||| ||  || ||:||  |:
Db        686 KWMAPESIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPE 745

Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVE 951
                || :|:|:||  ||:::| |||:|  : :::|
Db        746 HAPAEMYDIMKTCWDADPLKRPTFKQIVQLIE 777


RESULT 35
TVCHFG
fibroblast growth factor receptor 1 precursor - chicken
N;Alternate names: basic fibroblast growth factor receptor
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) cek1
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41345; A33908
R;Lee, P.L.; Johnson, D.E.; Cousens, L.S.; Fried, V.A.; Williams, L.T.
Science 245, 57-60, 1989
A;Title: Purification and complementary DNA cloning of a receptor for basic fibroblast gr
A;Reference number: A41345; MUID:89298406; PMID:2544996
A;Accession: A41345
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-819 <LEE>
A;Cross-references: UNIPROT:P21804; UNIPARC:UPI00001725FE
A;Note: part of the sequence was confirmed by protein sequencing
R;Pasquale, E.B.; Singer, S.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 5449-5453, 1989
A;Title: Identification of a developmentally regulated protein-tyrosine kinase by using a
A;Reference number: A33908; MUID:89315814; PMID:2473471
A;Accession: A33908
A;Molecule type: mRNA
A;Residues: 1-89,'A',91-685,'M',687-819 <PAS>
A;Cross-references: UNIPARC:UPI00001725FF; GB:M24637
A;Note: this protein is expressed in embryonic tissues and, at low levels, in adult brain
C;Genetics:
A;Gene: cek1
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-819/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
F;22-374/Domain: extracellular #status predicted <EXT>
F;125-132/Region: acidic
F;169-230/Domain: immunoglobulin homology <IMM>
F;375-395/Domain: transmembrane #status predicted <TMM>
F;396-819/Domain: intracellular #status predicted <INT>
F;474-759/Domain: protein kinase homology <KIN>
F;482-490/Region: protein kinase ATP-binding motif
```

```
F;54-100,176-228,275-339/Disulfide bonds: #status predicted
F;76,116,225,238,262,294,315,328/Binding site: carbohydrate (Asn) (covalent) #status pre
F;512,529,621/Active site: Lys, Glu, Asp #status predicted
F;626,639/Binding site: magnesium (Asn, Asp) #status predicted
F;652/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match           15.3%;  Score 863;  DB 1;  Length 819;
  Best Local Similarity  27.0%;  Pred. No. 2.8e-31;
  Matches  292;  Conservative  131;  Mismatches  330;  Indels  330;  Gaps   38;

Qy         13 CLLTGLSLILCQLS-------LP-SILPNENEKVVQLNSS----FSLRCFGESEV---SW 57
Db          6 CLILWAVLVTATLSAARPAPTLPDQALPKANIEVESHSAHPGDLLQLRCRLRDDVQSINW 65

Qy         58 -----QYPMSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENEL 112
Db         66 VRDGVQLP----ENNRTRITGEE---------VEVRDRVPEDSGLYACMTNSPSGSE--- 109

Qy        113 EGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASY 172
Db        110 ------------TTYFSVNVSDALPSAEDDDD--------EDDSSSEEKEADNTKPNQ- 147

Qy        173 DSRQGFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIV 232
Db        148 ----------AVAPYWTYPEKMEKKLHAVP----------------------AAKTVK 173

Qy        233 VTCAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY---TLTVPEATVKDSGDYE 289
Db        174 FKCPSGGTPNPTLRWLKNGK------EFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYT 227

Qy        290 CAARQATREVKEMKKVTIS-VHEKGFIEIKPTFSQLEA-------VNLHEVKHFVVEVRA 341
Db        228 C--------IVENKYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFVCKVYS 279

Qy        342 YPPPRISWLK-----------NNLTLIENLTEI---TTDVEKIQEIRYRSKLKLIRAKEE 387
Db        280 DPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKE--MEV-----LHLRNVSFE 332

Qy        388 DSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEW 447
Db        333 DAGEYTCLAGNSIGI-------------------SHH--SAWLTVLEATEQSPAMMTSP 370

Qy        448 MICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLL 507
Db        371 LYLEIIIYCTG--AFLISCMVVTVIIYKMKSTTKKT--------DFNSQLAVHKLAKSI- 419

Qy        508 GAENRELKLVAPTLRSELTVAAAVL------VLLVIVIISLIVLVVIWKQKPRYEIRWRV 561
Db        420 ------------PLRRQVTVSADSSSSMNSGVMLV--------------RP-------- 444

Qy        562 IESISPDGHEYIY-VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP 620
Db        445 -SRLSSSGTPMLAGVSEYELPEDPRWELPRDRLILGKPLGEGCFGQVVLAEAIGLDKDKP 503

Qy        621 --VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCF 678
Db        504 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYAS 563

Qy        679 YGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQAD 738
Db        564 KGNLREYLQARR---------PPGME---YCYNP----TR-------------------- 587

Qy        739 TTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSF 798
Db        588 ----IP-----------------------------------------EEQLSFKDLVSC 601

Qy        799 TYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLP 858
Db        602 AYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLP 661

Qy        859 VKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKP 918
Db        662 VKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELF-KLLKEGHRMDKP 720

Qy        919 DHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA 978
Db        721 SNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRI---------------------- 755

Qy        979 RMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRN 1038
Db        756 -VAMTSNQEYLDLSV-----PLDQYSPGFPATRSSTCSSGEDSVFSHDPLPDEPCLPRCP 809

Qy       1039 RHS 1041
Db        810 PHS 812
```

RESULT 36
TVHUFG
fibroblast growth factor receptor 1 precursor - human
N;Alternate names: basic fibroblast growth factor receptor; heparin-binding growth factor
N;Contains: HBGFR 3; HBGFR alpha b1; HBGFR beta a1; HBGFR beta b1; HBGFR gamma a1; HBGFR
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S11692; B40862; S09226; A61533; A61536; S26739; S26738; S17374; S17375; S17
R;Dionne, C.A.; Crumley, G.; Bellot, F.; Kaplow, J.M.; Searfoss, G.; Ruta, M.; Burgess,
EMBO J. 9, 2685-2692, 1990
A;Title: Cloning and expression of two distinct high-affinity receptors cross-reacting wi
A;Reference number: S11691; MUID:90360977; PMID:1697263
A;Accession: S11692
A;Molecule type: mRNA
A;Residues: 1-822 <DIO>
A;Cross-references: UNIPROT:P11362; UNIPARC:UPI00000534B8; EMBL:X52833; NID:g31377; PIDN
R;Hou, J.; Kan, M.; McKeehan, K.; McBride, G.; Adams, P.; McKeehan, W.L.
Science 251, 665-668, 1991
A;Title: Fibroblast growth factor receptors from liver vary in three structural domains.
A;Reference number: A40862; MUID:91126480; PMID:1846977
A;Accession: B40862
A;Molecule type: mRNA
A;Residues: 1-822 <HOU>
A;Cross-references: UNIPARC:UPI00000534B8; GB:M63887
A;Note: potentially twelve variants may arise by alternative splicing in liver cells
R;Isacchi, A.; Bergonzoni, L.; Sarmientos, P.
Nucleic Acids Res. 18, 1906, 1990
A;Title: Complete sequence of a human receptor for acidic and basic fibroblast growth fac
A;Reference number: S09226; MUID:90245600; PMID:2159626
A;Accession: S09226
A;Molecule type: mRNA
A;Residues: 1-816,'R',818-822 <ISA>
A;Cross-references: UNIPARC:UPI00001432A9; EMBL:X51803; NID:g31367; PIDN:CAA36101.1; PID:
R;Wennstroem, S.; Sandstroem, C.; Claesson-Welsh, L.
Growth Factors 4, 197-208, 1991
A;Title: cDNA cloning and expression of a human FGF receptor which binds acidic and basic
A;Reference number: A61533; MUID:92118394; PMID:1722683
A;Accession: A61533
A;Molecule type: mRNA
A;Residues: 1-147,150-193,'S',195-822 <WEN>
A;Cross-references: UNIPARC:UPI000016A8EC; GB:M34641; NID:g182529; PIDN:AAA35835.1; PID:g
A;Experimental source: teracarcinoma cell line Tera-2
R;Kiefer, M.C.; Baird, A.; Nguyen, T.; George-Nascimento, C.G.; Mason, O.B.; Boley, L.J.;
Growth Factors 5, 115-127, 1991
A;Title: Molecular cloning of a human basic fibroblast growth factor receptor cDNA and ex
A;Reference number: A61536; MUID:92118399; PMID:1662973
A;Accession: A61536
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-147,150-822 <KIE>
A;Cross-references: UNIPARC:UPI000002A997
R;Tronick, S.R.
submitted to the EMBL Data Library, January 1991
A;Reference number: S19167
A;Accession: S26739
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-822 <TR1>
A;Cross-references: UNIPARC:UPI00000534B8; EMBL:X57121; NID:g31392; PIDN:CAA40403.1; PID:
```
```

A;Accession: S26738
A;Molecule type: mRNA
A;Residues: 1-147,150-822 <TR2>
A;Cross-references: UNIPARC:UPI000002A997; EMBL:X57120; NID:g31390; PIDN:CAA40402.1; PID
R;Eisemann, A.; Ahn, J.A.; Graziani, G.; Tronick, S.R.; Ron, D.
Oncogene 6, 1195-1202, 1991
A;Title: Alternative splicing generates at least five different isoforms of the human ba
A;Reference number: S17373; MUID:91319400; PMID:1650441
A;Accession: S17374
A;Molecule type: mRNA
A;Residues: 1-30,120-147,150-822 <EI4>
A;Cross-references: UNIPARC:UPI0000167BB6; EMBL:X57122; NID:g31386; PIDN:CAA40404.1; PID
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Prc
A;Note: this form is designated isoform I
A;Accession: S17375
A;Molecule type: mRNA
A;Residues: 1-30,120-822 <EI3>
A;Cross-references: UNIPARC:UPI000002A994; EMBL:X57119; NID:g31388; PIDN:CAA40401.1; PID
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Prc
A;Note: this form is designated isoform II
A;Accession: S17377
A;Molecule type: mRNA
A;Residues: 1-90,'D',91-822 <EI2>
A;Cross-references: UNIPARC:UPI00001725F7; EMBL:X57121
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Prc
A;Note: this form is designated isoform III
A;Accession: S17376
A;Molecule type: mRNA
A;Residues: 1-90,'D',91-147,150-822 <EIS>
A;Cross-references: UNIPARC:UPI00001725F8; EMBL:X57120
A;Note: this form is designated isoform IV
R;Itoh, N.; Terachi, T.; Ohta, M.; Seo, M.K.
Biochem. Biophys. Res. Commun. 169, 680-685, 1990
A;Title: The complete amino acid sequence of the shorter form of human basic fibroblast
A;Reference number: A35479; MUID:90290512; PMID:2162671
A;Accession: A35479
A;Molecule type: mRNA
A;Residues: 1-30,120-147,150-468,'L',470-822 <ITO>
A;Cross-references: UNIPARC:UPI00001562DD; GB:M37722; NID:g179413; PIDN:AAA75007.1; PID:
A;Note: both the longer and shorter forms are expressed in the placenta
R;Johnson, D.E.; Lee, P.L.; Lu, J.; Williams, L.T.
Mol. Cell. Biol. 10, 4728-4736, 1990
A;Title: Diverse forms of a receptor for acidic and basic fibroblast growth factors.
A;Reference number: A36464; MUID:90355989; PMID:2167437
A;Accession: A36464
A;Molecule type: mRNA
A;Residues: 1-30,120-822 <JOH>
A;Cross-references: UNIPARC:UPI000002A994; GB:M34185; NID:g182531; PIDN:AAA35836.1; PID:
A;Accession: B36464
A;Molecule type: mRNA
A;Residues: 1-30,120-147,150-191,'E',193-822 <JO2>
A;Cross-references: UNIPARC:UPI00001432AA; GB:M34186; NID:g182533; PIDN:AAA35837.1; PID:
A;Accession: E36464
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 71-132 <JO3>
A;Cross-references: UNIPARC:UPI00001725F9
R;Ruta, M.; Howk, R.; Ricca, G.; Drohan, W.; Zabelshansky, M.; Laureys, G.; Barton, D.E.
Oncogene 3, 9-15, 1988
A;Title: A novel protein tyrosine kinase gene whose expression is modulated during endot
A;Reference number: A28361
A;Accession: A28361
A;Molecule type: mRNA
A;Residues: 201-671,'IYLTGS',677-822 <RUT>
A;Cross-references: UNIPARC:UPI00001725FA; EMBL:Y00665
R;Hattori, Y.; Odagiri, H.; Katoh, O.; Sakamoto, H.; Morita, T.; Shimotohno, K.; Tobinai
Cancer Res. 52, 3367-3371, 1992
A;Title: K-sam-related gene, N-sam, encodes fibroblast growth factor receptor and is exp
A;Reference number: S25420; MUID:92282615; PMID:1317750
A;Accession: S25420
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-822 <HAT>
A;Cross-references: UNIPARC:UPI00000534B8; EMBL:X66945; NID:g35109; PIDN:CAA47375.1; PID
R;Rusnati, M.; Coltrini, D.; Caccia, P.; Dell'Era, P.; Zoppetti, G.; Oreste, P.; Valsasi
Biochem. Biophys. Res. Commun. 203, 450-458, 1994
A;Title: Distinct role of 2-O-, N-, and 6-O-sulfate groups of heparin in the formation o
A;Reference number: PC2394; MUID:94354840; PMID:8074689
A;Accession: PC2394
A;Molecule type: protein
A;Residues: 81-100 <RUS>
A;Cross-references: UNIPARC:UPI00001725FB
A;Experimental source: recombinant soluble form of extracellular domain after expression
A;Note: this sequence represents the amino end of a 33K fragment protected from trypsin
C;Comment: This receptor binds acidic and basic fibroblast growth factors with high affi
C;Genetics:
A;Gene: GDB:FGFR1; FLT2
A;Cross-references: GDB:119913; OMIM:136350
A;Map position: 8p11.2-8p11.1
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
yrosine-specific protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-822/Product: fibroblast growth factor receptor 1, form alpha a1 #status predicted <
F;22-427,430-822/Product: fibroblast growth factor receptor 1, form alpha b1 #status pre
F;22-376/Domain: extracellular #status predicted <EXT>
F;22-147,150-822/Product: fibroblast growth factor receptor 1, form 3 #status predicted
F;22-30,120-822/Product: fibroblast growth factor receptor 1, form beta a1 #status predi
F;22-30,120-427,430-822/Product: fibroblast growth factor receptor 1, form beta b1 #stat
F;126-133/Region: acidic
F;161-822/Product: fibroblast growth factor receptor 1, form gamma a1 #status predicted
F;161-427,430-822/Product: fibroblast growth factor receptor 1, form gamma b1 #status pr
F;171-232/Domain: immunoglobulin homology <IMM>
F;377-397/Domain: transmembrane #status predicted <TMM>
F;398-822/Domain: intracellular #status predicted <INT>
F;476-761/Domain: protein kinase homology <KIN>
F;484-492/Region: protein kinase ATP-binding motif
F;55-101,178-230,277-341/Disulfide bonds: #status predicted
F;77,117,227,240,264,296,317,330/Binding site: carbohydrate (Asn) (covalent) #status pre
F;514,531,623/Active site: Lys, Glu, Asp #status predicted
F;628,641/Binding site: magnesium (Asn, Asp) #status predicted
F;654/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match 15.2%; Score 859.5; DB 1; Length 822;
Best Local Similarity 26.0%; Pred. No. 4e-31;
Matches 285; Conservative 135; Mismatches 322; Indels 355; Gaps 36;

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Qy         13 CLLTGLSLI---LCQLSLPSILPNENEK----------VVQLNSSFSLRCFGESEV---S 56
                |||    |:   ||       || : :           :|      |||    :|   :
Db          6 CLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDLLQLRCRLRDDVQSIN 65

Qy         57 W-QYPMSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGR 115
               | :  :   ||:   |  ||          :||  :  | :|||  |  :
Db         66 WLRDGVQLAESNRTRITGEE---------VEVQDSVPADSGLYACVTSSPS--------- 107

Qy        116 HIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSR 175
                     |  :  : ::| |   ||||         | ::      ::   |
Db        108 -------GSDTTYFSVNVSDALPSSEDDDD--------DDDSSSEEKETDNTKP------ 146

Qy        176 QGFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTC 235
                    | ||         ||   :|                        : :|:   |
Db        147 ----NRMPVAPYWTSPEKMEKKLHAVP----------------------AAKTVKFKC 178

Qy        236 AVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY---TLTVPEATVKDSGDYECAA 292
                     |:|   |:          : ::   |: |   :: :       | |:| |
Db        179 PSSGTPNPTLRWLKNGK------EFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIV 232

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEA-------VNLHEVKHFVVEVRAYPPP 345
                  :    :: :        :|  |    |:|       | |     |: :| : | |
Db        233 ENEYGSINHTYQLDV-------VERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQP 285

Qy        346 RISWLK-----------NNLTLIENLTEI---TTDVEKIQEIRYRSKLKLIRAKEEDSGH 391
                | |||          :||  :: |      ||| |   |:     | |     ||:|
Db        286 HIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKE--MEV-----LHLRNVSFEDAGE 338

Qy        392 YTIVAQNEDAVKSYT-----FELLTQVPSSI-----LDLVDDHHGSTGGQTVRCTAEGTP 441
```

```
Db        339 YTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEII---IYCTGAFLISCMVGSV- 394

Qy        442 LPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRC 501

Db        395 ---IVYKMKSGTKK-----------------SDFHSQ----------------MAVHK 416

Qy        502 LAKNLLGAENRELKLVAPTLRSELTVAA---AVL---VLLVIVIISLIVLVVIWKQKPRY 555

Db        417 LAKSI------------PLRRQVTVSADSSASMNSGVLLV--------------RP-- 446

Qy        556 EIRWRVIESISPDGHEYIY-VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYG 614

Db        447 -------SRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIG 499

Qy        615 LSRSQP--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYI 672

Db        500 LDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYV 559

Qy        673 ITEYCFYGDLVNYLHKNRDSFL------SHHPEKPKKELDIFGLNPADESTRSYVILSFE 726

Db        560 IVEYASKGNLREYLQARRPPGLEYCYNPSHNPE-------------------------- 592

Qy        727 NNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDN 786

Db        593 ------------------------------------------------------------ 592

Qy        787 SEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHD 846

Db        593 -EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHI 651

Qy        847 SNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFY 906

Db        652 DYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELF- 710

Qy        907 NKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIH 966

Db        711 KLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRI------------- 757

Qy        967 LDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDID 1026

Db        758 ------------VALTSNQEYLDLSM-----PLDQYSPSFPDTRSSTCSSGEDSVFSHE 799

Qy       1027 PVPEEEDLGKRNRHSSQ 1043

Db        800 PLPEEPCL---PRHPAQ 813
```

RESULT 37
S29840
fibroblast growth factor receptor 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S29840
R;Yazaki, N.; Fujita, H.; Ohta, M.; Kawasaki, T.; Itoh, N.
Biochim. Biophys. Acta 1172, 37-42, 1993
A;Title: The structure and expression of the FGF receptor-1 mRNA isoforms in rat tissues
A;Reference number: S29840; MUID:93176824; PMID:8382532
A;Accession: S29840
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-822 <YAZ>
A;Cross-references: UNIPROT:Q04589; UNIPARC:UPI000012A727; EMBL:D12498; NID:g220737; PID
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; autophosphorylation; growth factor receptor; phosphoprotein; transmembr
F;171-232/Domain: immunoglobulin homology <IMM>
F;476-761/Domain: protein kinase homology <KIN>
F;484-492/Region: protein kinase ATP-binding motif

Query Match 15.1%; Score 855; DB 2; Length 822;
Best Local Similarity 26.6%; Pred. No. 6.3e-31;
Matches 291; Conservative 133; Mismatches 324; Indels 344; Gaps 38;

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Qy          7 AFLVLGCLLTGL-SLILCQLSLPSILPNENEK-VVQLNSSFSLRCFGESEV---SW-QYP 60

Db         11 AVLVTATLCTARPAPTLPEQAQPWGVPVEVESLLVHPGDLLQLRCRLRDDVQSINWLRDG 70

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Db         71 VQLAESNRTRITGEE---------VEVRDSIPADSGLYACVTNSPS------------- 107

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Db        108 --GSDTTYFSVNVSDALPSSEDDDD--------DDDSSSEEKETDNTKP----NRR---- 149

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Db        150 --PVAPYWTSPEKMEKKLHAVP----------------------AAKTVKFKCPSSGT 183

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY---TLTVPEATVKDSGDYECAARQATR 297

Db        184 PSPTLRWLKNGK------EFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYG 237

Qy        298 EVKEMKKVTISVHEKGFIEIKPTFSQLEA-------VNLHEVKHFVVEVRAYPPPRISWL 350

Db        238 SINHTYQLDV-------VERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWL 290

Qy        351 K-----------NNL---TLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVA 396

Db        291 KHIEVNGSKIGPDNLPYDQILKTAGVNTTDKE--MEV-----LHLRNVSFEDAGEYTCLA 343

Qy        397 QNEDAVKSYT-----FELLTQVPSSI-----LDLVDDHHGSTGGQTVRCTAEGTPLPDIE 446

Db        344 GNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEII---IYCTGAFLISCMVGSV----II 396

Qy        447 WMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNL 506

Db        397 YKMKSGTKK-----------------SDFHSQ----------------MAVHKLAKSI 421

Qy        507 LGAENRELKLVAPTLRSELTVAA---AVL---VLLVIVIISLIVLVVIWKQKPRYEIRWR 560

Db        422 ------------PLRRQVTVSADSSASMNSGVLLV--------------RP------- 446

Qy        561 VIESISPDGHEYIY-VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 619

Db        447 --SRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDK 504

Qy        620 P--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYC 677

Db        505 PNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYA 564

Qy        678 FYGDLVNYLHKNRDSFL------SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDY 731

Db        565 SKGNLREYLQARRPPGLEYCYNPSHNPE---------------------------------- 592

Qy        732 MDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLT 791

Db        593 ------------------------------------------------------EQLS 596

Qy        792 LLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVS 851

Db        597 SKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKK 656

Qy        852 KGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKS 911

Db        657 TTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPNPGVPVEELF-KLLKE 715

Qy        912 GYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLK 971

Db        716 GHRMDKPSNCTNELYMMMRDCWNAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMP-LD 774

Qy        972 SDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEE 1031

Db        775 QDSPSFPDTR--------SSTCSSGEDSVFSHE---------------------PFPEE 804

Qy       1032 EDLGKRNRHSSQ 1043
```

```
Db        805 PCL---PRHPTQ 813


RESULT 38
A36477
fibroblast growth factor receptor A2 precursor - African clawed frog
N;Contains: fibroblast growth factor receptor A2, short splice form; protein-tyrosine ki
C;Species: Xenopus laevis (African clawed frog)
C;Date: 08-Mar-1991 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A36477; C39752
R;Musci, T.J.; Amaya, E.; Kirschner, M.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 8365-8369, 1990
A;Title: Regulation of the fibroblast growth factor receptor in early Xenopus embryos.
A;Reference number: A36477; MUID:91045998; PMID:2172985
A;Accession: A36477
A;Molecule type: mRNA
A;Residues: 1-812 <MUS>
A;Cross-references: UNIPROT:P22182; UNIPARC:UPI000012A728; GB:U24491; GB:M37201; NID:g85
A;Note: 45-Arg, 49-Thr, 50-Val, and 64-Ser also found
R;Friesel, R.; Dawid, I.B.
Mol. Cell. Biol. 11, 2481-2488, 1991
A;Title: cDNA cloning and developmental expression of fibroblast growth factor receptore
A;Reference number: A39752; MUID:91203867; PMID:1850097
A;Accession: C39752
A;Molecule type: mRNA
A;Residues: 1-30,119-189,'G',191-418,'L',420-636,'R',638-788,'V',790-812 <FRI>
A;Cross-references: UNIPARC:UPI00000FDA99; GB:M62322; NID:g214899; PIDN:AAA49993.1; PID:
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-812/Product: fibroblast growth factor receptor A2, long splice form #status predict
F;22-372/Domain: extracellular #status predicted <EXT>
F;22-30,119-812/Product: fibroblast growth factor receptor A2, short splice form #status
F;47-102/Domain: immunoglobulin homology <IM1>
F;125-132/Region: acidic
F;167-228/Domain: immunoglobulin homology <IM2>
F;266-339/Domain: immunoglobulin homology <IM3>
F;373-393/Domain: transmembrane #status predicted <TMM>
F;394-812/Domain: intracellular #status predicted <INT>
F;470-755/Domain: protein kinase homology <KIN>
F;478-486/Region: protein kinase ATP-binding motif
F;54-100,174-226,273-337/Disulfide bonds: #status predicted
F;76,116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent) #st
F;508,525,617/Active site: Lys, Glu, Asp #status predicted
F;622,635/Binding site: magnesium (Asn, Asp) #status predicted
F;648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match             15.1%;  Score 854;  DB 1;  Length 812;
  Best Local Similarity   28.9%;  Pred. No. 6.9e-31;
  Matches  262;  Conservative  120;  Mismatches  288;  Indels  238;  Gaps   29;

Qy        228 GETIVVTCAVFNNEVVDLQWTYPG----EVKGKGITMLEEIKVPSIKLVYTLTVPEATVK 283
              |: | : | :   :|  : |   |     |     ||  |||:: :           |  :
Db         47 GDRITLQCRL-REDVQSINWVKNGVQLSETNRTRITG-EEIQISN-----------AGPE 93

Qy        284 DSGDYECAARQATREVKEMKKVTI----------------SVHEKGFIEIKPT------ 320
              |:| | |     :|    :  | :                |  ||     ||
Db         94 DNGVYACVTNGPSRTYTVLCSVNVSDALPSAEDDDEDDDNSSSEEKAAENSKPNRPLWSH 153

Qy        321 ----FSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYR 376
                  :| ||   :   |      | | : |||||   ::      ::|  : |
Db        154 PEKMEKKLHAVPAAKTVKFRCPANGTPTPTLRWLKNNRAFQQD--------QRIGGYKVR 205

Qy        377 SK---LKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTV 433
              |:   | :       | |:|| : :|:    ::|::|     |    ::     :    ||
Db        206 SQTWSLIMDSVVPSDKGNYTCIVENKYGAINHTYQLDVVERSPHRPILQAGLPANTSVTV 265

Qy        434 RCTAE------GTPLPDIEWMICKDIKKCN--------NETSWTILANNVSNIITEIHSR 479
              |||        | | |:|:   :|             |   |    |     :  :| |
Db        266 GTTAEFSCKVYSDPQPHIQWLRHIEINGSRVASDGFPYVEILKTAGVNTSDKDMEVLHLR 325

Qy        480 DRSTVEGRVTFAKVEETIAVRCLAKNLLG-----------AENRELKLVAPTLRSEL-- 525
              :       |||   |:     ||| | :|           |: :  |:|  |: |:
Db        326 N-------VTF---EDAGQYTCLAANSIGISHHSAWLTVLKVEDNKPALLASPLQLEIII 375

Qy        526 --TVAAAVLVLLVIVII------------SLIVLVVIWKQKPRYEIRWRV--------- 561
                | || |  ::| :||            | : :  : |  |   :| :|
Db        376 YCTGAAFVSAMVVTIIIFKMKHPSKKSDFNSQLAVHKLAKSIP---VRRQVTVSGDSSSS 432

Qy        562 -------IESISPDGHEYIY-VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAY 613
                    :  :|  |   :  :   :|| | |||  || |:|| || | ||:||   |
Db        433 MNSGVILVRRLSSSGTPMLSGLSEYELPEDPRWEVARDRLILGKPLGEGCFGQVVMAEAI 492

Qy        614 GLSRSQP--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIY 671
              || : :|  | |||||||||  |   :   |:||:::|  :| | ||:|||||||: ||:|
Db        493 GLDKEKPNKVTKVAVKMLKSDASEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLY 552

Qy        672 IITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDY 731
              :| ||   |:|  ||   |          |  |   :  ||
Db        553 VIVEYTSKGNLREYLRARR---------PPAME---YCYNPT----------------- 582

Qy        732 MDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLT 791
                      ||                  |:  |:|
Db        583 ----------CVP-----------------DQLLSFK---------------------- 592

Qy        792 LLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVS 851
              ||:|  |||||||::|||| |:||||||||||: :  |:|| |||||||| |   |
Db        593 --DLVSCAYQVARGMDYLASKKCIHRDLAARNVLVTEDNIMKIADFGLARDIHHIDYYKK 650

Qy        852 KGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKS 911
              :  |||||||||::|| :||  |||||:|:|||||:|||:||||: ::   |   :|
Db        651 TTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPMEELF-KLLKE 709

Qy        912 GYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLK 971
              |:|| || : |:|:| :|  ||:: | :||:|  | | :: :|     : |  : :  :
Db        710 GHRMDKPTNCTNELYMMMKDCWHAMPSQRPTFNQLVEDLDRILALSSNQEYLDLSMP-VN 768

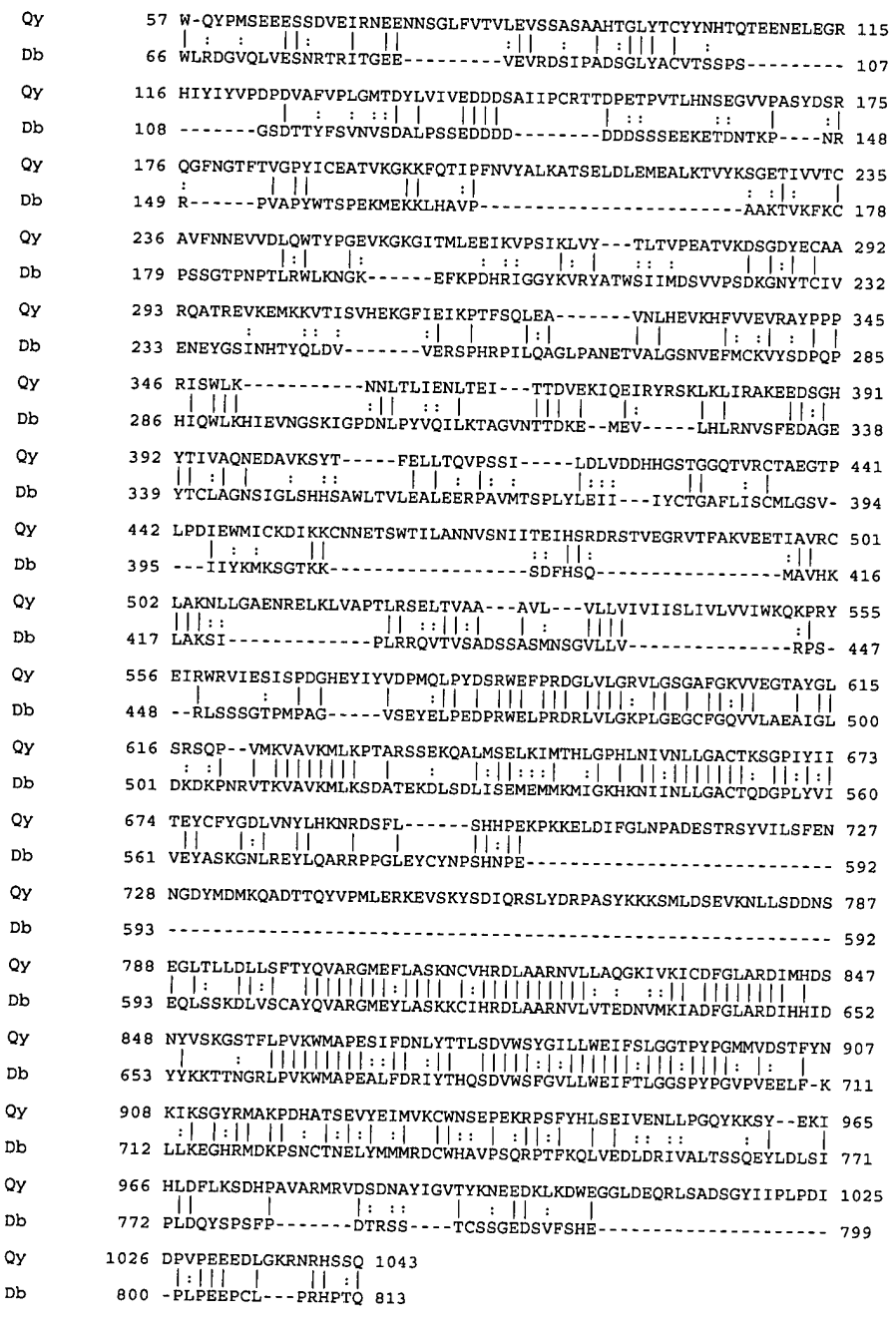
Qy        972 SDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEE 1031
                |     |          |  : || :           | |     ||||   :|:
Db        769 QYSPCFPDTR--------SSTCSSGEDSM----------FSHD-----PLPDEPCLPKY 804

Qy       1032 EDLGKRNR 1039
                : | : |
Db        805 SNGGLKKR 812


RESULT 39
I49289
fibroblast growth factor receptor-1, long isoform precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49289
R;Jin, Y.; Pasumarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A;Title: Cloning and expression of fibroblast growth factor receptor-1 isoforms in the m
A;Reference number: I49289; MUID:95205422; PMID:7897669
A;Accession: I49289
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-822 <RES>
A;Cross-references: UNIPROT:Q60818; UNIPARC:UPI000003F144; EMBL:U22324; NID:g722340; PID
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C;Keywords: ATP; growth factor receptor
F;270-343/Domain: immunoglobulin homology <IMM>
F;476-761/Domain: protein kinase homology <KIN>
F;484-492/Region: protein kinase ATP-binding motif

  Query Match             15.1%;  Score 852.5;  DB 2;  Length 822;
  Best Local Similarity   26.5%;  Pred. No. 8.1e-31;
  Matches  291;  Conservative  133;  Mismatches  317;  Indels  357;  Gaps   39;

Qy         13 CLLTGLSLI---LCQLSLPSILPNENEK----------VVQLNSSFSLRCFGESEV---S 56
              |||    |:   ||       || : :           :|       |||    :|   :
Db          6 CLLFWAVLVTATLCTARPAPTLPEQAQPWGVPVEVESLLVHPGDLLQLRCRLRDDVQSIN 65
```



RESULT 40
TVMSFG
fibroblast growth factor receptor 1 precursor - mouse
N;Alternate names: basic fibroblast growth factor receptor
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) flg
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A34849; B34849; S09953; A35794; A43025; PC2277
R;Reid, H.H.; Wilks, A.F.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 87, 1596-1600, 1990
A;Title: Two forms of the basic fibroblast growth factor receptor-like mRNA are expressed
A;Reference number: A34849; MUID:90160373; PMID:1689490
A;Accession: A34849
A;Molecule type: mRNA
A;Residues: 1-822 <REI>
A;Cross-references: UNIPROT:P16092; UNIPARC:UPI0000161D54; GB:M28998; NID:g192164; PIDN:
A;Accession: B34849
A;Molecule type: mRNA
A;Residues: 1-30,120-822 <RE2>
A;Cross-references: UNIPARC:UPI00001725FC; GB:M28998
A;Note: the shorter form is expressed at higher levels in neuronal cells at early stages
R;Safran, A.; Avivi, A.; Orr-Urtereger, A.; Neufeld, G.; Lonai, P.; Givol, D.; Yarden, Y
Oncogene 5, 635-643, 1990
A;Title: The murine flg gene encodes a receptor for fibroblast growth factor.
A;Reference number: S09953; MUID:90265603; PMID:2161096
A;Accession: S09953
A;Molecule type: mRNA
A;Residues: 1-147,150-255,'ILQ',259-439,'A',441-755,'R',757-822 <SAF>
A;Cross-references: UNIPARC:UPI000016CD4D; EMBL:X51893; NID:g50959; PIDN:CAA36175.1; PID
R;Mansukhani, A.; Moscatelli, D.; Talarico, D.; Levytska, V.; Basilico, C.
Proc. Natl. Acad. Sci. U.S.A. 87, 4378-4382, 1990
A;Title: A murine fibroblast growth factor (FGF) receptor expressed in CHO cells is activ
A;Reference number: A35794; MUID:90272715; PMID:2161540
A;Accession: A35794
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-628,'LV',631-755,'
A;Cross-references: UNIPARC:UPI00001725FD; GB:M33760
R;Basilico, C.
submitted to GenBank, March 1990
A;Reference number: A43025
A;Accession: A43025
A;Molecule type: mRNA
A;Residues: 1-30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-755,'R',757-764,'I
A;Cross-references: UNIPARC:UPI000016CD53; GB:M33760; NID:g193298; PIDN:AAA37622.1; PID:g
R;Harada, T.; Saito, H.; Kouhara, H.; Kurebayashi, S.; Kasayama, S.; Terakawa, N.; Kishin
Biochem. Biophys. Res. Commun. 205, 1057-1063, 1994
A;Title: Murine fibroblast growth factor receptor 1 gene generates multiple messenger RNA
A;Reference number: PC2277; MUID:95100926; PMID:7802632
A;Accession: PC2277
A;Molecule type: DNA
A;Residues: 1-15 <HAR>
A;Cross-references: UNIPARC:UPI0000170CA4; GB:S74765; NID:g833887; PIDN:AAB32845.1; PID:g
C;Comment: This protein mediates the biological actions of heparin-binding growth factors
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gr
protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-822/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
F;22-376/Domain: extracellular #status predicted <EXT>
F;22-30,120-822/Product: fibroblast growth factor receptor 1, short form #status predicte
F;126-133/Region: acidic
F;171-232/Domain: immunoglobulin homology <IMM>
F;377-397/Domain: transmembrane #status predicted <TMM>
F;398-822/Domain: intracellular #status predicted <INT>
F;476-761/Domain: protein kinase homology <KIN>
F;484-492/Region: protein kinase ATP-binding motif
F;55-101,178-230,277-341/Disulfide bonds: #status predicted
F;77,117,227,240,264,296,317,330/Binding site: carbohydrate (Asn) (covalent) #status pred
F;514,531,623/Active site: Lys, Glu, Asp #status predicted
F;628,641/Binding site: magnesium (Asn, Asp) #status predicted
F;654/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

```
  Query Match           15.0%;  Score 849.5;  DB 1;  Length 822;
  Best Local Similarity  28.4%;  Pred. No. 1.1e-30;
  Matches  268;  Conservative  118;  Mismatches  275;  Indels  282;  Gaps   35;

Qy        216 LEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPG----EVKGKGITMLEEIKVPSIKL 271
              :|:|:|  :   |: : : | :  ::|  : |   |     |     ||  ||::|
Db         38 VEVESL--LVHPGDLLQLRCRL-RDDVQSINWLRDGVQLVESNRTRITG-EEVEVRD--- 90

Qy        272 VYTLTVPEATVKDSGDYECAARQATREVKEMKKVTI----------------SVHEKGFI 315
                ::|     ||| | |      :         | :                | ||
Db         91 ----SIP----ADSGLYACVTSSPSGSDTTYFSVNVSDALPSSEDDDDDDDSSSEEKETD 142

Qy        316 EIKPT--------------FSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLT 361
               ||                 :| ||   :   |        | | : ||||
Db        143 NTKPNRRPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNG-------K 195

Qy        362 EITTDVEKI--QEIRYRS-KLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSIL 418
              |  |  :|   ::|| :  : :       | |:|| : :||    ::|::          |
Db        196 EFKPD-HRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ---------L 245

Qy        419 DLVD--DH--HGSTG---------GQTVR--CTAEGTPLPDIEWMICKDIKKCNNETS-- 461
              |:|:   |  | | |          |  |   |      | | |:|:  | |:   ::
Db        246 DVVERSPHRPHPSAGLPANKTVALGSNVEFMCKVYSDPQPHIQWL--KHIEVNGSKIGPD 303

Qy        462 --------WTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRE 513
                      |   |     :  :| |:      |:|   |:      ||| | :|  :
Db        304 NLPYVQILKTAGVNTTDKEMEVLHLRN-------VSF---EDAGEYTCLAGNSIGLSHHS 353

Qy        514 LKL-VAPTLRSELTVAAAVLVLLVIV-------IISLIVLVVIWKQK------------- 552
              | |   |      |  : | | :|:       |  ::  |:|:| |
Db        354 AWLTVLEALEERPAVMTSPLYLEIIIYCTGAFLISCMLGSVIIYKMKSGTKKSDFHSQMA 413

Qy        553 -----PRYEIRWRVIES-----------------ISPDGHEYIY-VDPMQLPYDSRWEF 588
                    :| :|  |                   :|  |   :  |   :|| | |||
Db        414 VHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWEL 473

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP--VMKVAVKMLKPTARSSEKQALMSELK 646
              ||| ||||: || | ||:||    | || : :|  | ||||||||  |   :   |:||::
Db        474 PRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEME 533

Qy        647 IMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFL------SHHPEK 700
              :|  :| | ||:|||||||: ||:|:| ||   |:|  ||   |   |       ||:||
Db        534 MMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPE- 592

Qy        701 PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRS 760

Db        593 ------------------------------------------------------------ 592

Qy        761 LYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLA 820
                                       | |:  ||:|  |||||||:|||| |:|||||
Db        593 -------------------------EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLA 625

Qy        821 ARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWS 880
              |||||: :  ::|| |||||||| |    |     :  |||||||||::|| :||  |||||
Db        626 ARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWS 685

Qy        881 YGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKR 940
              :|:||||||:|||:||||: |:  |    :| |:|| || : |:|:| :|   ||::  | :|
Db        686 FGVLLWEIFTLGGSPYPGVPVEELF-KLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQR 744

Qy        941 PSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKL 1000
              |:|    ::||:|                ||      : : |:  |: ::          |
Db        745 PTF---KQLVEDL------------------DH----IVALTSNQEYLDLSI-----PL 773

Qy       1001 KDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQ 1043
                :      : | |  |      :   :|:|||  |    || :|
Db        774 DQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL---PRHPTQ 813


RESULT 41
A39752
fibroblast growth factor receptor A1 precursor - African clawed frog
N;Contains: fibroblast growth factor receptor A1, short splice form; protein-tyrosine kir
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Feb-1992 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A39752; B39752
R;Friesel, R.; Dawid, I.B.
Mol. Cell. Biol. 11, 2481-2488, 1991
A;Title: cDNA cloning and developmental expression of fibroblast growth factor receptors
A;Reference number: A39752; MUID:91203867; PMID:1850097
A;Accession: A39752
A;Molecule type: mRNA
A;Residues: 1-814 <FRI>
A;Cross-references: UNIPROT:Q91897; UNIPARC:UPI00000FC58F; GB:M55163; NID:g214893; PIDN:A
A;Accession: B39752
A;Molecule type: mRNA
A;Residues: 1-30,119-814 <FR2>
A;Cross-references: UNIPARC:UPI0000172600; GB:M55163
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-814/Product: fibroblast growth factor receptor A1, long splice form #status experim
F;22-372/Domain: extracellular #status predicted <EXT>
F;22-30,119-814/Product: fibroblast growth factor receptor A1, short splice form #status
F;47-102/Domain: immunoglobulin homology <IM1>
F;125-132/Region: acidic
F;167-228/Domain: immunoglobulin homology <IM2>
F;266-339/Domain: immunoglobulin homology <IM3>
F;373-393/Domain: transmembrane #status predicted <TMM>
F;394-814/Domain: intracellular #status predicted <INT>
F;472-757/Domain: protein kinase homology <KIN>
F;480-488/Region: protein kinase ATP-binding motif
F;54-100,174-226,273-337/Disulfide bonds: #status predicted
F;76,116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent) #sta
F;510,527,619/Active site: Lys, Glu, Asp #status predicted
F;624,637/Binding site: magnesium (Asn, Asp) #status predicted
F;650/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

  Query Match           15.0%;  Score 846;  DB 1;  Length 814;
  Best Local Similarity  27.2%;  Pred. No. 1.6e-30;
  Matches  252;  Conservative  128;  Mismatches  279;  Indels  266;  Gaps   29;

Qy        226 KSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITML---------EEIKVPSIKLVYTLT 276
              : |:|: : | :   :|  : |     ||  |: :|         |||:: :
Db         45 RPGDTVTLQCRL-REDVQSISW-----VK-NGVQLLETNRTRITGEEIQISN-------- 89

Qy        277 VPEATVKDSGDYECAA-----------------RQATREVKEMKKVTISVHEKGFIEIKP 319
                |  :|:| | |                    | : |  :      |  ||     ||
Db         90 ---AGPEDNGLYACVTIGPSGTYTVLFSINVSDAQPSAEDDDDDDDNSSSEEKASENSKP 146

Qy        320 T----------FSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEK 369
                       :| ||   :   |       | | : ||||          |   | ::
Db        147 NRPFWSHPEKMEKKLHAVPAAKTVKFRCPANGTPSPALRWLKNG-------KEFRPD-QR 198

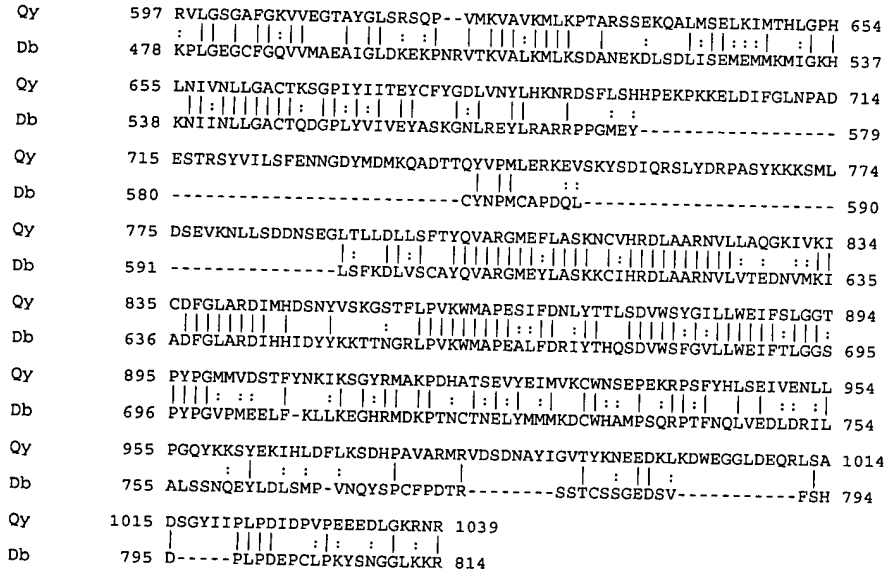
Qy        370 IQEIRYRSK---LKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVD---- 422
              |   : ||:   | :       | |:|| : :|:    ::|::          ||:|:
Db        199 IGGYKVRSQTWSLIMDSVVPSDKGNYTCIVENKYGTLNHTYQ---------LDVVERSPH 249

Qy        423 ---------DHHGSTGGQTVR--CTAEGTPLPDIEWMICKDIKKCN--------NETSWT 463
                      :   | | |      |     | | |:|:   :|             |   |
Db        250 RPILQAGLPANTSVTVGSTAEFSCKVYSDPQPHIQWLRHIEINGSRVASDGFPYVEILKT 309

Qy        464 ILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRS 523
              |     :  :| |:       |||   |:    ||| | :|  :    |   :
Db        310 AGVNTSDKDMEVLHLRN-------VTF---EDAGQYTCLAANSIGISHHSAWLTVLEVED 359

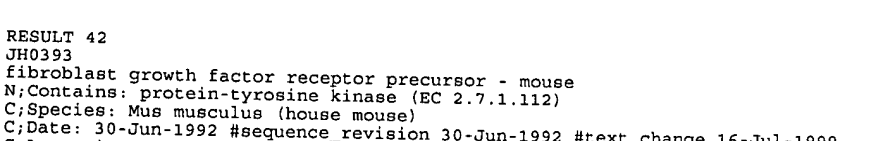
Qy        524 EL-TVAAAVLVLLVIV-------IISLIVLVVIWKQK-----------------PRYEI 557
              :   : |: | | :|:       : :::| ::|:| |                  :
Db        360 DKPALLASPLQLEIIIYCTGAAFVSAMVVTIIIFKMKHPSKKSDFNSQLAVHKLAKSIPL 419

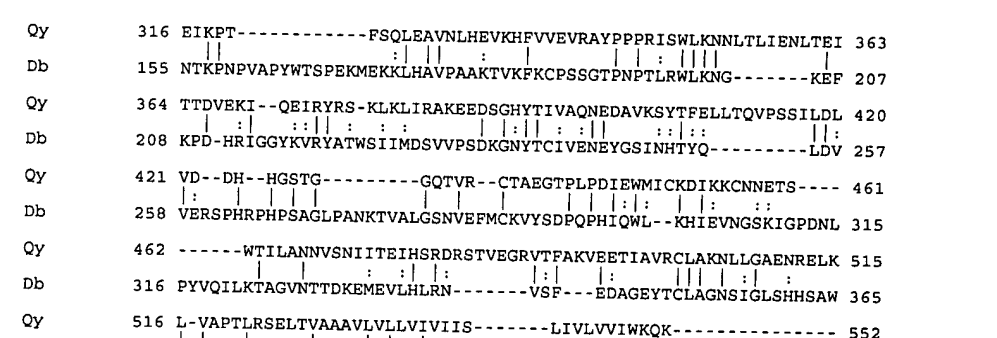
Qy        558 RWRVIESISPDGHEYIY--------------------VDPMQLPYDSRWEFPRDGLVLG 596
              | :|  ::| | :  ::                   |   :|| | |||  || |:||
Db        420 RRQV--TVSGDSNSSMHSGVILVRPSRLSSSGTPMLSGVSEYELPEDPRWEVARDRLILG 477
```



RESULT 42
JH0393
fibroblast growth factor receptor precursor - mouse
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C;Accession: JH0393
R;Kouhara, H.; Kasayama, S.; Saito, H.; Matsumoto, K.; Sato, B.
Biochem. Biophys. Res. Commun. 176, 31-37, 1991
A;Title: Expression cDNA cloning of fibroblast growth factor (FGF) receptor in mouse bre
A;Reference number: JH0393; MUID:91207411; PMID:1708247
A;Accession: JH0393
A;Molecule type: mRNA
A;Residues: 1-832 <KOU>
A;Cross-references: UNIPARC:UPI000016CD52; GB:M65053; NID:g193292; PIDN:AAA37620.1; PID:
A;Experimental source: breast cancer cell line SC-3
A;Note: the authors translated the codon ATG for residue 397 as Ile and CTG for residue
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-832/Product: fibroblast growth factor receptor #status predicted <FGF>
F;181-242/Domain: immunoglobulin homology <IMM>
F;387-409/Domain: transmembrane #status predicted <TMM>
F;486-771/Domain: protein kinase homology <KIN>
F;494-502/Region: protein kinase ATP-binding motif
F;67-113,188-240,287-351/Disulfide bonds: #status predicted
F;524,541,633/Active site: Lys, Glu, Asp #status predicted

Query Match 14.9%; Score 843.5; DB 2; Length 832;
Best Local Similarity 28.3%; Pred. No. 2.1e-30;
Matches 267; Conservative 117; Mismatches 275; Indels 284; Gaps 35;





RESULT 43
A49151
fibroblast growth factor receptor 1 - Iberian ribbed newt
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49151
R;Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.
Development 116, 261-273, 1992
A;Title: Differential expression and regulation of two distinct fibroblast growth factor
A;Reference number: A49151; MUID:93130775; PMID:1483392
A;Accession: A49151
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-816 <SHI>
A;Cross-references: UNIPROT:Q91285; UNIPARC:UPI0000175634
A;Note: sequence extracted from NCBI backbone (NCBIN:122562, NCBIP:122597)

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor
F;169-230/Domain: immunoglobulin homology <IMM>
F;472-757/Domain: protein kinase homology <KIN>
F;480-488/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 841.5; DB 2; Length 816;
Best Local Similarity 27.7%; Pred. No. 2.5e-30;
Matches 263; Conservative 124; Mismatches 281; Indels 281; Gaps 34;

```
Qy      200 TIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPG----EVKG 255
            |:|  |     : :  :|:|:    :  |: : : | :  ::|  : |   |     |
Db       26 TLPEQV-----SPKAKVEVESYSAHH--GDLLQLRCRL-RDDVHSINWEKDGVQLAETNR 77

Qy      256 KGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTI-----SVH 310
              ||  |                : | :|  :||| | |   : :          | :    ||
Db       78 TRITGAE------------VEVRDAVQEDSGLYACMTHRPSGTETTFFAVNVSDRIPSVE 125

Qy      311 EKGFIEIKPTFSQLEAVN-------------------LHEVK-----HFVVEVRAYPPPR 346
            :    : | :  : || |                    || |          |       | |
Db      126 DDDDDDEKSSSEEKEAENSKPNPVAPFWAHPEKMEKKLHAVPAAKTVKFRCPAGGTPSPT 185

Qy      347 ISWLKNNLTLIENLTEITTDVEKI--QEIRYRS-KLKLIRAKEEDSGHYTIVAQNEDAVK 403
            : ||||          |   |  :|   ::||::  : :       | | || : :|
Db      186 LRWLKNG-------KEFKPD-HRIGGYKVRYQTWSIIMDSVVPSDKGPYTCLVENNYGSI 237

Qy      404 SYTFELLTQVPSSILDLVD--DHH-----GSTGGQTVR--------CTAEGTPLPDIEWM 448
            ::|::         ||:|:   |       |   |||          |     | | |:|:
Db      238 NHTYQ---------LDVVERSPHRPILQAGLPANQTVPVGSNVDFVCKVYSDPQPHIQWL 288

Qy      449 ---------------ICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAK 492
                          : : :|           |      :  :| |:        |:|
Db      289 KHVTVNGSKYGSDGLPLVQVLKAAG--------VNTTDKEMEVLHLRN-------VSF-- 331

Qy      493 VEETIAVRCLAKNLLGAENRELKL-VAPTLRSELTVAAAVLVLLVIV-------IISLIV 544
             |:     ||| | :|  :    | |   :      :  : | | :|:       |  ::|
Db      332 -EDAGEYTCLAGNSIGISHHSAWLTVVEAISENPVIMTSPLYLEIIIYCTGAFLISCMLV 390

Qy      545 LVVIWKQK-----------------PRYEIRWRVI---------------ESISPDGH 570
             |:|:| |                  : :: :|              :|  |
Db      391 TVIIYKMKNTTKKTDFNSQPAVHKLAKSFPLQRQVSADSSSSMSSGVMLVRPSRLSSSGS 450

Qy      571 EYIY-VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP--VMKVAVK 627
              :  |   :|| | |||| || |:||: || | ||:|| | | || : :|  | |||||
Db      451 PMLTGVSEYELPEDPRWEFSRDRLILGKPLGEGCFGQVVMGEAIGLDKEKPNRVTKVAVK 510

Qy      628 MLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLH 687
            |||  |   :  |:||:::|  :| | ||:|||||||: ||:|:| ||   |:|  ||
Db      511 MLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLR 570

Qy      688 KNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLE 747
             |          |  |   :  ||
Db      571 ARR---------PPGME---YCYNPI---------------------------------- 584

Qy      748 RKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGME 807
             |||                                 : |:  ||:|  ||||||||
Db      585 --HVSK---------------------------------DMLSFKDLVSCAYQVARGME 608

Qy      808 FLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESI 867
            :|||| |:|||||||||: :  ::|| |||||||| |    |     :  |||||||::
Db      609 YLASKKCIHRDLAARNVLVTEDSVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPEAL 668

Qy      868 FDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYE 927
            || :||  |||||:|:|||||:|||:||||: |:   |   :| |:|| || : |:|:|
Db      669 FDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELF-KLLKEGHRMDKPGNCTNELYM 727

Qy      928 IMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNA 987
            :|  ||:: | :||:|  | | :: ::     : |    ||          | ||
Db      728 MMRDCWHAVPSQRPTFKQLVEDLDRIVAMTSNQEY----LDL---------SMPVD---- 770

Qy      988 YIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGK 1036
                      :  |  : | |  |      :   ||:|:|  | |
Db      771 -------------QYSPGFPDTRSSTCSSGEDSVFSHDPLPDEPCLPK 805
```

RESULT 44
S38579
fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment)
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38579
R;Shi, D.L.; Fromentoux, V.; Launay, C.; Umbhauer, M.; Boucaut, J.C.
submitted to the EMBL Data Library, November 1993
A;Description: Expression of FGFR-3 in amphibian embryos.
A;Reference number: S38579
A;Accession: S38579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-797 <SHI>
A;Cross-references: UNIPROT:Q91287; UNIPARC:UPI0000175635; EMBL:X75603
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor
F;258-331/Domain: immunoglobulin homology <IMM>
F;456-741/Domain: protein kinase homology <KIN>
F;464-472/Region: protein kinase ATP-binding motif

Query Match 14.9%; Score 841; DB 2; Length 797;
Best Local Similarity 28.2%; Pred. No. 2.5e-30;
Matches 236; Conservative 124; Mismatches 256; Indels 222; Gaps 26;

```
Qy      224 VYKSGETIVVTCAVFNNEV----------VD-LQWTYPGEVKGKGITMLEEIKVPSIKLV 272
            :: :|:|| ::|    : |          ||  |:: |:                  ||:
Db       46 LFGTGDTIELSCTTPGSSVSVVWFKDGISVDPPTWSHTGQ----------------KLL 88

Qy      273 YTLTVPEATVKDSGDYECAARQATREVKEMKKVTISV-----------HEKGFIEIKPT 320
              : |   :  ||| | | |||::   : :: ||: |             |:      |
Db       89 KIINV---SYDDSGVYSCKARQSS---EVLRNVTVRVTDSPSSGDDEDDDEESESANAPK 142

Qy      321 FSQLE-------AVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEI 373
            |:: |        ||       |     | | |:|||             :|  |
Db      143 FTRPEWMEKKLLAVPAANTVRFRCPAAGKPTPSITWLKNGKEF--------KGEHRIGGI 194

Qy      374 RYRSK---LKLIRAKEEDSGHYTIVAQNEDAV--KSYTFELLTQVP-SSILDLVDDHHGS 427
            : | :   | :      | |:|| |  |:     ::|| ::| : |   ||       |
Db      195 KLRHQQWSLVMESVVPSDRGNYTCVVANKYGTIRETYTLDVLERTPHRPILQA-----GF 249

Qy      428 TGGQTV--------RCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSR 479
              :||          |        | |:|:  | :     | : :    : :  :| : :
Db      250 RSNKTVVVGSDVEFHCKVYSDAQPHIQWL--KHV-----EVNGSKFGPDGNPYVTVLKTA 302

Qy      480 DRSTVE--------GRVTFAKVEETIAVRCLAKNLLGAENRELKLV-------APTLRSE 524
              :| :          |||   |:     ||| | :|  :     |              | : :
Db      303 GVNTSDKELEIQFLRNVTF---EDAGEYTCLAGNSIGYSHHSAWLTVLPPAEPVPDVDTS 359

Qy      525 LTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESI------------------- 565
            ::: ||   : |:::: :|:     |   :  :    :  :
Db      360 VSILAAAGCVAVVILVVIIIFTYKMKMPSKKTMNTATVHKVSKFPLKRQVSLESNSSMNS 419

Qy      566 -----------SPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYG 614
                       | ||      |  ::|| | :||   |  | ||: || | ||:||   | |
Db      420 NTPLVRITRLSSSDGPMLANVSELELPADPKWELSRSRLTLGKPLGEGCFGQVVMADAVG 479

Qy      615 LSRSQP--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYI 672
            : : :|     |||||||  |   :   |:||:::|  :| | ||:|||||||: ||:|:
Db      480 IEKDKPNKATSVAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQDGPLYV 539

Qy      673 ITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYM 732
            : ||   |:|  ||    |   : :                          ||:
Db      540 LVEYASKGNLREYLRARRPPGMDY--------------------------SFD------ 566

Qy      733 DMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTL 792
                | :|                                              | ||
Db      567 -------TCKLP-------------------------------------------EEQLTF 577

Qy      793 LDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSK 852
             ||:|  ||||||||:|||: |:||||||||||:    ::|| |||||||: |: :|  |
```

```
Db        578 KDLVSCAYQVARGMEYLASQKCIHRDLAARNVLVTDDNVMKIADFGLARDV-HNIDYYKK 636

Qy        853 GST-FLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKS 911

Db        637 TTNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELF-KLLKE 695

Qy        912 GYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDF 969

Db        696 GHRMDKPANCTHELYMIMRECWHAVPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSVPF 753


RESULT 45
TVHUF2
fibroblast growth factor receptor 2 precursor - human
N;Alternate names: fibroblast growth factor receptor K-sam
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) bek; receptor-like protein-tyrosine k
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
C;Accession: A42691; B42691; S11691; A36210; B44775; D44775
R;Katoh, M.; Hattori, Y.; Sasaki, H.; Tanaka, M.; Sugano, K.; Yazaki, Y.; Sugimura, T.;
Proc. Natl. Acad. Sci. U.S.A. 89, 2960-2964, 1992
A;Title: K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase.
A;Reference number: A42691; MUID:92212948; PMID:1313574
A;Accession: A42691
A;Molecule type: mRNA
A;Residues: 1-821 <KAT>
A;Cross-references: UNIPARC:UPI000012A72A; GB:M87770; NID:g186779; PIDN:AAA59470.1; PID:
A;Accession: B42691
A;Molecule type: mRNA
A;Residues: 1-313,430-821 <KA2>
A;Cross-references: UNIPARC:UPI000002A9A6; GB:M87771; NID:g186781; PIDN:AAA59471.1; PID:
R;Dionne, C.A.; Crumley, G.; Bellot, F.; Kaplow, J.M.; Searfoss, G.; Ruta, M.; Burgess,
EMBO J. 9, 2685-2692, 1990
A;Title: Cloning and expression of two distinct high-affinity receptors cross-reacting w
A;Reference number: S11691; MUID:90360977; PMID:1697263
A;Accession: S11691
A;Molecule type: mRNA
A;Residues: 1-821 <DIO>
A;Cross-references: UNIPARC:UPI000012A72A; EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID
R;Houssaint, E.; Blanquet, P.R.; Champion-Arnaud, P.; Gesnel, M.C.; Torriglia, A.; Court
Proc. Natl. Acad. Sci. U.S.A. 87, 8180-8184, 1990
A;Title: Related fibroblast growth factor receptor genes exist in the human genome.
A;Reference number: A36210; MUID:91045961; PMID:2172978
A;Accession: A36210
A;Molecule type: mRNA
A;Residues: 1-313,'VLK',314-428,431-821 <HOU>
A;Cross-references: UNIPARC:UPI000002A9A7; GB:M55614; GB:M37715; NID:g339710; PIDN:AAA61
R;Champion-Arnaud, P.; Ronsin, C.; Gilbert, E.; Gesnel, M.C.; Houssaint, E.; Breathnach,
Oncogene 6, 979-987, 1991
A;Title: Multiple mRNAs code for proteins related to the BEK fibroblast growth factor re
A;Reference number: A44775; MUID:91296403; PMID:1648704
A;Accession: B44775
A;Molecule type: DNA
A;Residues: 263-361 <CH2>
A;Cross-references: UNIPARC:UPI000006D144; GB:S40858; NID:g232799; PIDN:AAB19320.1; PID:
A;Accession: D44775
A;Molecule type: DNA
A;Residues: 759-821 <CHA>
A;Cross-references: UNIPARC:UPI0000172602; GB:S41873
C;Comment: This receptor binds basic fibroblast growth factor and, with lower affinity,
C;Genetics:
A;Gene: GDB:FGFR2
A;Cross-references: GDB:127273; OMIM:176943
A;Map position: 10q25.3-10q26
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-821/Product: fibroblast growth factor receptor 2 #status predicted <MAT>
F;22-377/Domain: extracellular #status predicted <EXT>
F;132-138/Region: acidic
F;172-233/Domain: immunoglobulin homology <IMM>
F;378-398/Domain: transmembrane #status predicted <TMM>
F;399-821/Domain: intracellular #status predicted <INT>
F;479-764/Domain: protein kinase homology <KIN>
F;487-495/Region: protein kinase ATP-binding motif
F;62-107,179-231,278-342/Disulfide bonds: #status predicted
F;83,123,228,241,265,297,318,331/Binding site: carbohydrate (Asn) (covalent) #status prec
F;517,534,626/Active site: Lys, Glu, Asp #status predicted
F;631,644/Binding site: magnesium (Asn, Asp) #status predicted
F;657/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

  Query Match             14.7%;  Score 833.5;  DB 1;  Length 821;
  Best Local Similarity   29.0%;  Pred. No. 5.7e-30;
  Matches  262;  Conservative  112;  Mismatches  279;  Indels  251;  Gaps   31;

Qy        185 GPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYK----------SGETIVVT 234

Db          5 GRFICLVVV---TMATLSLARPSFSLVEDTTLEPEEPPTKYQISQPEVYVAAPGESLEVR 61

Qy        235 CAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYT---LTVPEATVKDSGDYECA 291

Db         62 CLLKDAAVI--SWTKDGVHLG----------PNNRTVLIGEYLQIKGATPRDSGLYACT 108

Qy        292 ARQATREVKE-----MKKVT--IS--------------VHEKGFIEIKPTFSQLEAV--N 328

Db        109 ---ASRTVDSETWYFMVNVTDAISSGDDEDDTDGAEDFVSENSNNKRAPYWTNTEKMEKR 165

Qy        329 LHEVK-----HFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSK---LK 380

Db        166 LHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQE--------HRIGGYKVRNQHWSLI 217

Qy        381 LIRAKEEDSGHYTIVAQNEDAVKSYTFEL--LTQVP-SSILDLVDDHHGST---GGQTVR 434

Db        218 MESVVPSDKGNYTCVVENEYGSINHTYHLDVVERSPHRPILQAGLPANASTVVGGDVEFV 277

Qy        435 CTAEGTPLPDIEWMICKDIKKCNNETSWTIL----------ANNVSNIITEIHSRDRSTV 484

Db        278 CKVYSDAQPHIQWI--KHVEKNGSKYGPDGLPYLKVLKAAGVNTTDKEIEVLYIRN---- 331

Qy        485 EGRVTFAKVEETIAVRCLAKNLLGAENRELKLV---APTLRSELTVA-----AAVLVLLV 536

Db        332 ---VTF---EDAGEYTCLAGNSIGISFHSAWLTVLPAPGREKEITASPDYLEIAIYCIGV 385

Qy        537 IVIISLIVLVVIWKQK----------------------------------------PRY 555

Db        386 FLIACMVVTVILCRMKNTTKKPDFSSQPAVHKLTKRIPLRRQVTVSAESSSSMNSNTPLV 445

Qy        556 EIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGL 615

Db        446 RITTRL--SSTADTPMLAGVSEYELPEDPKWEFPRDKLTLGKPLGEGCFGQVVMAEAVGI 503

Qy        616 SRSQP--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYII 673

Db        504 DKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIINLLGACTQDGPLYVI 563

Qy        674 TEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMD 733

Db        564 VEYASKGNLREYLRARRP---------------------------------------- 581

Qy        734 MKQADTTQYVPMLERKEVSKYS-DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTL 792

Db        582 ----------PGME------YSYDINRV------------------------PEEQMTF 600

Qy        793 LDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSK 852

Db        601 KDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLARDINNIDYYKKT 660

Qy        853 GSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSG 912

Db        661 TNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELF-KLLKEG 719

Qy        913 YRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLP----------GQY 958

Db        720 HRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEQY 779
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Qy        959 KKSY 962
Db        780 SPSY 783


RESULT 46
A56795
fibroblast growth factor receptor 1 beta-isoform - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A56795
R;Kim, E.G.; Kwon, H.M.; Burrow, C.R.; Ballermann, B.J.
Am. J. Physiol. 264, F66-F73, 1993
A;Title: Expression of rat fibroblast growth factor receptor 1 as three splicing variant
A;Reference number: A56795; MUID:93158788; PMID:8381605
A;Contents: Sprague-Dawley, kidneys
A;Accession: A56795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-729 <KIM>
A;Cross-references: UNIPROT:Q63827; UNIPARC:UPI00000E59E7; GB:S54008; NID:g264804; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:124259, NCBIP:124270)
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; growth factor receptor
F;80-141/Domain: immunoglobulin homology <IMM>
F;383-668/Domain: protein kinase homology <KIN>
F;391-399/Region: protein kinase ATP-binding motif

  Query Match             14.7%;  Score 830.5;  DB 2;  Length 729;
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  Matches  244;  Conservative  110;  Mismatches  262;  Indels  231;  Gaps   24;

Qy        276 TVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHF 335
Db         26 TLPEQDALPSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKF 85

Qy        336 VVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKI--QEIRYRS-KLKLIRAKEEDSGHY 392
Db         86 KCPSSGTPSPTLRWLKNG-------KEFKPD-HRIGGYKVRYATWSIIMDSVVPSDKGNY 137

Qy        393 TIVAQNEDAVKSYTFELLTQVPSSILDLVD--DHH-----GSTGGQTV--------RCTA 437
Db        138 TCIVENEYGSINHTYQ---------LDVVERSPHRPILQAGLPANKTVALGSNVEFMCKV 188

Qy        438 EGTPLPDIEWMICKDIKKCNNETS----------WTILANNVSNIITEIHSRDRSTVEGR 487
Db        189 YSDPQPHIQWL--KHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRN------- 239

Qy        488 VTFAKVEETIAVRCLAKNLLGAENRELKL-VAPTLRSELTVAAAVLVLLVIV------II 540
Db        240 VSF---EDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEIIIYCTGAFLI 296

Qy        541 SLIV-LVVIWKQK------------------PRYEIRWRVIESISPDGHEYIY------- 574
Db        297 SCMVGSVIIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVSADSSASMNSGVLLVRPSRL 356

Qy        575 ----------VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP--VM 622
Db        357 SSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVT 416

Qy        623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL 682
Db        417 KVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNL 476

Qy        683 VNYLHKNRDSFL------SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQ 736
Db        477 REYLQARRPPGLEYCYNPSHNPE---------------------------------- 499

Qy        737 ADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLL 796
Db        500 ------------------------------------------------------EQLSSKDLV 508

Qy        797 SFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTF 856
Db        509 SCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGR 568

Qy        857 LPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMA 916
Db        569 LPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELF-KLLKEGHRMD 627

Qy        917 KPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPA 976
Db        628 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRI---------------------- 664

Qy        977 VARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGK 1036
Db        665 ---VALTSNQEYLDLSM-----PLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL-- 714

Qy       1037 RNRHSSQ 1043
Db        715 -PRHPTQ 720


RESULT 47
I49293
fibroblast growth factor receptor-1, short isoform precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49293
R;Jin, Y.; Pasumarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A;Title: Cloning and expression of fibroblast growth factor receptor-1 isoforms in the m
A;Reference number: I49289; MUID:95205422; PMID:7897669
A;Accession: I49293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-733 <RES>
A;Cross-references: UNIPROT:Q60830; UNIPARC:UPI00000E7FD9; EMBL:U23445; NID:g733537; PIDN
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C;Keywords: ATP; growth factor receptor
F;181-254/Domain: immunoglobulin homology <IMM>
F;387-672/Domain: protein kinase homology <KIN>
F;395-403/Region: protein kinase ATP-binding motif

  Query Match             14.7%;  Score 829.5;  DB 2;  Length 733;
  Best Local Similarity   29.8%;  Pred. No. 7.5e-30;
  Matches  241;  Conservative   97;  Mismatches  224;  Indels  247;  Gaps   26;

Qy        323 QLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKI--QEIRYRS-KL 379
Db         75 KLHAVPAAKTVKFKCPSSGTPNPTLRWLKNG-------KEFKPD-HRIGGYKVRYATWSI 126

Qy        380 KLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVD--DHH-----GSTGGQT 432
Db        127 IMDSVVPSDKGNYTCIVENEYGSINHTYQ---------LDVVERSPHRPILQAGLPANET 177

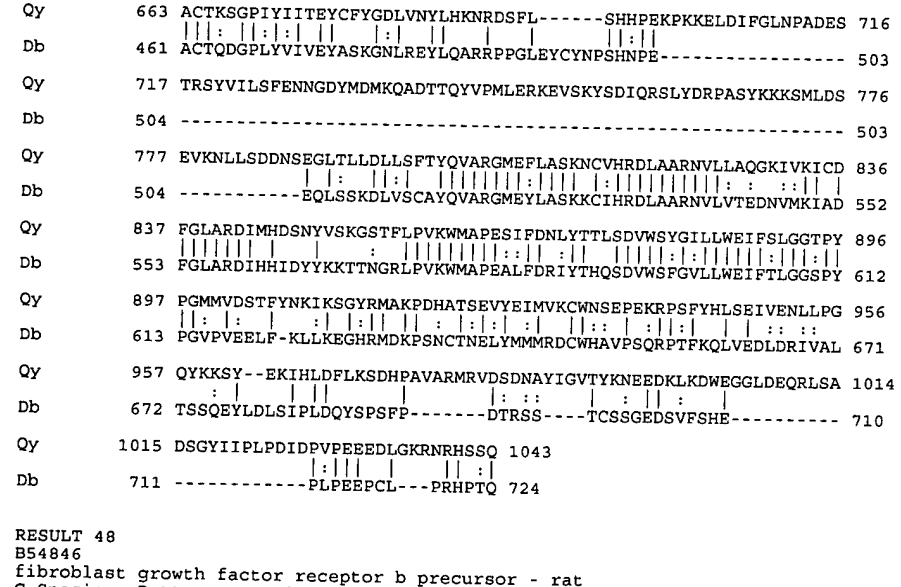
Qy        433 V--------RCTAEGTPLPDIEWMICKDIKKCNNETS----------WTILANNVSNIIT 474
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Qy        475 EIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKL-VAPTLRSELTVAAAVLV 533
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Qy        534 LLVIV-------IISLIVLVVIWKQKP---------------------RYEIRWRVIES 564
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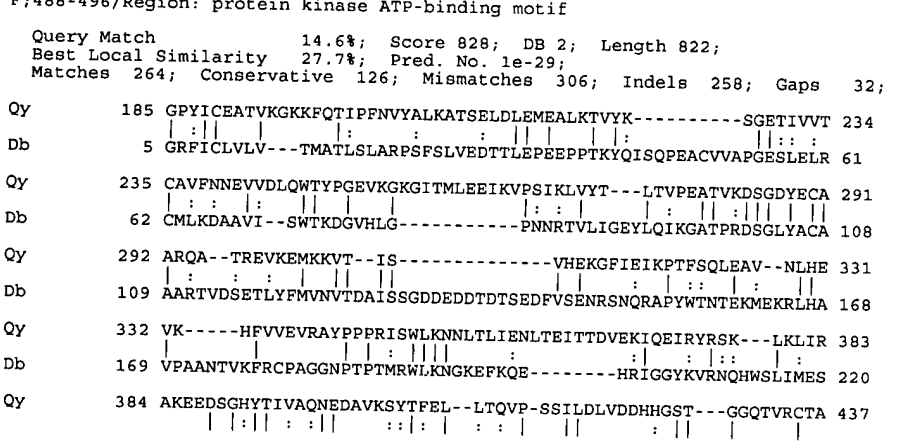
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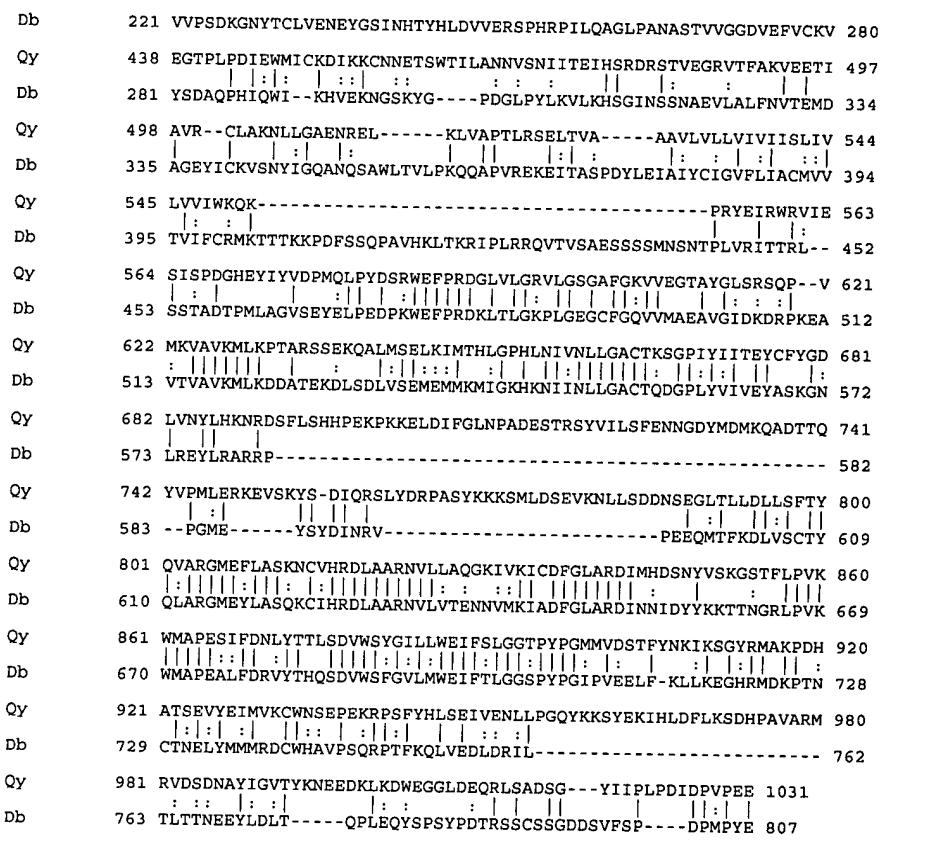
Qy        605 GKVVEGTAYGLSRSQP--VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 662
Db        401 GQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLG 460
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RESULT 48
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fibroblast growth factor receptor b precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: B54846
R;Takagi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.
J. Biol. Chem. 269, 23743-23749, 1994
A;Title: Molecular cloning and expression of the acidic fibroblast growth factor receptc
ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors.
A;Reference number: A54846; MUID:94375484; PMID:8089146
A;Accession: B54846
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-822 <TAK>
A;Cross-references: UNIPARC:UPI00000E6187
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor
F;172-233/Domain: immunoglobulin homology <IMM>
F;480-765/Domain: protein kinase homology <KIN>
F;488-496/Region: protein kinase ATP-binding motif

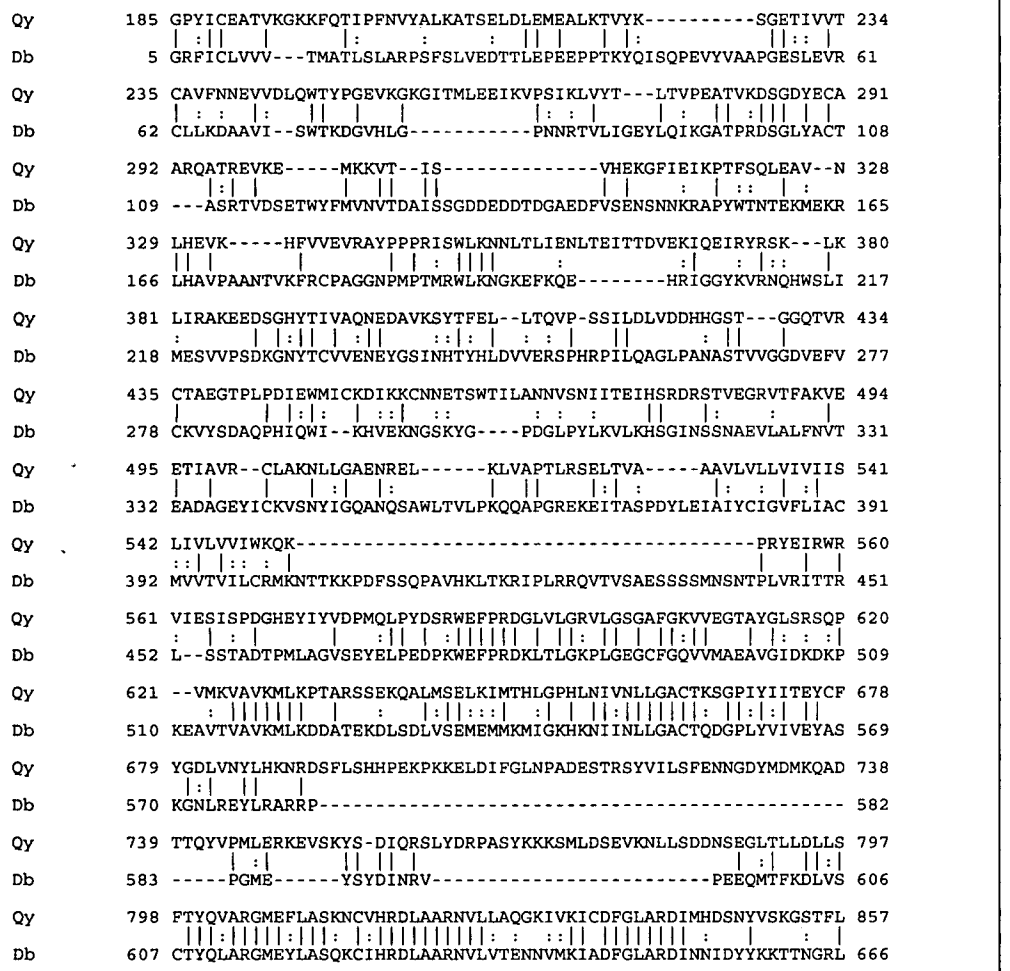
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Matches 264; Conservative 126; Mismatches 306; Indels 258; Gaps 32;





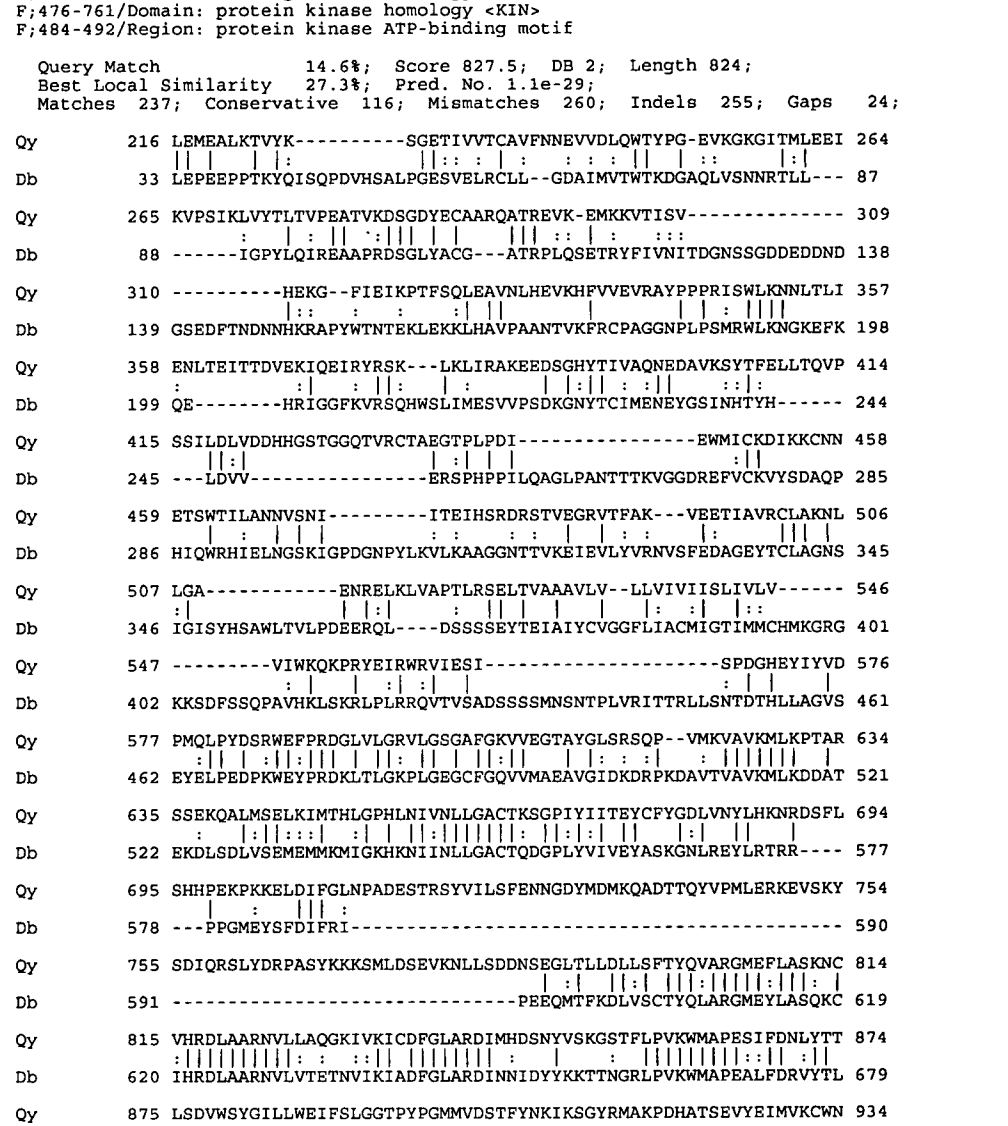
RESULT 49
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fibroblast growth factor receptor 2 IIIb, FGFR2 IIIb - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A45081
R;Dell, K.R.; Williams, L.T.
J. Biol. Chem. 267, 21225-21229, 1992
A;Title: A novel form of fibroblast growth factor receptor 2. Alternative splicing of the
A;Reference number: A45081; MUID:93016048; PMID:1400433
A;Accession: A45081
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-822 <DEL>
A;Cross-references: UNIPROT:P21802; UNIPARC:UPI000002A99A; GB:M97193; NID:g182566; PIDN:A
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:116207)
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F;172-233/Domain: immunoglobulin homology <IMM>
F;379-399/Domain: transmembrane #status predicted <TMM>
F;480-765/Domain: protein kinase homology <KIN>
F;488-496/Region: protein kinase ATP-binding motif
F;62-107,179-231,278-340/Disulfide bonds: #status predicted
F;518,535,627/Active site: Lys, Glu, Asp #status predicted

Query Match 14.6%; Score 828; DB 2; Length 822;
Best Local Similarity 28.8%; Pred. No. 1e-29;
Matches 259; Conservative 114; Mismatches 286; Indels 240; Gaps 30;



RESULT 50
S36439
fibroblast growth factor receptor 2 - Iberian ribbed newt
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: I51127; S36439
R;Shi, D.L.; Launay, C.; Fromentoux, V.; Feige, J.J.; Boucaut, J.C.
Dev. Biol. 164, 173-182, 1994
A;Title: Expression of fibroblast growth factor receptor-2 splice variants is developmen
A;Reference number: I51127; MUID:94299014; PMID:8026621
A;Accession: I51127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-824 <SH2>
A;Cross-references: UNIPROT:Q91286; UNIPARC:UPI00000FB46B; EMBL:X74332; NID:g396744; PID
C;Genetics:
A;Gene: FGFR-2
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor
F;171-232/Domain: immunoglobulin homology <IMM>
F;476-761/Domain: protein kinase homology <KIN>
F;484-492/Region: protein kinase ATP-binding motif

Query Match 14.6%; Score 827.5; DB 2; Length 824;
Best Local Similarity 27.3%; Pred. No. 1.1e-29;
Matches 237; Conservative 116; Mismatches 260; Indels 255; Gaps 24;



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Db        680 QSDVWSFGVLMWEIFTLGGSPYPGIPVEELF-KLLKEGHRMVKPGNCTNELYTMMTDCWR 738

Qy        935 SEPEKRPSFYHLSEIVENLLPGQYKKSY 962
              : | :||:|  | | :: :|     : |
Db        739 AVPSQRPTFKQLVEDLDRILTQTTNEEY 766


Search completed: May 15, 2006, 08:52:54
Job time : 58 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 08:51:46 ; Search time 249 Seconds
(without alignments)
3085.624 Million cell updates/sec

Title: US-08-439-095-1
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5652	100.0	1089	1	PGFRA_HUMAN	P16234 homo sapien
2	5400	95.5	1079	2	Q6E7G6_CANFA	Q6e7g6 canis famil
3	5232	92.6	1089	2	Q7TSJ3_MOUSE	Q7tsj3 mus musculu
4	5229	92.5	1089	1	PGFRA_MOUSE	P26618 mus musculu
5	5190.5	91.8	1088	1	PGFRA_RAT	P20786 rattus norv
6	4577	81.0	1087	2	Q9PUF6_CHICK	Q9puf6 gallus gall
7	4246	75.1	1087	1	PGFRA_XENLA	P26619 xenopus lae
8	4228	74.8	1087	2	Q7ZY71_XENLA	Q7zy71 xenopus lae
9	3715	65.7	743	2	Q6P4H5_HUMAN	Q6p4h5 homo sapien
10	3592	63.6	790	2	Q8C4N3_MOUSE	Q8c4n3 mus musculu
11	3419.5	60.5	1062	2	Q8AXC7_FUGRU	Q8axc7 fugu rubrip
12	3363	59.5	1059	2	Q9DE49_BRARE	Q9de49 brachydanio
13	3352	59.3	1101	2	Q5TZB6_BRARE	Q5tzb6 brachydanio
14	3296	58.3	1078	2	Q8AXC8_FUGRU	Q8axc8 fugu rubrip
15	3250.5	57.5	1337	2	Q4RKW0_TETNG	Q4rkw0 tetraodon n
16	2692	47.6	849	2	Q7Z608_HUMAN	Q7z608 homo sapien
17	2354.5	41.7	1106	1	PGFRB_HUMAN	P09619 homo sapien
18	2336.5	41.3	1098	1	PGFRB_MOUSE	P05622 mus musculu
19	2327	41.2	1099	2	Q7TMR8_MOUSE	Q7tmr8 mus musculu
20	2326	41.2	1097	1	PGFRB_RAT	Q05030 rattus norv
21	2285.5	40.4	1103	2	Q6QNF3_CANFA	Q6qnf3 canis famil
22	2182.5	38.6	1048	2	P79749_FUGRU	P79749 fugu rubrip
23	2132.5	37.7	686	2	Q75WK5_ORYLA	Q75wk5 oryzias lat
24	2104	37.2	1094	2	Q4RZA4_TETNG	Q4rza4 tetraodon n
25	2043	36.1	486	2	Q8CGH8_MOUSE	Q8cgh8 mus musculu
26	1914.5	33.9	457	2	Q90269_BRARE	Q90269 brachydanio
27	1863	33.0	777	2	Q59F04_HUMAN	Q59f04 homo sapien
28	1835.5	32.5	986	2	Q8UVR9_FUGRU	Q8uvr9 fugu rubrip
29	1554.5	27.5	976	2	Q5RID5_BRARE	Q5rid5 brachydanio
30	1554.5	27.5	976	2	Q9W755_BRARE	Q9w755 brachydanio
31	1553.5	27.5	976	2	Q8JFR5_BRARE	Q8jfr5 brachydanio
32	1527	27.0	984	2	Q8AXC6_FUGRU	Q8axc6 fugu rubrip
33	1501	26.6	966	2	Q4RKW2_TETNG	Q4rkw2 tetraodon n
34	1489	26.3	978	1	KIT_CAPHI	Q28317 capra hircu
35	1481.5	26.2	977	1	KIT_BOVIN	P43481 bos taurus
36	1472	26.0	964	2	O97744_PIG	O97744 sus scrofa
37	1472	26.0	964	2	Q9TQQ0_PIG	Q9tqq0 sus scrofa
38	1470.5	26.0	975	2	Q7YRV7_CANFA	Q7yrv7 canis famil
39	1469.5	26.0	979	2	Q8WN23_CANFA	Q8wn23 canis famil
40	1469	26.0	964	2	Q9TQQ1_PIG	Q9tqq1 sus scrofa
41	1469	26.0	978	2	Q9XS93_CANFA	Q9xs93 canis famil
42	1463.5	25.9	975	1	KIT_CANFA	O97799 canis famil
43	1461.5	25.9	960	1	KIT_CHICK	Q08156 gallus gall
44	1460	25.8	974	2	Q63702_RATRT	Q63702 rattus ratt
45	1458	25.8	978	2	Q63116_RAT	Q63116 rattus norv
46	1457.5	25.8	972	2	Q99662_HUMAN	Q99662 homo sapien
47	1454.5	25.7	976	1	KIT_HUMAN	P10721 homo sapien
48	1453.5	25.7	979	2	Q8C8K9_MOUSE	Q8c8k9 mus musculu
49	1452	25.7	972	2	Q76II0_CALJA	Q76ii0 callithrix
50	1450.5	25.7	975	2	Q6QJB8_MOUSE	Q6qjb8 mus musculu
51	1450.5	25.7	975	2	Q7TS86_MOUSE	Q7ts86 mus musculu
52	1448.5	25.6	975	2	Q6QJB7_MOUSE	Q6qjb7 mus musculu
53	1448	25.6	992	2	Q8AXU0_ONCMY	Q8axu0 oncorhynchu
54	1447.5	25.6	948	2	Q9TTD7_TRIVU	Q9ttd7 trichosurus
55	1446.5	25.6	967	2	Q76KE8_ONCMY	Q76ke8 oncorhynchu
56	1446.5	25.6	975	1	KIT_MOUSE	P05532 mus musculu
57	1446	25.6	978	1	KIT_FELCA	Q28889 felis silve
58	1443.5	25.5	976	2	Q6IQ28_HUMAN	Q6iq28 homo sapien
59	1440.5	25.5	945	2	O77589_HORSE	O77589 equus cabal
60	1439.5	25.5	939	2	Q5FYR8_HORSE	Q5fyr8 equus cabal
61	1417.5	25.1	935	2	Q640T5_XENTR	Q640t5 xenopus tro
62	1416.5	25.1	954	2	Q91909_XENLA	Q91909 xenopus lae
63	1412.5	25.0	980	1	CSF1R_FELCA	P13369 felis silve
64	1403.5	24.8	979	2	Q4GWZ1_SPAAU	Q4gwz1 sparus aura
65	1399.5	24.8	978	1	KFMS_FSVMD	P00545 feline sarc
66	1395	24.7	975	2	P79750_FUGRU	P79750 fugu rubrip
67	1384	24.5	953	2	Q6P6Y9_XENLA	Q6p6y9 xenopus lae
68	1382	24.5	975	2	Q4L1N7_CARAU	Q4l1n7 carassius a
69	1374.5	24.3	968	2	Q4W447_HORSE	Q4w447 equus cabal
70	1367.5	24.2	977	1	CSF1R_MOUSE	P09581 mus musculu
71	1362.5	24.1	977	2	Q6NXV8_MOUSE	Q6nxv8 mus musculu
72	1352.5	23.9	978	1	CSF1R_RAT	Q00495 rattus norv
73	1346.5	23.8	972	1	CSF1R_HUMAN	P07333 homo sapien
74	1344.5	23.8	972	2	Q86VW7_HUMAN	Q86vw7 homo sapien
75	1340	23.7	1019	2	Q8UVR8_FUGRU	Q8uvr8 fugu rubrip
76	1339	23.7	819	2	Q4T5K0_TETNG	Q4t5k0 tetraodon n
77	1337.5	23.7	724	2	Q9MYN0_BOVIN	Q9myn0 bos taurus
78	1312	23.2	977	2	Q98SU4_9TELE	Q98su4 danio albol
79	1312	23.2	977	2	Q98SU2_DANKE	Q98su2 danio kerri
80	1307	23.1	891	2	Q5ND91_SPAAU	Q5nd91 sparus aura
81	1305.5	23.1	974	2	Q98SU3_9TELE	Q98su3 danio dangi
82	1305.5	23.1	977	2	Q9I8N6_BRARE	Q9i8n6 brachydanio
83	1301	23.0	977	2	Q98SU1_9TELE	Q98su1 danio nigro
84	1287	22.8	1338	1	VGFR1_HUMAN	P17948 h vascular
85	1287	22.8	1338	2	Q5TAR1_HUMAN	Q5tar1 homo sapien
86	1282.5	22.7	923	2	O97745_PIG	O97745 sus scrofa
87	1280	22.6	1333	1	VGFR1_MOUSE	P35969 mus musculu
88	1278	22.6	1336	1	VGFR1_RAT	P53767 rattus norv
89	1266	22.4	995	2	Q4SQ14_TETNG	Q4sq14 tetraodon n
90	1238	21.9	898	2	Q5D4S1_HORSE	Q5d4s1 equus cabal
91	1226	21.7	1348	1	VGFR2_COTJA	P52583 coturnix co
92	1224	21.7	1348	2	Q677M1_CHICK	Q677m1 gallus gall
93	1221.5	21.6	1327	2	Q8QHL3_CHICK	Q8qhl3 gallus gall
94	1218.5	21.6	1356	1	VGFR2_HUMAN	P35968 homo sapien
95	1217.5	21.5	1451	2	Q59EB0_HUMAN	Q59eb0 homo sapien
96	1214.5	21.5	1357	2	Q5MD89_BRARE	Q5md89 brachydanio
97	1214.5	21.5	1357	2	Q5GIT2_BRARE	Q5git2 brachydanio
98	1211.5	21.4	1357	2	Q5GIT4_BRARE	Q5git4 brachydanio
99	1205	21.3	1328	2	Q4RKW3_TETNG	Q4rkw3 tetraodon n
100	1199	21.2	1272	2	Q5GIT3_BRARE	Q5git3 brachydanio
101	1198.5	21.2	1379	2	P79701_COTCO	P79701 coturnix co
102	1194.5	21.1	846	2	Q4RZA3_TETNG	Q4rza3 tetraodon n
103	1188	21.0	1343	2	Q5PQU0_RAT	Q5pqu0 rattus norv
104	1187	21.0	1272	2	Q4JDD5_BRARE	Q4jdd5 brachydanio

105	1185	21.0	993	2	Q4ZHV8_CANFA	Q4zhv8	canis famil
106	1185	21.0	1387	2	Q4SJQ3_TETNG	Q4sjq3	tetraodon n
107	1183	20.9	1343	1	VGFR2_RAT	O08775	rattus norv
108	1181.5	20.9	1302	1	VGFR2_BRARE	Q8axb3	brachydanio
109	1166	20.6	993	1	FLT3_HUMAN	P36888	homo sapien
110	1163.5	20.6	1298	1	VGFR3_HUMAN	P35916	homo sapien
111	1162.5	20.6	996	2	Q5VTU6_HUMAN	Q5vtu6	homo sapien
112	1162	20.6	1345	2	Q8VCD0_MOUSE	Q8vcd0	mus musculu
113	1161.5	20.6	1298	2	Q86W08_HUMAN	Q86w08	homo sapien
114	1161.5	20.6	1363	2	Q86W07_HUMAN	Q86w07	homo sapien
115	1152.5	20.4	992	1	FLT3_MOUSE	Q00342	mus musculu
116	1152.5	20.4	1363	1	VGFR3_MOUSE	P35917	mus musculu
117	1152.5	20.4	1363	2	Q5SU94_MOUSE	Q5su94	mus musculu
118	1152	20.4	1367	1	VGFR2_MOUSE	P35918	mus musculu
119	1151.5	20.4	1363	2	Q91ZT1_RAT	Q91zt1	rattus norv
120	1102.5	19.5	817	2	Q4H2M8_CIOIN	Q4h2m8	ciona intes
121	1062	18.8	370	1	KIT_FSVHZ	P04048	feline sarc
122	1043	18.5	553	2	Q4SQ12_TETNG	Q4sq12	tetraodon n
123	1042.5	18.4	207	2	Q9PSG8_CHICK	Q9psg8	gallus gall
124	993	17.6	829	2	Q5TZ34_BRARE	Q5tz34	brachydanio
125	976	17.3	1474	2	Q8T4M0_DROME	Q8t4m0	drosophila
126	974.5	17.2	1509	2	Q95P10_DROME	Q95p10	drosophila
127	974.5	17.2	1509	2	Q8IPG1_DROME	Q8ipg1	drosophila
128	973.5	17.2	1503	2	Q8T4L8_DROME	Q8t4l8	drosophila
129	973.5	17.2	1503	2	Q7KTI8_DROME	Q7kti8	drosophila
130	960.5	17.0	1509	2	Q9VLQ8_DROME	Q9vlq8	drosophila
131	955.5	16.9	1461	2	Q8T9F6_DROME	Q8t9f6	drosophila
132	954.5	16.9	323	2	Q9EQ22_RAT	Q9eq22	rattus norv
133	937.5	16.6	441	2	Q4S569_TETNG	Q4s569	tetraodon n
134	937	16.6	551	2	Q59GQ9_HUMAN	Q59gq9	homo sapien
135	915	16.2	401	2	Q9U8U9_EPTBU	Q9u8u9	eptatretus
136	914	16.2	487	2	Q75WK4_ORYLA	Q75wk4	oryzias lat
137	912.5	16.1	323	2	Q9EQ24_RAT	Q9eq24	rattus norv
138	900.5	15.9	464	2	Q5RIP2_BRARE	Q5rip2	brachydanio
139	885	15.7	1215	2	Q7KTI7_DROME	Q7kti7	drosophila
140	884	15.6	468	2	Q4RP85_TETNG	Q4rp85	tetraodon n
141	870.5	15.4	458	2	Q5MD88_BRARE	Q5md88	brachydanio
142	868	15.4	819	1	FGFR1_CHICK	P21804	gallus gall
143	859.5	15.2	822	1	FGFR1_HUMAN	P11362	homo sapien
144	858.5	15.2	820	2	Q5R8Q3_PONPY	Q5r8q3	pongo pygma
145	855	15.1	822	1	FGFR1_RAT	Q04589	rattus norv
146	854.5	15.1	820	2	Q8CIM9_MOUSE	Q8cim9	mus musculu
147	854.5	15.1	822	1	FGFR1_MOUSE	P16092	mus musculu
148	854	15.1	812	1	FGFR1_XENLA	P22182	xenopus lae
149	853.5	15.1	820	2	Q53H63_HUMAN	Q53h63	homo sapien
150	852.5	15.1	822	2	Q60818_MOUSE	Q60818	mus musculu
151	850	15.0	959	2	Q6PUA9_AMBME	Q6pua9	ambystoma m
152	849	15.0	345	2	Q9PVU7_LAMRE	Q9pvu7	lampetra re
153	848	15.0	445	2	Q9U8U8_BRABE	Q9u8u8	branchiosto
154	847	15.0	810	2	Q9PS96_XENLA	Q9ps96	xenopus lae
155	846	15.0	814	2	Q59H40_HUMAN	Q59h40	homo sapien
156	846	15.0	814	2	Q91897_XENLA	Q91897	xenopus lae
157	842.5	14.9	816	2	Q91285_PLEWA	Q91285	pleurodeles
158	842	14.9	350	2	Q91416_XENLA	Q91416	xenopus lae
159	841	14.9	796	2	Q91287_PLEWA	Q91287	pleurodeles
160	837	14.8	1254	2	Q674V1_PODCA	Q674v1	podocoryne
161	833.5	14.7	821	1	FGFR2_HUMAN	P21802	homo sapien
162	832.5	14.7	1092	2	Q91ZT0_RAT	Q91zt0	rattus norv
163	831.5	14.7	733	2	Q9QZM7_MOUSE	Q9qzm7	mus musculu
164	831.5	14.7	800	2	Q9I8X3_BRARE	Q9i8x3	brachydanio
165	830.5	14.7	729	2	Q63827_RAT	Q63827	rattus norv
166	830.5	14.7	731	2	Q5BJG2_HUMAN	Q5bjg2	homo sapien
167	830.5	14.7	731	2	Q8CFK8_MOUSE	Q8cfk8	mus musculu
168	830.5	14.7	782	2	Q9TTZ3_RABIT	Q9ttz3	oryctolagus
169	830	14.7	972	2	Q26614_STRPU	Q26614	strongyloce
170	829.5	14.7	733	2	Q60830_MOUSE	Q60830	mus musculu
171	829.5	14.7	806	2	Q90Z00_BRARE	Q90z00	brachydanio
172	828	14.6	822	2	Q9QVV7_9MURI	Q9qvv7	rattus sp.
173	827.5	14.6	824	2	Q91286_PLEWA	Q91286	pleurodeles
174	827.5	14.6	827	2	Q6GNS5_XENLA	Q6gns5	xenopus lae
175	826.5	14.6	804	2	Q800Z1_BRARE	Q800z1	brachydanio
176	821	14.5	821	1	FGFR2_MOUSE	P21803	mus musculu
177	821	14.5	823	1	CEK3_CHICK	P18461	gallus gall
178	820.5	14.5	635	2	Q4S1S8_TETNG	Q4s1s8	tetraodon n
179	818	14.5	802	2	O42127_XENLA	O42127	xenopus lae
180	815.5	14.4	709	2	Q8IXC7_HUMAN	Q8ixc7	homo sapien
181	815	14.4	829	2	Q9PSV8_XENLA	Q9psv8	xenopus lae
182	814	14.4	817	2	Q8JG38_BRARE	Q8jg38	brachydanio
183	813.5	14.4	952	2	Q4SPY1_TETNG	Q4spy1	tetraodon n
184	811	14.3	824	2	Q90749_CHICK	Q90749	gallus gall
185	808	14.3	756	2	Q800Z0_BRARE	Q800z0	brachydanio
186	808	14.3	822	2	Q91288_PLEWA	Q91288	pleurodeles
187	807	14.3	769	2	Q8NI15_HUMAN	Q8ni15	homo sapien
188	807	14.3	806	1	FGFR3_HUMAN	P22607	homo sapien
189	806.5	14.3	802	2	Q95M13_BOVIN	Q95m13	bos taurus
190	806.5	14.3	818	2	Q91742_XENLA	Q91742	xenopus lae
191	806	14.3	314	2	Q9PVU8_LAMRE	Q9pvu8	lampetra re
192	806	14.3	815	2	Q8AYP3_BRARE	Q8ayp3	brachydanio
193	804.5	14.2	259	2	Q9BDK8_PIG	Q9bdk8	sus scrofa
194	804	14.2	1106	2	P79726_BRARE	P79726	brachydanio
195	802.5	14.2	807	2	Q6DD66_XENLA	Q6dd66	xenopus lae
196	802.5	14.2	818	2	Q9PSV9_XENLA	Q9psv9	xenopus lae
197	802	14.2	782	2	Q61563_MOUSE	Q61563	mus musculu
198	801.5	14.2	729	2	Q91147_NOTVI	Q91147	notophthalm
199	801.5	14.2	828	2	Q9DGK3_XENLA	Q9dgk3	xenopus lae
200	800.5	14.2	922	2	Q90413_BRARE	Q90413	brachydanio
201	800	14.2	815	2	Q805B9_BRARE	Q805b9	brachydanio
202	799.5	14.1	723	2	Q86YI4_HUMAN	Q86yi4	homo sapien
203	798.5	14.1	692	2	Q800Y9_BRARE	Q800y9	brachydanio
204	798	14.1	771	2	Q8NI16_HUMAN	Q8ni16	homo sapien
205	798	14.1	806	1	CEK2_CHICK	P18460	gallus gall
206	796	14.1	707	2	Q9TT07_CANFA	Q9tt07	canis famil
207	796	14.1	800	2	Q7TSI8_MOUSE	Q7tsi8	mus musculu
208	796	14.1	821	2	Q4S2G2_TETNG	Q4s2g2	tetraodon n
209	795	14.1	800	2	Q99052_MOUSE	Q99052	mus musculu
210	794	14.0	800	2	Q9JHX9_RAT	Q9jhx9	rattus norv
211	793.5	14.0	308	2	Q9U8V0_EPTBU	Q9u8v0	eptatretus
212	792	14.0	707	2	Q5BJ23_MOUSE	Q5bj23	mus musculu
213	792	14.0	877	2	Q9GSH3_HALRO	Q9gsh3	halocynthia
214	790	14.0	705	2	Q63710_RATRT	Q63710	rattus ratt
215	789	14.0	671	2	Q63711_RATRT	Q63711	rattus ratt
216	786.5	13.9	731	2	Q91150_NOTVI	Q91150	notophthalm
217	785.5	13.9	683	2	Q5TTJ6_ANOGA	Q5ttj6	anopheles g
218	785	13.9	1106	2	O42362_BRARE	O42362	brachydanio
219	784.5	13.9	678	2	Q5XUI1_SHEEP	Q5xui1	ovis aries
220	784	13.9	1064	2	Q90601_CHICK	Q90601	gallus gall
221	782	13.8	1331	2	Q4S572_TETNG	Q4s572	tetraodon n
222	781	13.8	888	2	Q4VBK2_BRARE	Q4vbk2	brachydanio
223	780.5	13.8	630	2	Q7QBL9_ANOGA	Q7qbl9	anopheles g
224	778.5	13.8	801	1	FGFR3_MOUSE	Q61851	mus musculu
225	778	13.8	814	2	Q6GNP8_XENLA	Q6gnp8	xenopus lae
226	775	13.7	828	2	Q91743_XENLA	Q91743	xenopus lae
227	772	13.7	1059	2	Q9DGL0_XENLA	Q9dgl0	xenopus lae
228	771.5	13.7	713	2	Q90330_COTCO	Q90330	coturnix co
229	770.5	13.6	813	1	FGFR2_XENLA	Q03364	xenopus lae
230	769	13.6	799	2	Q8C3V5_MOUSE	Q8c3v5	mus musculu
231	768.5	13.6	1052	1	FGFR2_DROME	Q09147	drosophila
232	768	13.6	799	2	Q8CIB8_MOUSE	Q8cib8	mus musculu
233	765.5	13.5	891	2	Q25177_HYDAT	Q25177	hydra atten
234	763	13.5	763	2	Q95YM9_HALRO	Q95ym9	halocynthia
235	760	13.4	1106	2	Q9YH35_TETFL	Q9yh35	tetraodon f
236	760	13.4	1114	1	RET_HUMAN	P07949	homo sapien
237	758.5	13.4	650	2	Q63709_9MURI	Q63709	rattus sp.
238	758	13.4	388	2	Q91146_NOTVI	Q91146	notophthalm
239	757.5	13.4	1115	1	RET_MOUSE	P35546	mus musculu
240	756	13.4	1072	2	Q9BTB0_HUMAN	Q9btb0	homo sapien
241	755.5	13.4	713	2	Q4S6E0_TETNG	Q4s6e0	tetraodon n
242	755	13.4	1107	2	Q9PSD4_CHICK	Q9psd4	gallus gall
243	752.5	13.3	453	2	Q9CW58_MOUSE	Q9cw58	mus musculu
244	752.5	13.3	808	1	FGFR4_MOUSE	Q03142	mus musculu
245	751.5	13.3	1091	2	Q9UMQ4_HUMAN	Q9umq4	homo sapien
246	748	13.2	802	2	Q8TDA0_HUMAN	Q8tda0	homo sapien
247	744	13.2	802	1	FGFR4_HUMAN	P22455	homo sapien
248	740.5	13.1	1034	2	Q59F30_HUMAN	Q59f30	homo sapien
249	739	13.1	762	2	Q71TW8_HUMAN	Q71tw8	homo sapien
250	737.5	13.0	415	2	Q64334_RAT	Q64334	rattus norv

251	736.5	13.0	384	2	Q5RF81_PONPY	Q5rf81	pongo pygma
252	726.5	12.9	816	2	Q86PM4_HYDAT	Q86pm4	hydra atten
253	721	12.8	791	2	Q7PWP1_ANOGA	Q7pwp1	anopheles g
254	718	12.7	592	2	Q96KE5_HUMAN	Q96ke5	homo sapien
255	718	12.7	1074	2	Q9EPC3_RAT	Q9epc3	rattus norv
256	718	12.7	1116	2	Q9EPA1_RAT	Q9epa1	rattus norv
257	714.5	12.6	348	2	Q8CBY7_MOUSE	Q8cby7	mus musculu
258	712	12.6	725	2	Q59HE0_HUMAN	Q59he0	homo sapien
259	700.5	12.4	435	2	Q15850_HUMAN	Q15850	homo sapien
260	698	12.3	729	1	FGFR1_DROME	Q07407	drosophila
261	697	12.3	593	2	Q15300_HUMAN	Q15300	homo sapien
262	689.5	12.2	1040	1	EGL15_CAEEL	Q10656	caenorhabdi
263	685	12.1	1051	2	Q7JL68_CAEEL	Q7jl68	caenorhabdi
264	685	12.1	1096	2	Q8MQ14_CAEEL	Q8mq14	caenorhabdi
265	679	12.0	1348	2	Q25199_HYDAT	Q25199	hydra atten
266	673	11.9	747	2	Q4H3K6_CIOIN	Q4h3k6	ciona intes
267	672	11.9	374	2	Q63240_RAT	Q63240	rattus norv
268	671	11.9	987	2	Q7YZM8_CAEEL	Q7yzm8	caenorhabdi
269	658	11.6	1235	2	Q7KA88_DROME	Q7ka88	drosophila
270	658	11.6	1235	2	Q7KT06_DROME	Q7kt06	drosophila
271	658	11.6	1237	2	Q8INU0_DROME	Q8inu0	drosophila
272	657	11.6	282	2	Q9QVY9_9MURI	Q9qvy9	mus sp. c-r
273	656	11.6	1235	2	Q9BHA9_DROME	Q9bha9	drosophila
274	655.5	11.6	582	2	Q95N25_BOVIN	Q95n25	bos taurus
275	645	11.4	817	2	Q7JQD5_DROME	Q7jqd5	drosophila
276	641.5	11.3	1227	2	Q21038_CAEEL	Q21038	caenorhabdi
277	637.5	11.3	329	2	Q9U8W3_BRABE	Q9u8w3	branchiosto
278	637	11.3	693	2	Q7PYY7_ANOGA	Q7pyy7	anopheles g
279	631	11.2	333	2	Q9U8W4_EPTBU	Q9u8w4	eptatretus
280	631	11.2	773	1	CAD96_DROME	Q9vbw3	drosophila
281	630	11.1	854	2	Q8MY86_DUGJA	Q8my86	dugesia jap
282	627	11.1	991	2	Q7Z1L9_APLCA	Q7z1l9	aplysia cal
283	623	11.0	1237	2	Q610C8_CAEBR	Q610c8	caenorhabdi
284	618	10.9	326	2	Q9U8W5_EPTBU	Q9u8w5	eptatretus
285	605.5	10.7	395	2	Q70W10_CIOIN	Q70w10	ciona intes
286	604	10.7	227	2	Q5EGE5_BRARE	Q5ege5	brachydanio
287	602.5	10.7	941	2	Q5J1R9_BRARE	Q5j1r9	brachydanio
288	601.5	10.6	868	1	MUSK_MOUSE	Q61006	mus musculu
289	601.5	10.6	868	1	MUSK_RAT	Q62838	rattus norv
290	595	10.5	906	2	Q61KG5_CAEBR	Q61kg5	caenorhabdi
291	594	10.5	867	2	Q5VZW7_HUMAN	Q5vzw7	homo sapien
292	593.5	10.5	903	2	O76385_CAEEL	O76385	caenorhabdi
293	592	10.5	404	2	Q9PUL0_BRARE	Q9pul0	brachydanio
294	590	10.4	753	2	Q5J7D9_MOUSE	Q5j7d9	mus musculu
295	590	10.4	869	1	MUSK_HUMAN	O15146	homo sapien
296	590	10.4	875	2	Q5VZW8_HUMAN	Q5vzw8	homo sapien
297	589.5	10.4	978	2	Q4RJ67_TETNG	Q4rj67	tetraodon n
298	589	10.4	394	2	Q9PVV3_LAMRE	Q9pvv3	lampetra re
299	588.5	10.4	752	2	Q9XYS4_HYDAT	Q9xys4	hydra atten
300	583.5	10.3	1199	2	Q21041_CAEEL	Q21041	caenorhabdi
301	582	10.3	1122	1	TIE2_MOUSE	Q02858	mus musculu
302	581.5	10.3	1072	2	Q80YS4_MOUSE	Q80ys4	mus musculu
303	581	10.3	367	2	Q91356_COTCO	Q91356	coturnix co
304	580	10.3	1083	2	Q9QW24_9MURI	Q9qw24	rattus sp.
305	580	10.3	2311	1	ROS_CHICK	P08941	gallus gall
306	578	10.2	1124	1	TIE2_HUMAN	Q02763	homo sapien
307	575	10.2	1157	2	Q59HG2_HUMAN	Q59hg2	homo sapien
308	574.5	10.2	1081	2	O76809_HYDAT	O76809	hydra atten
309	573.5	10.1	1125	1	TIE2_BOVIN	Q06807	bos taurus
310	573	10.1	803	2	Q5DM52_TRICA	Q5dm52	tribolium c
311	573	10.1	1101	2	Q8IV34_HUMAN	Q8iv34	homo sapien
312	573	10.1	1124	2	Q5TCU2_HUMAN	Q5tcu2	homo sapien
313	572.5	10.1	715	2	Q5K4G5_SUBDO	Q5k4g5	suberites d
314	571	10.1	1607	1	MIPR_LYMST	Q25410	l putative
315	570.5	10.1	1123	2	Q5RDI5_PONPY	Q5rdi5	pongo pygma
316	568	10.0	1124	2	Q5RDB0_PONPY	Q5rdb0	pongo pygma
317	564.5	10.0	804	2	Q7YT64_CRAGI	Q7yt64	crassostrea
318	563.5	10.0	334	2	Q5UBV6_HUMAN	Q5ubv6	homo sapien
319	562.5	10.0	1443	2	Q4RUB0_TETNG	Q4rub0	tetraodon n
320	561.5	9.9	1083	2	O76698_CAEEL	O76698	caenorhabdi
321	560	9.9	341	2	Q8CD05_MOUSE	Q8cd05	mus musculu
322	560	9.9	887	2	Q8MY85_DUGJA	Q8my85	dugesia jap
323	558	9.9	1062	2	Q8BKG3_MOUSE	Q8bkg3	mus musculu
324	557.5	9.9	346	2	O42570_XENLA	O42570	xenopus lae
325	556.5	9.8	1138	1	TIE1_HUMAN	P35590	homo sapien
326	556	9.8	1134	1	TIE1_MOUSE	Q06806	mus musculu
327	555.5	9.8	1000	2	Q4TBR4_TETNG	Q4tbr4	tetraodon n
328	555	9.8	1134	2	Q8BGI2_MOUSE	Q8bgi2	m mus muscu
329	550	9.7	1136	1	TIE1_BOVIN	Q06805	bos taurus
330	549	9.7	2317	2	Q63130_RAT	Q63130	rattus norv
331	549	9.7	2338	2	Q63132_RAT	Q63132	rattus norv
332	547.5	9.7	1192	2	Q610E4_CAEBR	Q610e4	caenorhabdi
333	546	9.7	757	2	Q9VQN7_DROME	Q9vqn7	drosophila
334	545.5	9.7	808	2	Q8IQ00_DROME	Q8iq00	drosophila
335	545.5	9.7	821	1	NTRK2_RAT	Q63604	rattus norv
336	545.5	9.7	1476	2	Q8WRF4_MONBE	Q8wrf4	monosiga br
337	545	9.6	495	1	KIN16_CAEEL	P34892	caenorhabdi
338	544	9.6	367	2	Q7Q840_ANOGA	Q7q840	anopheles g
339	543.5	9.6	430	2	Q9TZS7_CAEEL	Q9tzs7	caenorhabdi
340	543.5	9.6	818	1	NTRK2_CHICK	Q91987	gallus gall
341	543.5	9.6	923	1	TOR_DROME	P18475	drosophila
342	543.5	9.6	2341	2	Q5TDB4_HUMAN	Q5tdb4	homo sapien
343	543.5	9.6	2347	2	Q5TDB5_HUMAN	Q5tdb5	homo sapien
344	542.5	9.6	947	1	MUSK_CHICK	Q8axy6	gallus gall
345	542	9.6	821	1	NTRK2_MOUSE	P15209	mus musculu
346	541.5	9.6	2347	1	ROS_HUMAN	P08922	homo sapien
347	540	9.6	822	1	NTRK2_HUMAN	Q16620	homo sapien
348	540	9.6	822	2	Q5VVP4_HUMAN	Q5vvp4	homo sapien
349	540	9.6	838	2	Q8WXJ7_HUMAN	Q8wxj7	homo sapien
350	540	9.6	1477	1	HTK7_HYDAT	Q25197	hydra atten
351	539	9.5	221	2	Q9N111_SHEEP	Q9n111	ovis aries
352	537.5	9.5	402	1	ROS_AVISU	P00529	avian sarco
353	537.5	9.5	759	2	Q7YZH7_MONBE	Q7yzh7	monosiga br
354	537	9.5	1030	2	Q8NFA8_HUMAN	Q8nfa8	homo sapien
355	537	9.5	1363	1	ILPR_BRALA	O02466	branchiosto
356	536	9.5	421	2	Q9HBS4_HUMAN	Q9hbs4	homo sapien
357	534.5	9.5	666	2	O76167_DUGJA	O76167	dugesia jap
358	534.5	9.5	1116	1	TIE2_BRARE	O73791	brachydanio
359	534.5	9.5	1245	2	Q9YGH8_SCOMX	Q9ygh8	scophthalmu
360	533	9.4	825	1	NTRK3_MACFA	Q5ifj9	macaca fasc
361	532	9.4	207	2	Q9N112_SHEEP	Q9n112	ovis aries
362	532	9.4	2340	2	Q78DX7_MOUSE	Q78dx7	mus musculu
363	531.5	9.4	1367	1	IGF1R_HUMAN	P08069	h insulin-l
364	531	9.4	676	2	Q5J1R8_BRARE	Q5j1r8	brachydanio
365	530	9.4	669	2	Q6B515_POEGU	Q6b515	poephila gu
366	530	9.4	825	1	NTRK3_PANTR	Q5is37	pan troglod
367	527	9.3	354	2	Q9DDA2_XENLA	Q9dda2	xenopus lae
368	527	9.3	825	2	Q5IS82_9PRIM	Q5is82	saimiri bol
369	526.5	9.3	553	2	Q7ZZ92_BRARE	Q7zz92	brachydanio
370	525.5	9.3	557	2	Q61BE3_CAEBR	Q61be3	caenorhabdi
371	525.5	9.3	1369	2	Q8UW86_PAROL	Q8uw86	paralichthy
372	525	9.3	1389	2	Q4REV4_TETNG	Q4rev4	tetraodon n
373	524	9.3	946	2	Q07153_TORCA	Q07153	torpedo cal
374	524	9.3	2340	2	Q60705_MOUSE	Q60705	mus musculu
375	522	9.2	392	2	Q7Q0U2_ANOGA	Q7q0u2	anopheles g
376	522	9.2	797	2	Q52V39_BRAFL	Q52v39	branchiosto
377	521.5	9.2	1070	2	Q4S2F2_TETNG	Q4s2f2	tetraodon n
378	521	9.2	797	2	Q52V40_BRAFL	Q52v40	branchiosto
379	521	9.2	994	1	MERTK_MOUSE	Q60805	mus musculu
380	521	9.2	1070	2	Q6IQ54_HUMAN	Q6iq54	homo sapien
381	521	9.2	1070	2	Q5T650_HUMAN	Q5t650	homo sapien
382	520	9.2	879	2	Q59FL9_HUMAN	Q59fl9	homo sapien
383	519	9.2	476	2	O73845_ONCMY	O73845	oncorhynchu
384	519	9.2	658	2	Q90X17_XENLA	Q90x17	xenopus lae
385	519	9.2	827	1	NTRK3_CHICK	Q91044	gallus gall
386	518.5	9.2	609	2	Q91776_XENLA	Q91776	xenopus lae
387	518.5	9.2	874	2	Q9YI66_BRARE	Q9yi66	brachydanio
388	518	9.2	226	2	Q9PS75_CHICK	Q9ps75	gallus gall
389	518	9.2	839	1	NTRK3_HUMAN	Q16288	homo sapien
390	518	9.2	839	2	O75682_HUMAN	O75682	homo sapien
391	518	9.2	888	2	Q8VIA0_RAT	Q8via0	rattus norv
392	517.5	9.2	880	1	TYRO3_RAT	P55146	rattus norv
393	516	9.1	1358	2	O73798_XENLA	O73798	xenopus lae
394	515.5	9.1	1064	2	Q5RCL1_PONPY	Q5rcl1	pongo pygma
395	515	9.1	1671	2	Q9NJV5_BIOGL	Q9njv5	biomphalari
396	514.5	9.1	698	2	Q8C481_MOUSE	Q8c481	mus musculu

397	514.5	9.1	974	2	Q90777_CHICK	Q90777 gallus gall
398	514	9.1	825	1	NTRK3_PIG	P24786 sus scrofa
399	514	9.1	825	2	Q6VNS1_MOUSE	Q6vns1 mus musculu
400	514	9.1	1158	2	Q8SWV4_DROME	Q8swv4 drosophila
401	514	9.1	1701	2	Q9V3E8_DROME	Q9v3e8 drosophila
402	513.5	9.1	823	2	Q9TTY2_CANFA	Q9tty2 canis famil
403	513.5	9.1	951	2	Q59FM9_HUMAN	Q59fm9 homo sapien
404	513.5	9.1	1043	2	Q6PA07_XENLA	Q6pa07 xenopus lae
405	513	9.1	810	2	Q4S351_TETNG	Q4s351 tetraodon n
406	513	9.1	822	1	FER_HUMAN	P16591 homo sapien
407	513	9.1	887	1	UFO_HUMAN	P30530 homo sapien
408	512.5	9.1	879	2	Q8VI99_RAT	Q8vi99 rattus norv
409	512.5	9.1	1064	2	Q5W0C5_HUMAN	Q5w0c5 homo sapien
410	512.5	9.1	1092	2	Q7Z301_HUMAN	Q7z301 homo sapien
411	512.5	9.1	1167	2	Q6NZY6_HUMAN	Q6nzy6 homo sapien
412	512.5	9.1	1182	1	ABL2_HUMAN	P42684 homo sapien
413	512.5	9.1	1182	2	Q5T0X6_HUMAN	Q5t0x6 homo sapien
414	512	9.1	894	2	Q8N5L2_HUMAN	Q8n5l2 homo sapien
415	512	9.1	1182	2	Q4JIM5_MOUSE	Q4jim5 mus musculu
416	512	9.1	1390	1	INSR_AEDAE	Q93105 aedes aegyp
417	511.5	9.0	1102	2	Q6P2B2_XENLA	Q6p282 xenopus lae
418	511	9.0	880	1	TYRO3_MOUSE	P55144 mus musculu
419	511	9.0	880	2	Q6NZM6_MOUSE	Q6nzm6 mus musculu
420	510.5	9.0	1358	2	Q6PA47_XENLA	Q6pa47 xenopus lae
421	510	9.0	1418	2	Q8UW83_PAROL	Q8uw83 paralichthy
422	509.5	9.0	765	2	Q6PEE5_MOUSE	Q6pee5 mus musculu
423	509.5	9.0	799	1	NTRK1_RAT	P35739 rattus norv
424	509.5	9.0	1037	1	EPHA5_HUMAN	P54756 homo sapien
425	509	9.0	989	2	Q9PWN6_CHICK	Q9pwn6 gallus gall
426	508.5	9.0	640	1	IGF1R_BOVIN	Q05688 bos taurus
427	508.5	9.0	890	2	Q86VR3_HUMAN	Q86vr3 homo sapien
428	506.5	9.0	515	2	Q8UUY9_BRARE	Q8uuy9 brachydanio
429	506.5	9.0	890	1	TYRO3_HUMAN	Q06418 homo sapien
430	506	9.0	1014	2	Q8NFA6_HUMAN	Q8nfa6 homo sapien
431	505	8.9	449	2	Q80UI3_MOUSE	Q80ui3 mus musculu
432	505	8.9	823	2	P70451_MOUSE	P70451 mus musculu
433	504	8.9	940	2	Q8NFA7_HUMAN	Q8nfa7 homo sapien
434	503.5	8.9	1219	2	Q7PV77_ANOGA	Q7pv77 anopheles g
435	502.5	8.9	1383	1	INSR_RAT	P15127 rattus norv
436	502	8.9	323	1	FLK_RAT	P09760 rattus norv
437	502	8.9	1051	1	PTK7_CHICK	Q91048 gallus gall
438	502	8.9	1412	2	Q8UW84_PAROL	Q8uw84 paralichthy
439	501.5	8.9	671	2	O73846_ONCMY	O73846 oncorhynchu
440	501.5	8.9	1362	2	Q9PVZ4_XENLA	Q9pvz4 xenopus lae
441	501.5	8.9	1370	1	IGF1R_RAT	P24062 rattus norv
442	501.5	8.9	1472	2	Q9U5A8_BOMMO	Q9u5a8 bombyx mori
443	501	8.9	570	2	O97191_GEOCY	O97191 geodia cydo
444	501	8.9	767	2	Q5DIB5_MUGCE	Q5dib5 mugil cepha
445	501	8.9	1371	2	Q9QVW4_9MURI	Q9qvw4 rattus sp.
446	501	8.9	2069	2	Q9Y1Y9_9METZ	Q9y1y9 ephydatia f
447	500.5	8.9	879	2	Q6PE80_MOUSE	Q6pe80 mus musculu
448	500.5	8.9	885	2	Q4RFS5_TETNG	Q4rfs5 tetraodon n
449	500	8.8	178	2	Q9XS54_RABIT	Q9xs54 oryctolagus
450	500	8.8	1070	1	PTK7_HUMAN	Q13308 homo sapien
451	499.5	8.8	1418	2	O93457_SCOMX	O93457 scophthalmu
452	499.5	8.8	1466	2	Q7Q7W3_ANOGA	Q7q7w3 anopheles g
453	499	8.8	209	2	Q9DE16_BRARE	Q9de16 brachydanio
454	499	8.8	873	2	Q98949_CHICK	Q98949 gallus gall
455	499	8.8	888	2	Q80YQ3_MOUSE	Q80yq3 mus musculu
456	499	8.8	1373	1	IGF1R_MOUSE	Q60751 mus musculu
457	499	8.8	2144	1	INSR_DROME	P09208 drosophila
458	498.5	8.8	856	2	Q62121_MOUSE	Q62121 mus musculu
459	498.5	8.8	1649	2	Q5TUS8_ANOGA	Q5tus8 anopheles g
460	498	8.8	833	2	Q59H98_HUMAN	Q59h98 homo sapien
461	498	8.8	888	1	UFO_MOUSE	Q00993 mus musculu
462	498	8.8	994	1	MERTK_RAT	P57097 rattus norv
463	497	8.8	180	2	Q8MI23_SHEEP	Q8mi23 ovis aries
464	497	8.8	453	2	Q61561_MOUSE	Q61561 mus musculu
465	497	8.8	1368	2	Q8UW85_PAROL	Q8uw85 paralichthy
466	496.5	8.8	811	2	Q9YH43_XENLA	Q9yh43 xenopus lae
467	496.5	8.8	1372	1	INSR_MOUSE	P15208 mus musculu
468	496	8.8	969	2	Q7Z3F2_HUMAN	Q7z3f2 homo sapien
469	496	8.8	1382	1	INSR_HUMAN	P06213 homo sapien
470	495	8.8	143	2	Q60515_MOUSE	Q60515 mus musculu
471	494.5	8.7	1005	1	EPHA5_RAT	P54757 rattus norv
472	494.5	8.7	1013	1	EPHA5_CHICK	P54755 gallus gall
473	494.5	8.7	1123	1	ABL1_MOUSE	P00520 mus musculu
474	494	8.7	526	2	Q6E5A8_SUBDO	Q6e5a8 suberites d
475	494	8.7	1325	1	FPS_DROME	P18106 drosophila
476	494	8.7	1341	2	Q6VGS6_RABIT	Q6vgs6 oryctolagus
477	493.5	8.7	538	2	Q7Q5D3_ANOGA	Q7q5d3 anopheles g
478	493.5	8.7	821	2	Q9YH44_XENLA	Q9yh44 xenopus lae
479	493	8.7	138	2	Q6H8S6_ONCMY	Q6h8s6 oncorhynchu
480	493	8.7	439	2	Q8JID1_BRARE	Q8jid1 brachydanio
481	493	8.7	790	2	Q5VZS2_HUMAN	Q5vzs2 homo sapien
482	493	8.7	820	1	FES_FELCA	P14238 felis silve
483	493	8.7	1620	1	ABL_DROME	P00522 drosophila
484	492.5	8.7	746	1	ABL_MLVAB	P00521 abelson mur
485	492.5	8.7	981	2	O92809_MLVAB	O92809 abelson mur
486	492	8.7	681	2	Q4SEJ9_TETNG	Q4sej9 tetraodon n
487	491.5	8.7	488	1	KIN15_CAEEL	P34891 caenorhabdi
488	491.5	8.7	507	1	LCK_CHICK	P42683 gallus gall
489	491.5	8.7	888	1	LTK_MOUSE	P08923 mus musculu
490	491.5	8.7	1017	2	Q59FT4_HUMAN	Q59ft4 homo sapien
491	491.5	8.7	1138	2	Q4RUE3_TETNG	Q4rue3 tetraodon n
492	491	8.7	563	2	Q6R1Y3_ASTMI	Q6r1y3 asterina mi
493	491	8.7	1145	2	Q9BKL8_APLCA	Q9bkl8 aplysia cal
494	490.5	8.7	1192	2	Q53RZ4_HUMAN	Q53rz4 homo sapien
495	490.5	8.7	1620	1	ALK_HUMAN	Q9um73 homo sapien
496	490.5	8.7	1626	2	Q59FI3_HUMAN	Q59fi3 homo sapien
497	490	8.7	796	1	NTRK1_HUMAN	P04629 homo sapien
498	490	8.7	1419	2	Q4RWP2_TETNG	Q4rwp2 tetraodon n
499	490	8.7	1456	2	Q5I4E2_BRUMA	Q5i4e2 brugia mala
500	489.5	8.7	502	2	Q9DDK6_SALSA	Q9ddk6 salmo salar

ALIGNMENTS

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RESULT 1
PGFRA_HUMAN
ID   PGFRA_HUMAN     STANDARD;      PRT;  1089 AA.
AC   P16234; Q96KZ7;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-alpha) (CD140a antigen).
GN   Name=PDGFRA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX   MEDLINE=89130149; PubMed=2536956;
RA   Matsui T., Heidaran M., Miki T., Popescu N., la Rochelle W., Kraus M.,
RA   Pierce J., Aaronson S.;
RT   "Isolation of a novel receptor cDNA establishes the existence of two
RT   PDGF receptor genes.";
RL   Science 243:800-804(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX   MEDLINE=89296915; PubMed=2544881;
RA   Claesson-Welsh L., Eriksson A., Westermark B., Heldin C.H.;
RT   "cDNA cloning and expression of the human A-type platelet-derived
RT   growth factor (PDGF) receptor establishes structural similarity to the
RT   B-type PDGF receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4917-4921(1989).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC   TISSUE=Blood;
RX   MEDLINE=96163874; PubMed=8586421;
RA   Kawagishi J., Ku T.;
RT   "Structure, organization, and transcription units of the human alpha-
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RT   platelet-derived growth factor receptor gene, PDGFRA.";
RL   Genomics 30:224-232(1995).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   DISEASE.
RX   MEDLINE=22547205; PubMed=12660384; DOI=10.1056/NEJMoa025217;
RA   Cools J., DeAngelo D.J., Gotlib J., Stover E.H., Legare R.D.,
RA   Cortes J., Kutok J., Clark J., Galinsky I., Griffin J.D., Cross N.C.,
RA   Tefferi A., Malone J., Alam R., Schrier S.L., Schmid J., Rose M.,
RA   Vandenberghe P., Verhoef G., Boogaerts M., Wlodarska I.,
RA   Kantarjian H., Marynen P., Coutre S.E., Stone R., Gilliland D.G.;
RT   "A tyrosine kinase created by fusion of the PDGFRA and FIP1L1 genes as
RT   a therapeutic target of imatinib in idiopathic hypereosinophilic
RT   syndrome.";
RL   N. Engl. J. Med. 348:1201-1214(2003).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1185-1189 IN COMPLEX WITH
RP   SLC9A3R1 AND PDGFRB.
RX   MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;
RA   Karthikeyan S., Leung T., Ladias J.A.A.;
RT   "Structural determinants of the Na+/H+ exchanger regulatory factor
RT   interaction with the beta 2 adrenergic and platelet-derived growth
RT   factor receptors.";
RL   J. Biol. Chem. 277:18973-18978(2002).
CC   -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a
CC       tyrosine-protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P16234-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P16234-2; Sequence=VSP_007833, VSP_007834;
CC         Note=No experimental confirmation available;
CC   -!- DISEASE: A fusion of PDGFRA and FIP1L1 (FIP1L1-PDGFRA), due to an
CC       interstitial chromosomal deletion, is the cause of some cases of
CC       hypereosinophilic syndrome (HES) [MIM:607685]. HES is a rare
CC       hematologic disorder characterized by sustained overproduction of
CC       eosinophils in the bone marrow, eosinophilia, tissue infiltration
CC       and organ damage.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M21574; AAA96715.1; -; mRNA.
DR   EMBL; M22734; AAA60048.1; -; mRNA.
DR   EMBL; D50017; BAA08742.1; -; Genomic_DNA.
DR   EMBL; BC015186; AAH15186.1; -; mRNA.
DR   PIR; A40162; PFHUGA.
DR   PDB; 1GQ5; X-ray; -.
DR   Ensembl; ENSG00000134853; Homo sapiens.
DR   HGNC; HGNC:8803; PDGFRA.
DR   MIM; 173490; -.
DR   MIM; 607685; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005018; F:platelet-derived growth factor alpha-recept. . .; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; ReceptTyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   3D-structure; Alternative splicing; ATP-binding; Glycoprotein;
KW   Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation;
KW   Receptor; Repeat; Signal; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
FT   SIGNAL        1     23
FT   CHAIN        24   1089       Alpha platelet-derived growth factor
FT                                 receptor.
FT   TOPO_DOM     24    524       Extracellular (Potential).
FT   TRANSMEM    525    549       Potential.
FT   TOPO_DOM    550   1089       Cytoplasmic (Potential).
FT   DOMAIN       24    113       Ig-like C2-type 1.
FT   DOMAIN      202    306       Ig-like C2-type 2.
FT   DOMAIN      319    410       Ig-like C2-type 3.
FT   DOMAIN      593    954       Protein kinase.
FT   NP_BIND     599    607       ATP (By similarity).
FT   COMPBIAS   1041   1087       Ser-rich.
FT   ACT_SITE    818    818       By similarity.
FT   BINDING     627    627       ATP (By similarity).
FT   MOD_RES     849    849       Phosphotyrosine (by autocatalysis) (By
FT                                 similarity).
FT   CARBOHYD     42     42       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     76     76       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    179    179       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    353    353       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    359    359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    468    468       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    210    218       ATSELDLEM -> GTCIISFLL (in isoform 2).
FT                                 /FTId=VSP_007833.
FT   VARSPLIC    219   1089       Missing (in isoform 2).
FT                                 /FTId=VSP_007834.
SQ   SEQUENCE   1089 AA;  122670 MW;  5E3FB9940ACD1BE8 CRC64;

  Query Match           100.0%;  Score 5652;  DB 1;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-294;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 2
Q6E7G6_CANFA
ID   Q6E7G6_CANFA PRELIMINARY;   PRT; 1079 AA.
AC   Q6E7G6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Platelet-derived growth factor receptor alpha (Fragment).
GN   Name=PDGFRA;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dickinson P.J., Roberts B.N., Mallen-StClair J., LeCouteur R.A.;
RT   "Evaluation of Receptor Tyrosine Kinase Expression in Canine Brain
RT   Tumors.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Mallen-StClair J., London C.A.;
RT   "The Role of PDGFRA in Canine Cancer.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY525124; AAS91495.2; -; mRNA.
DR   Ensembl; ENSCAFG00000002057; Canis familiaris.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW   Receptor; Transferase; Transmembrane.
FT   NON_TER   1   1
SQ   SEQUENCE   1079 AA; 121935 MW; 3DA424B9C1339D6B CRC64;

  Query Match   95.5%; Score 5400; DB 2; Length 1079;
  Best Local Similarity   95.9%; Pred. No. 5e-281;
  Matches 1035; Conservative   24; Mismatches   20; Indels   0; Gaps   0;

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Qy         11 LGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVE 70
              ||||| | |||||||||||||||||||||||||||||||||||| || ||||: :||
Db          1 LGCLLAGPSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWHYPTSEEENPNVE 60
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Qy         71 IRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVP 130
              |||||||||||||||| :|||||||||||||||||:|||:||||||||||||||||||||
Db         61 IRNEENNSGLFVTVLEVVNASAAHTGLYTCYYNHTQTDENEIEGRHIYIYVPDPDVAFVP 120

Qy        131 LGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNGTFTVGPYICE 190
              |||||||||||||||||||||||||||||| ::::||| |||||||||||||:|||||||
Db        121 LGMTDYLVIVEDDDSAIIPCRTTDPETPVTLLSNDGVVHASYDSRQGFNGTFSVGPYICE 180

Qy        191 ATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYP 250
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATVRGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYP 240

Qy        251 GEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVH 310
              |||||||||||||||||||||||| |||||||||||||||||:|||||||||||||||||
Db        241 GEVKGKGITMLEEIKVPSIKLVYTLRVPEATVKDSGDYECAARQATKEVKEMKKVTISVH 300

Qy        311 EKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKI 370
              |||||||||  |||||||:|||||||||:|:||||||||||:|||||||||||||||:|:
Db        301 EKGFIEIKPNFSQLEAVDLHEVKHFVVDVQAYPPPRISWLKDNLTLIENLTEITTDIERT 360

Qy        371 QEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGG 430
              |||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||
Db        361 QEIRYRSKLKLIRAKEEDSGHYTIVVQNEDDVKSYTFELLTQVPSSILDLVDDHHGSTGG 420

Qy        431 QTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTF 490
              ||||| |||||||||||||||||||||||| |||||:||||||:| ||||||||||||
Db        421 QTVRCIAEGTPLPDIEWMICKDIKKCNNETSWAILANNISNIITEVHPRDRSTVEGRVTF 480

Qy        491 AKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWK 550
               :||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        481 TRVEETIAVRCLAKNLLGAESRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWK 540

Qy        551 QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEG 610
              ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        541 QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILGSGAFGKVVEG 600

Qy        611 TAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPI 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPI 660

Qy        671 YIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGD 730
              |||||||||||||||||||||| ||||||||||||||||:||||||||||||||||||||
Db        661 YIITEYCFYGDLVNYLHKNRDSFLSRHPEKPKKELDIFGLNPADDSTRSYVILSFENNGD 720

Qy        731 YMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGL 790
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        721 YMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSERL 780

Qy        791 TLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYV 850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYV 840

Qy        851 SKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIK 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIK 900

Qy        911 SGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFL 970
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        901 SGYRMAKPDHATSEVYEIMVKCWHSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFL 960

Qy        971 KSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPE 1030
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        961 KSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGSLDEQRLSADSGYIIPLPDIDPVPE 1020

Qy       1031 EEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 EEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1079
```

RESULT 3
Q7TSJ3_MOUSE
ID Q7TSJ3_MOUSE PRELIMINARY; PRT; 1089 AA.

AC Q7TSJ3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pdgfra protein.
GN Name=Pdgfra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC053036; AAH53036.1; -; mRNA.
DR HSSP; P36888; 1RJB.
DR MGI; MGI:97530; Pdgfra.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0048407; F:platelet-derived growth factor binding; IDA.
DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.
DR GO; GO:0030539; P:male genitalia morphogenesis; IMP.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); IMP.
DR GO; GO:0009887; P:organogenesis; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; ReceptTyrKinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 2.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ SEQUENCE 1089 AA; 122682 MW; 07AAFD2BAA12533A CRC64;

Query Match 92.6%; Score 5232; DB 2; Length 1089;
Best Local Similarity 91.8%; Pred. No. 5.2e-272;
Matches 1000; Conservative 48; Mismatches 41; Indels 0; Gaps 0;

```
Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| |||||  || ||| ||||||||||:|||||||||| |||||||:|
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:||||||||||||| :||||||| ||||||||||:|:|:||||||||
Db         61 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:|||||||||||||| |||||:  :|||||||||||||
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:||||||||||||: |:|  ||||||||||||:|||:| :||||:|||||||||||||
Db        181 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:||||||||||||:|||||||:|||||||||:|||
Db        241 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:||||||||||:||:||| |||||||||: |||||:||| |||||||:||||||||
Db        301 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:||||||||||||||||: |||| |||||||| | ||:||||||
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||:|:||||| ||||||:||||:||:||||||||:  |
Db        421 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||| |     ||||||||||||||||||||||||||||:
Db        481 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 4
PGFRA_MOUSE
ID   PGFRA_MOUSE   STANDARD;   PRT; 1089 AA.
AC   P26618; Q62046;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-alpha).
GN   Name=Pdgfra;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91061789; PubMed=2174116;
RA   Stiles C.D., Wang C.;
RT   "Retinoic acid promotes transcription of the platelet-derived growth
RT   factor alpha-receptor gene.";
RL   Mol. Cell. Biol. 10:6781-6784(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92334866; PubMed=1321404;
RA   Do M.S., Fitzer-Attas C., Gubbay J., Greenfeld L., Feldman M.,
RA   Eisenbach L.;
RT   "Mouse platelet-derived growth factor alpha receptor: sequence,
RT   tissue-specific expression and correlation with metastatic
RT   phenotype.";
RL   Oncogene 7:1567-1575(1992).
CC   -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a
CC   tyrosine-protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC   tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC   receptor subfamily.
CC   -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC   domains.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; M84607; AAA39904.1; -; mRNA.
DR   EMBL; M57683; AAA39733.1; -; mRNA.
DR   PIR; I57511; S33727.
DR   HSSP; P11362; 1FGK.
DR   Ensembl; ENSMUSG00000029231; Mus musculus.
DR   MGI; MGI:97530; Pdgfra.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0048407; F:platelet-derived growth factor binding; IDA.
DR   GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.
DR   GO; GO:0030539; P:male genitalia morphogenesis; IMP.
DR   GO; GO:0042475; P:odontogenesis (sensu Vertebrata); IMP.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.

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DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Receptor; Repeat; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25   1089       Alpha platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM     25    525       Extracellular (Potential).
FT   TRANSMEM    526    549       Potential.
FT   TOPO_DOM    550   1089       Cytoplasmic (Potential).
FT   DOMAIN       25    113       Ig-like C2-type 1.
FT   DOMAIN      214    306       Ig-like C2-type 2.
FT   DOMAIN      319    410       Ig-like C2-type 3.
FT   DOMAIN      593    954       Protein kinase.
FT   NP_BIND     599    607       ATP (By similarity).
FT   ACT_SITE    818    818       By similarity.
FT   BINDING     627    627       ATP (By similarity).
FT   CARBOHYD     42     42       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     76     76       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     89     89       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    179    179       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    353    353       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    359    359       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    458    458       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    468    468       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    506    506       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    192    192       T -> A (in Ref. 1).
FT   CONFLICT    202    202       E -> A (in Ref. 1).
FT   CONFLICT    252    252       E -> G (in Ref. 1).
FT   CONFLICT    271    271       L -> V (in Ref. 1).
FT   CONFLICT    322    322       G -> S (in Ref. 1).
FT   CONFLICT    326    326       A -> P (in Ref. 1).
FT   CONFLICT    439    440       GT -> EG (in Ref. 1).
FT   CONFLICT    529    529       A -> E (in Ref. 1).
FT   CONFLICT    737    737       A -> D (in Ref. 1).
FT   CONFLICT    849    849       Y -> D (in Ref. 1).
FT   CONFLICT    936    936       E -> D (in Ref. 1).
FT   CONFLICT    950    950       V -> L (in Ref. 1).
FT   CONFLICT   1005   1005       S -> G (in Ref. 1).
SQ   SEQUENCE   1089 AA;  122727 MW;  B3A3B246716249E0 CRC64;

  Query Match             92.5%;  Score 5229;  DB 1;  Length 1089;
  Best Local Similarity   91.8%;  Pred. No. 7.6e-272;
  Matches 1000;  Conservative   47;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| |||||  || ||| ||||||||||:|||||||||| ||||||||:|
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||  :||||:|||||||||||||| :||||||| ||||||||||:|:|:||||||||
Db         61 MSEEEDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||:|||||||||| |||||:|||||||||||||||| |||||:  :|||||||||||||
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:||||||||||||: |:|  ||||||||||||:|||:| :||||:|||||||||||||
Db        181 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:|||||||||||||:|||||||:|||||||||:|||
Db        241 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:|||||||||:||:||| |||||||||: |||||:||| |||||||:||||||||
Db        301 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:|||||||||||||||: |||| |||||||| | ||:|||||
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||||:|:|||||  ||||||:||||:||:||||||||:  |
Db        421 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||||| |    |||||||||||||||||||||||||||:
Db        481 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWESGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 5
PGFRA_RAT
ID   PGFRA_RAT      STANDARD;      PRT;  1088 AA.
AC   P20786;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-alpha).
GN   Name=Pdgfra;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=90220609; PubMed=2157969;
RA   Lee K.H., Bowen-Pope D.F., Reed R.R.;
RT   "Isolation and characterization of the alpha platelet-derived growth
RT   factor receptor from rat olfactory epithelium.";
RL   Mol. Cell. Biol. 10:2237-2246(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 33-524.
RX   MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;
RA   Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
RT   "Conservation in sequence and affinity of human and rodent PDGF
RT   ligands and receptors.";
RL   Biochim. Biophys. Acta 1173:294-302(1993).
CC   -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a
CC       tyrosine-protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M63837; AAA40743.1; ALT_INIT; mRNA.
DR   EMBL; Z14118; CAA78488.1; -; mRNA.
DR   PIR; A34710; PFRTGA.
DR   HSSP; P11362; 1FGK.
DR   Ensembl; ENSRNOG00000002244; Rattus norvegicus.
DR   RGD; 3284; Pdgfra.
DR   GO; GO:0005018; F:platelet-derived growth factor alpha-recept. . .; TAS.
DR   GO; GO:0046983; F:protein dimerization activity; NAS.
DR   GO; GO:0042063; P:gliogenesis; NAS.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Receptor; Repeat; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL       1     23
FT   CHAIN       24   1088       Alpha platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM     24    524       Extracellular (Potential).
FT   TRANSMEM    525    548       Potential.
FT   TOPO_DOM    549   1088       Cytoplasmic (Potential).
FT   DOMAIN       25    112       Ig-like C2-type 1.
FT   DOMAIN      213    305       Ig-like C2-type 2.
FT   DOMAIN      318    409       Ig-like C2-type 3.
FT   DOMAIN      592    953       Protein kinase.
FT   NP_BIND     598    606       ATP (By similarity).
FT   ACT_SITE    817    817       By similarity.
FT   BINDING     626    626       ATP (By similarity).
FT   MOD_RES     848    848       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     41     41       O-linked (Potential).
FT   CARBOHYD     75     75       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    178    178       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    352    352       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    358    358       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    457    457       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    467    467       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    150    150       L -> R (in Ref. 2).
FT   CONFLICT    519    519       S -> T (in Ref. 2).
SQ   SEQUENCE   1088 AA;  122642 MW;  590C8BB0418801E7 CRC64;

  Query Match             91.8%;  Score 5190.5;  DB 1;  Length 1088;
  Best Local Similarity   90.9%;  Pred. No. 8.8e-270;
  Matches  990;  Conservative   55;  Mismatches   43;  Indels    1;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||  |||||  |||||  |||:||| ||||||||||:| |:||||||||||||||:|
Db          1 MGTSQ-AFLVLSCLLTGPSLIVCQLLLPSILPNENEKIVPLSSSFSLRCFGESEVSWQHP 59

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||  :|||| |||||  |||||||| :||||||| ||||||||||||:|:|||||||
Db         60 MSEEEDPNVEIRTEENNSSLFVTVLEVVNASAAHTGWYTCYYNHTQTEESEIEGRHIYIY 119

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:|||||||| ||||:| |||||:  :|||||||||||||
Db        120 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCLTTDPDTEVTLHNNGRLVPASYDSRQGFNG 179

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:||||||||||:|: |:|  |||||||||||:|||:  :||||:|||||||||||||
Db        180 TFSVGPYICEATVRGRTFKTSEFNVYALKATSELNLEMDTRQTVYKAGETIVVTCAVFNN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: ||||||||||:||||||||||||:|||||||||||||||||:|||
Db        240 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGDYECAARQATKEVK 299

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||| |||||||||::|:|||  || ||||:|: |||||:||| |||||||:||||||||
Db        300 EMKTVTISVHEKGFVQIRPTFGHLETVNLHQVREFVVEVQAYPTPRISWLKDNLTLIENL 359

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:: || ||:||||||||||||||||: ||:| :||||||| | ||:|||:|
Db        360 TEITTDVQRSQETRYQSKLKLIRAKEEDSGHYTIIVQNDDDMKSYTFELSTLVPASILEL 419

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||:|||||||||||||:||||:||:|||||||| | |
Db        420 VDDHHGSGGGQTVRCTAEGTPLPNIEWMICKDIKKCNNDTSWTVLASNVSNIITEFHQRG 479

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||| ||  |||||||:||||||||||||||||||||||||:
Db        480 RSTVEGRVSFAKVEETIAVRCLAKNDLGIGNRELKLVAPSLRSELTVAAAVLVLLVIVIV 539

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        540 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 599

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 659

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||||:| |||||||:||||||||||||||||
Db        660 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSRHPEKPKKDLDIFGLNPADESTRSY 719

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 VILSFENNGDYVDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEAKN 779

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        780 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 839

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Db        840 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGVLLWEIFSLGGTPYPGMM 899

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Db        900 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 959

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db        960 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKEWEGGLDEQRLSADSGYII 1019

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Db       1020 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1079

Qy       1081 SDLVEDSFL 1089

Db       1080 SDLVEDSFL 1088


RESULT 6
Q9PUF6_CHICK
ID   Q9PUF6_CHICK PRELIMINARY;      PRT;  1087 AA.
AC   Q9PUF6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Platelet-derived growth factor receptor alpha.
GN   Name=PDGFR-a;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20302546; PubMed=10842055; DOI=10.1016/S0925-4773(00)00321-X;
RA   Ataliotis P.;
RT   "Platelet-derived growth factor A modulates limb chondrogenesis both
RT   in vivo and in vitro.";
RL   Mech. Dev. 94:13-24(2000).
DR   EMBL; AF188842; AAF01460.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   Ensembl; ENSGALG00000013929; Gallus gallus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.

SQ   SEQUENCE   1087 AA;  122939 MW;  F3306BDD3D983E31 CRC64;

  Query Match             81.0%;  Score 4577;  DB 2;  Length 1087;
  Best Local Similarity   80.3%;  Pred. No. 7.3e-237;
  Matches  875;  Conservative   95;  Mismatches  116;  Indels    4;  Gaps    4;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Db          1 MGTPPRTFLILGCFLTGPLLTLCQLPLPTIVPNRNEMVVQLNSNFTLKCSGDSEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Db         61 VT-EGSHRIDIRHEENNSGLFVTVLEVGNASAAHTGMYVCYYNHTQVEDGEVEGKDIYIY 119

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNS-EGVVPASYDSRQGFN 179

Db        120 VPDPDMPFVPSLPEDQFILVEEGDPTVIPCRTSDPSAEVTLVNSLDKPVYAFYDSKQGFV 179

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db        180 GNFLAGPYTCKTMVKGVEFKSDEFLIYILRATSQLPVEIEALKTVYKTGETIVVTCVVFD 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREV 299

Db        240 NEVVNLQWNYPGKVKEKGLIKLDDIKVPSQKLVYMLTIPDVLVKDTGDYECTARHATKEV 299

Qy        300 KEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIEN 359

Db        300 KENKKVVITVHDKGFIHLEPQFSPLEAVNLHEVKNFVVDVQAYPAPKMYWLKDNVTLIEN 359

Qy        360 LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 419

Db        360 LTEIVTSSNRVQETRFQSVLKLIRAKEEDSGTILWLLKNEDEIKRYTFSLLIQVPALILD 419

Qy        420 LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSR 479

Db        420 LMDDHQGSAGRQTVRCLAEGTPLPDVEWLVCKDIKKCSNDTSWTLLTNNISDIHMEAHLD 479

Qy        480 DRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVI 539

Db        480 ERNMVESQVTFQKVEETLAVRCVARNDLGAVTRELKLVAPTLRSELTVAAAVLVLLVIVI 539

Qy        540 ISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVL 599

Db        540 ISLIVLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRIL 599

Qy        600 GSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVN 659

Db        600 GSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVN 659

Qy        660 LLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719

Db        660 LLGACTKSGPIYIITEYCFYGDLVNYLHKNRDNFLSRHPEKPKKDLDIFGMNPADESTRS 719

Qy        720 YVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVK 779

Db        720 YVILSFENTGEYMDMKQADTTQYVPMLERKEGSKYSDIQRSVYDRPASYKKKSLSESEVK 779

Qy        780 NLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGL 839

Db        780 NLLSDDGSEGLSLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGL 839

Qy        840 ARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGM 899

Db        840 ARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGILYPGM 899

Qy        900 MVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYK 959

Db        900 MVDSTFYNKIKSGYRMAKPDHATNEVYEIMVKCWNNEPEKRPSFYHLSEIVESLLPGEYK 959

Qy        960 KSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYI 1019

Db        960 KSYEKIHLDFLKSDHPAVTRMRGDCDNAYIGVTYKN-EDKIKDRESGFDEQRLSADSGYI 1018
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Qy       1020 IPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGID 1079
              |||||||| |:| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TPLPDIDPVSEDE-LGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGID 1077

Qy       1080 SSDLVEDSFL 1089
              ||||||||||
Db       1078 SSDLVEDSFL 1087


RESULT 7
PGFRA_XENLA
ID   PGFRA_XENLA    STANDARD;      PRT;  1087 AA.
AC   P26619;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-alpha).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93365089; PubMed=8358864;
RA   Jones S.D., Ho L., Smith J.C., Yordan C., Stiles C.D., Mercola M.;
RT   "The Xenopus platelet-derived growth factor alpha receptor: cDNA
RT   cloning and demonstration that mesoderm induction establishes the
RT   lineage-specific pattern of ligand and receptor gene expression.";
RL   Dev. Genet. 14:185-193(1993).
CC   -!- FUNCTION: Receptor that binds both PDGFA and PDGFB and has a
CC       tyrosine-protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M80798; AAA49929.1; -; mRNA.
DR   PIR; I51552; I51552.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Receptor; Repeat; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25   1087       Alpha platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM     25    528       Extracellular (Potential).
FT   TRANSMEM    529    551       Potential.
FT   TOPO_DOM    552   1087       Cytoplasmic (Potential).
FT   DOMAIN       27    114       Ig-like C2-type 1.
FT   DOMAIN      205    311       Ig-like C2-type 2.
FT   DOMAIN      417    519       Ig-like C2-type 3.
FT   DOMAIN      595    970       Protein kinase.
FT   NP_BIND     601    609       ATP (By similarity).
FT   ACT_SITE    818    818       By similarity.
FT   BINDING     629    629       ATP (By similarity).
FT   MOD_RES     849    849       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     77     77       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    216    216       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    282    282       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    309    309       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    356    356       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    362    362       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    461    461       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    471    471       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   1087 AA;  122699 MW;  A621E6B0A5BADCA6 CRC64;

  Query Match             75.1%;  Score 4246;  DB 1;  Length 1087;
  Best Local Similarity   75.6%;  Pred. No. 4.2e-219;
  Matches  821;  Conservative  104;  Mismatches  153;  Indels    8;  Gaps    6;

Qy         7 AFLVLGCLL-TGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEE 65
             | |:||||| |   || :  ||:| |:::| |  |:|||:|:| |||||||| | |  |
Db         7 ASLILGCLLIIGPWAILAENPLPTIFPDKDELVQALHSSFTLKCTGESEVSWQNPNSNPE 66

Qy        66 SSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPD 125
               :| ||:||||||||||::|||| |||  |||||||:|||||||:|:||  ||||||||:
Db        67 KQNVVIRSEENNSGLFVSILEVSDASAFDTGLYTCYHNHTQTEESEIEGTDIYIYVPDPN 126

Qy       126 VAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFNGTFT 183
             | | | |: |::::||:|:||::|||||| : ||| | |    | | |||:||| | |
Db       127 VPFAPPGLFDHIIVVEEDESALVPCRTTDPSSEVTLKNIESSRTVFAFYDSKQGFAGNFP 186

Qy       184 VGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVV 243
               | |||| |     :|| |: :   |||  : :|||| ||::::|||| : | | :||||
Db       187 PGSYICETTSNKMVYQTEPYILQTWKATHNISVEMEAPKTMFRAGETIAIDCIVLDNEVV 246

Qy       244 DLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMK 303
             ||:|||||: :| ||  :|| |||  :||||||:  || :|||:|||| || : : :|
Db       247 DLKWTYPGKQRGVGIRNVEESKVPYQRLVYTLTLANATTEDSGEYECAVIHATLDNRVVK 306

Qy       304 KVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEI 363
             |  |:|||||||:::| |    |  |||||| |:| : ||| | : |||:| || ||||||
Db       307 KTNITVHEKGFIDLEPMFGSEEFANLHEVKSFIVNLHAYPTPGLFWLKDNRTLSENLTEI 366

Qy       364 TTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDD 423
             || :   :| |::|||||||||||||| ||:||||:   |||:| |  :||: ||:|||
Db       367 TTSIVTTKETRFQSKLKLIRAKEEDSGLYTLVAQNDRETKSYSFILQIKVPALILELVDK 426

Qy       424 HHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRST 483
             |||::| ||| | |:| |:||:||::|||||:|||:| |:||| | | |  | | :|
Db       427 HHGASGEQTVGCLAKGMPVPDVEWLVCKDIKRCNNDTLWSILATNGSEISMETH-QDDEQ 485

Qy       484 VEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLI 543
             :| :||| |:|||:|:|:|:||| ||   |||||||||||||||||||||||||||||||
Db       486 IESQVTFKKIEETMAIRCIAKNELGVVARELKLVAPTLRSELTVAAAVLVLLVIVIISLI 545

Qy       544 VLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGA 603
             |||:|||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db       546 VLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILGSGA 605

Qy       604 FGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGA 663
             ||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       606 FGKVVEGAAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGAHLNIVNLLGA 665
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Qy       664 CTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVIL 723
Db       666 CTKSGPIYIITEYCFYGDLVNYLHKNRDNFQSRHPEKPKKDLDIFGLNPADESTRSYVIL 725

Qy       724 SFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLS 783
Db       726 SFENNGDYMDMKQADTMQYVPMLEMKEPSKYSDIQRSLYDRPASYKKKPL--SEVKNILS 783

Qy       784 DDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDI 843
Db       784 DDGFEGLTVLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAHGKIVKICDFGLARDI 843

Qy       844 MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDS 903
Db       844 MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSFGILLWEIFSLGGTPYPGMIVDS 903

Qy       904 TFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYE 963
Db       904 TFYNKIKSGYRMAKPDHATHEVYDIMVKCWNSEPEKRPSFRHLSDIVESLLPMEYKRCYE 963

Qy       964 KIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLP 1023
Db       964 TVLHDFLKSDHPAVTRMRSDSDNSYIGVTYKNEH-KMKDRESGFDEQRLSADSGYIIPLP 1022

Qy      1024 DIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDL 1083
Db      1023 DIDPVSEDES-GKRNRHSSQTSEESAIETGSSSSTFIKRDDETIEDIDMMDDIGIDSSDL 1081

Qy      1084 VEDSFL 1089
Db      1082 VEDSFL 1087
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RESULT 8
Q7ZY71_XENLA
ID   Q7ZY71_XENLA PRELIMINARY;      PRT;  1087 AA.
AC   Q7ZY71;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Pdgfra-prov protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC043948; AAH43948.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   1087 AA;  122585 MW;  2C094A5FB7C43566 CRC64;
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Query Match 74.8%; Score 4228; DB 2; Length 1087;
Best Local Similarity 75.2%; Pred. No. 3.9e-218;
Matches 817; Conservative 105; Mismatches 156; Indels 8; Gaps 6;

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Qy         7 AFLVLGCLL-TGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEE 65
Db         7 ASLILGCLLIIGPWAILAENPLPTIFPDKDELVQALHSSFTLKCTGESEVSWQNPNSNPE 66

Qy        66 SSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPD 125
Db        67 KQNVVIRSEENNSGLFVSILEVSDASAFDTGLYTCYHNHTQTEESEIEGTDIYIYVPDPN 126

Qy       126 VAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFNGTFT 183
Db       127 VPFAPPGLFDHIIVVEEDESALVPCRTTDPSSEVMLKNIESSRTVFAFYDSKQGFAGNFP 186

Qy       184 VGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVV 243
Db       187 PGSYICETTSNKMVYQTEPYILQTWKATHNISVEMEAPKTMFRAGETIAIDCIVLDNEVV 246

Qy       244 DLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMK 303
Db       247 DLKWTYPGKQRGVGIRNVEESKVPYQRLVYTLTLANATTEDSGEYECAVIHATLDNRVVK 306

Qy       304 KVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEI 363
Db       307 KTNITVHEKGFIDLEPMFGSEEFANLHEVKSFIVNLHAYPTPGLFWLKDNRTLSENLTEI 366

Qy       364 TTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDD 423
Db       367 TTSIVTTKETRFQSKLKLIRAKEEDSGLYTLVAQNDAETKSYSFMLQIKVPALILELVDK 426

Qy       424 HHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRST 483
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Db        427 HHGASGEQTVGCLAKGMPVPDVEWLVCKDIKRCNNDTLWSILATNGSEISMETH-QDDEQ 485

Qy        484 VEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLI 543
              :| :||| |:|||:|:||:||| ||    |||||||||||||||||||||||||||||||
Db        486 IESQVTFKKIEETMAIRCIAKNELGVVARELKLVAPTLRSELTVAAAVLVLLVIVIISLI 545

Qy        544 VLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGA 603
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        546 VLVIIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILGSGA 605

Qy        604 FGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGA 663
              ||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        606 FGKVVEGAAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGAHLNIVNLLGA 665

Qy        664 CTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVIL 723
              |||||||||||||||||||||||||:| | |||||||:|||||||||||||||||||||
Db        666 CTKSGPIYIITEYCFYGDLVNYLHKNRDNFQSRHPEKPKKDLDIFGLNPADESTRSYVIL 725

Qy        724 SFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLS 783
              |||||||||||||||| ||||||| || |||||||||||||||||| :  |||||:||
Db        726 SFENNGDYMDMKQADTMQYVPMLEMKEPSKYSDIQRSLYDRPASYKKKPL--SEVKNILS 783

Qy        784 DDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDI 843
              ||  ||||:|||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        784 DDGFEGLTVLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAHGKIVKICDFGLARDI 843

Qy        844 MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDS 903
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||:|||
Db        844 MHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSFGILLWEIFSLGGTPYPGMIVDS 903

Qy        904 TFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYE 963
              |||||||||||| |||||| |||:|||||||||||||||| |||:|||:||| :||: ||
Db        904 TFYNKIKSGYRMTKPDHATHEVYDIMVKCWNSEPEKRPSFGHLSDIVESLLPTEYKRCYE 963

Qy        964 KIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLP 1023
              :  |||||||||| ||| ||||:|||||||||  |:|| | | |||||||||||||||||
Db        964 TVLHDFLKSDHPAVTRMRSDSDNSYIGVTYKNEH-KMKDRESGFDEQRLSADSGYIIPLP 1022

Qy       1024 DIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDL 1083
              ||||| ::|  |||||||||||||||||||||||||||||||||||:||||||| |||
Db       1023 DIDPVSDDES-GKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIEMMDDIGIDPSDL 1081

Qy       1084 VEDSFL 1089
              ||||||
Db       1082 VEDSFL 1087
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RESULT 9
Q6P4H5_HUMAN
ID   Q6P4H5_HUMAN PRELIMINARY;      PRT;   743 AA.
AC   Q6P4H5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PDGFRA protein.
GN   Name=PDGFRA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Director MGC Project;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063414; AAH63414.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   743 AA;  82818 MW;  24564E456607649F CRC64;
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  Query Match           65.7%;  Score 3715;  DB 2;  Length 743;
  Best Local Similarity   99.9%;  Pred. No. 7.8e-191;
  Matches  718;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHPRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRS 719


RESULT 10
Q8C4N3_MOUSE
ID   Q8C4N3_MOUSE PRELIMINARY;      PRT;   790 AA.
AC   Q8C4N3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE   library, clone:C130063B01 product:platelet derived growth factor
DE   receptor, alpha polypeptide, full insert sequence.
GN   Name=Pdgfra;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK081664; BAC38283.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   MGI; MGI:97530; Pdgfra.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0048407; F:platelet-derived growth factor binding; IDA.
DR   GO; GO:0030539; P:male genitalia morphogenesis; IMP.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   790 AA;  88629 MW;  FE13756876B68B95 CRC64;

  Query Match           63.6%;  Score 3592;  DB 2;  Length 790;
  Best Local Similarity  88.8%;  Pred. No. 3.4e-184;
  Matches  687;  Conservative   46;  Mismatches   41;  Indels    0;  Gaps    0;
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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| ||||  || ||| ||||||||||:||||||||||| ||||||||:|
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:||||||||||||| :||||||| ||||||||||:|:|:||||||||
Db         61 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:|||||||||||||| |||||:  :|||||||||||||
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:|||||||||||: |:|  |||||||||||:|||:| :||||:|||||||||||||
Db        181 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:|||||||||||||:|||||||:|||||||||:|||
Db        241 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:||||||||||:||:||| |||||||||: |||||:||| |||||||:||||||||
Db        301 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:|||||||||||||||||: |||| |||||||| | ||:|||||
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||:|:|||||| ||||||:||||:||:|||||||:  |
Db        421 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||| |     |||||||||||||||||||||||||||:
Db        481 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSML 774
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSML 774


RESULT 11
Q8AXC7_FUGRU
ID   Q8AXC7_FUGRU PRELIMINARY;      PRT;  1062 AA.
AC   Q8AXC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PDGFRalpha isoform 1.
GN   Name=PDGFRalpha;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22481137; PubMed=12592706; DOI=10.1080/1042517021000011627;
RA   Williams H., Brenner S., Venkatesh B.;
RT   "Characterization of the platelet-derived growth factor receptor alpha
RT   and c-kit genes in the pufferfish Fugu rubripes.";
RL   DNA Seq. 13:263-270(2002).
DR   EMBL; AF456419; AAN87554.1; -; Genomic_DNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q8AXC7; 765-918.
DR   Ensembl; SINFRUG00000126233; Fugu rubripes.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   1062 AA;  118636 MW;  5439854FE174B832 CRC64;

  Query Match             60.5%;  Score 3419.5;  DB 2;  Length 1062;
  Best Local Similarity   62.5%;  Pred. No. 9e-175;
  Matches  668;  Conservative  145;  Mismatches  240;  Indels   15;  Gaps    8;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | | :||   | || |:::|:| | ||: ::|  |:      ||  : :|:|||||||| :
Db          6 SAPLLLPQLEELVVPLHTAFTLTCQGEATIAWDVPL------DVPEKTQEDNSGLFVTTI 59

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
              | |||| ||| | |:|    ||: :   : ||:|||||| |||| :     :: | :
Db         60 SVDSASAMHTGYYRCFYRRNATEDADEAMQSIYVYVPDPDVPFVPLVVPFGNHVLSDHEE 119

Qy        146 AIIPCRTTDPETPVTLHN--SEGVVPASYDSRQGFNGTFTVGPYICEATVKGKKFQTIPF 203
              | || :||   ||| |  ::  ||  |||::|  | || | |:|:  | | :  :  :
Db        120 MEIQCRVSDPSANVTLINVDTQQPVPCMYDSKRGALGVFTAGTYVCKGVVNGAEHYSEDY 179

Qy        204 NVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITMLEE 263
              |:     | | :|: |  ||   |:|| | |    :|:::  | |||:|  :  : |
Db        180 IVHGWIGGSGLHVELTAKHTVLLVGDTITVNCLAQGSEILEDHWKYPGKVANRAIKTVHE 239

Qy        264 IKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQ 323
              |    :::||||||:|:|||:| | |:       : : |:: | |:   |: |:| | :
Db        240 NKKDQ-EILYTLTVPQASVKDTGIYSCSITDVVTNMSQTKQIAIRVYASEFMSIQPKFGE 298

Qy        324 LEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIR 383
              |:  | ||  |  |: ::|   ::| |::: |      ||:| ::|: |  | | | |||
Db        299 YESAELDEVCEFRAEITSFPTASVTWFKDSVPLSNVTAEISTSLQKLSETSYMSVLTLIR 358

Qy        384 AKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLP 443
              |||||||:||:  :| |  :: :  |  :||: |:||:| |||||  ||:| |    | | |
Db        359 AKEEDSGNYTMRVKNGDQSRTVSLILEVKVPAVIVDLMDIHHGSATGQSVVCITRGQPTP 418

Qy        444 DIEWMICKDIKKCNNET-SWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCL 502
              :|| :||:|| | |:| ||  |  | : :  :    : : :| :| |  :| |:|||||
Db        419 LVEWFVCKNIKHCANDTSSWVPLPVNSTEVTMDSRFDEDNNLETQVIFGHLENTLAVRCL 478

Qy        503 AKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVI 562
              |:| : | :||:|||:     |||||||||||||||||||||||||||||||||||||||
Db        479 ARNEMAAVSREIKLVSNGPHPELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVI 538

Qy        563 ESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVM 622
              ||:|||||||||||||||||||| |||||:|||||||||||||||||||||||||||||
Db        539 ESVSPDGHEYIYVDPMQLPYDSRWEFPRDRLVLGRILGSGAFGKVVEGTAYGLSRSQPVM 598
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Qy        623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 KVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL 658

Qy        683 VNYLHKNRDSFLSHHPEKP-KKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQ 741
              ||||||||:|||:  |||  ||||||||:||||||:|||||||||: ||||||||||| ||
Db        659 VNYLHKNRESFLNPKPEKSNKKELDIFGINPADESSRSYVILSFESKGDYMDMKQADNTQ 718

Qy        742 YVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQ 801
              ||||||    ||||:| | || | | |  :  | |:  ||||: |||||  ||||||||
Db        719 YVPMLEISNASKYSDLQGSNYDHPPSQKGSN--DGEMDQLLSDNMSEGLTTNDLLSFTYQ 776

Qy        802 VARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKW 861
              ||:||||||||||||||||||||:||||||||||||||||||:|||||||||||||||||
Db        777 VAKGMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPVKW 836

Qy        862 MAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHA 921
              ||||||||||||||||||||||||||||||||||||:|||:|||||||||||:||:||
Db        837 MAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMIVDSSFYNKIKSGYRMSKPEHA 896

Qy        922 TSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR 981
              :||::|:|||||||||||||  ||: : :|||  ||: ||::: :|||||||| |:
Db        897 PQDVYDMMMKCWNSEPEKRPSFLGLSDTIASLLPSSYKRHYERVNHEFLKSDHPAVTRVC 956

Qy        982 VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHS 1041
              ||:|:||||:|||| : |||| | | ||||||:||||||||||:||: :||  ||||||
Db        957 VDNDDAYIGITYKN-QGKLKDRESGFDEQRLSSDSGYIIPLPDLDPISDEE-YGKRNRHS 1014

Qy       1042 SQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              |||||||||||||||||| ||| ||:||| ::|:: :| |||||||||
Db       1015 SQTSEESAIETGSSSSTFAKREGETLEDITLLDEMCLDCSDLVEDSFL 1062
```

RESULT 12
Q9DE49_BRARE
ID Q9DE49_BRARE PRELIMINARY; PRT; 1059 AA.
AC Q9DE49;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Platelet-derived growth factor receptor alpha.
GN Name=pdgfra;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu L., Balasubramaniyan N.V., Ge R.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF200951; AAG43479.1; -; mRNA.
DR HSSP; P36888; 1RJB.
DR Ensembl; ENSDARG00000030379; Danio rerio.
DR ZFIN; ZDB-GENE-990415-208; pdgfra.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; ReceptttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Receptor.
SQ SEQUENCE 1059 AA; 118210 MW; 0AE93E2ABD9A72F3 CRC64;

  Query Match 59.5%; Score 3363; DB 2; Length 1059;
  Best Local Similarity 61.5%; Pred. No. 9.6e-172;
  Matches 659; Conservative 157; Mismatches 223; Indels 32; Gaps 14;

```
Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPM-SEEESSDVEIRNEENNSGLFVTVLE 86
              | | |       | |:|:| | | |::|:||  |:  :::::  |:         |||:: :
Db         12 PLIWPQRESMEVSLHSTFRLTCRGQTELSWNGPVFIDDQTNSVK-------KGLFISTVT 64

Qy         87 VSSASAAHTGLYTCY---YNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDY-LVIVED 142
              :|:|:| ||| | |    :| |::         ||||||||   |||  || :   ::
Db         65 ISNATAVHTGEYVCSSEPFNSTEST--------IYIYVPDPQTPFVP-SMTPFENHVLTS 115

Qy        143 DDSAIIPCRTTDPETPVTL--HNSEGVVPASYDSRQGFNGTFTVGPYICEATVKGKKFQT 200
              |   |||| |||   |:|    :: |:|::|||::|| | |  | | :|:| | : |:   :
Db        116 YDEMEIPCRVTDPSASVSLIHMGTDQVMPSAYDSKRGFIGLFGAGTYVCRALIHGQNHDS 175

Qy        201 IPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITM 260
              | : |:      |:| :|: |:|     |||| | |    :||::  | |||::  :|
Db        176 IEYIVHGWTGGSDLRVELRAVKRTLLVGETITVDCVAKGSEVLEDHWKYPGKLANRGPKT 235

Qy        261 LEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPT 320
              ::| |: :::: |||||  |: ||||  | |:         : |::||:|::  |: | |
Db        236 VKENKL-NLEIYYTLTVTNASPKDSGIYACSITDIMSNESQTKELTITVYDHEFVHINPL 294

Qy        321 FSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLK 380
                :|   | ||  | |:: ::| |:::|||::  | ::  ||:| : || |  |:  |
Db        295 IGPVETARLDEVPEFKVDIESFPAPKVTWLKDSSVLGDDTAEISTTLLKIGETSYQGVLN 354

Qy        381 LIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGT 440
              ||||| ||||:||: |:       ||:| |  :|| |:||:| ||||  || | ||| |:
Db        355 LIRAKAEDSGNYTVKAEIGSISTSYSFYLQVKVPPVIVDLIDVHHGSAAGQEVVCTAGGS 414

Qy        441 PLPDIEWMICKDIKKCNNETS-WTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAV 499
              | |:::| |||::| | |::| |  |  | ::|  |:     : :|  : |  :| |:||
Db        415 PFPEVDWDICKNLKHCANDSSQWMPLPINSTDITVELQMNVDNHIESHIIFHHLEGTVAV 474

Qy        500 RCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRW 559
              ||||:| :|  :||:||::  |||||||||||||||||||||||:|||||||||||
Db        475 RCLARNDMGVVSREVKLMSSGPHSELTVAAAVLVLLVIVIISLIVLVIIWKQKPRYEIRW 534

Qy        560 RVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 619
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 RVIESVSPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 594

Qy        620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFY 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFY 654

Qy        680 GDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADT 739
              |||||||||||| ||| | || ||:|||||:||||||:|||||||| |  ||||||||||
Db        655 GDLVNYLHKNRDGFLSRHTEKGKKDLDIFGINPADESSRSYVILSLEGKGDYMDMKQADT 714

Qy        740 TQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFT 799
              |||||||  | |||| |||| || | |:::    : | ::|||||::|||| :||||||
Db        715 MQYVPMLEMNEASKYSPIQRSDYDHPPSHRQ---FNDEAESLLSDDSAEGLTTMDLLSFT 771

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
              |||||||||||||||||||||||||:||||||||||||||||||:||||||||||||
Db        772 YQVARGMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPV 831

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
              |||||||||||||||||||||||||||||||||||||||:|||:|||||||||| ||:
Db        832 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMVVDSSFYNKIKSGYRMTKPE 891
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Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
              ||:|:|||:|:|||||||||||||: ||: | :||| :|: ||::: |||||||||| |
Db        892 HASSDVYELMMKCWNSEPEKRPSFHSLSDTVASLLPSGFKRCYERVNHDFLKSDHPAVTR 951

Qy        980 MR-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRN 1038
              :: :|:|:||:|| ||| : |:|  | | |||||||:||||||||||:||:   ||  |||
Db        952 VQCIDNDDAYMGVLYKN-QGKMKTRESGFDEQRLSSDSGYIIPLPDLDPL-SNEDYSKRN 1009

Qy       1039 RHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||||||||||||:|||||||  ||| ||:||| ::|:: :|| ||||||||
Db       1010 RHSSQTSEESAIDTGSSSST-TKREGETLEDITLLDEMCLDSGDLVEDSFL 1059


RESULT 13
Q5TZB6_BRARE
ID   Q5TZB6_BRARE PRELIMINARY;      PRT;  1101 AA.
AC   Q5TZB6;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Platelet derived growth factor receptor alpha.
GN   Name=pdgfra; ORFNames=CH211-176L11.3-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Hunter G.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX276097; CAH69120.1; -; Genomic_DNA.
DR   EMBL; BX276114; CAI11667.1; -; Genomic_DNA.
DR   EMBL; BX276114; CAH69120.1; JOINED; Genomic_DNA.
DR   EMBL; BX276097; CAI11667.1; JOINED; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   1101 AA;  123400 MW;  786692E370B7E63A CRC64;

  Query Match           59.3%;  Score 3352;  DB 2;  Length 1101;
  Best Local Similarity  61.4%;  Pred. No. 4e-171;
  Matches  655;  Conservative  159;  Mismatches  220;  Indels   32;  Gaps   14;

Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPM-SEEESSDVEIRNEENNSGLFVTVLE 86
              | | |       | |:|:| | | |::|:||  |:  ::::: |:        |||:: :
Db         12 PLIWPQRESMEVSLHSTFRLTCRGQAELSWNGPVFIDDQTNSVK-------KGLFISTVT 64

Qy         87 VSSASAAHTGLYTCY---YNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDY-LVIVED 142
              :|:|:| ||| | |     :| |::          ||||||||   |||  || :   ::
Db         65 ISNATAVHTGEYVCSSEPFNSTEST--------IYIYVPDPQTPFVP-SMTPFENHVLTS 115

Qy        143 DDSAIIPCRTTDPETPVTLHNSE--GVVPASYDSRQGFNGTFTVGPYICEATVKGKKFQT 200
              |   |||| |||   |:| : |   |:|::|||::|| | |  | |:| | : |:   :
Db        116 YDEMEIPCRVTDPSASVSLIHMETDQVMPSAYDSKRGFIGLFGAGTYVCRALIHGQNHDS 175

Qy        201 IPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITM 260
              | : |:      |:| :|: |:|     |||| | |    :|::: | |||::  :|
Db        176 IEYIVHGWTGGSDLRVELRAVKRTLLVGETITVDCVAKGSEMLEDHWKYPGKLANRGTKT 235

Qy        261 LEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPT 320
              ::| |: :::: |||||  |: |||| | |:          : |::||:|::  |: | |
Db        236 VKENKL-NLEIYYTLTVTNASPKDSGIYACSITDIMSNESQTKELTITVYDHEFVHINPL 294

Qy        321 FSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLK 380
              :|   | ||  | |:: ::| |:::|||::  | ::  ||:|:: || |  |: |
Db        295 IGPVETARLDEVPEFKVDIESFPAPKVTWLKDSAVLGDDTAEISTNLLKIGETSYKGVLN 354

Qy        381 LIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGT 440
              ||||| ||||:||: |:      ||:| |  :||  |:||:| ||||  || | ||| |:
Db        355 LIRAKAEDSGNYTVKAEIGSISTSYSFYLQVKVPPVIVDLIDVHHGSAAGQEVVCTAGGS 414

Qy        441 PLPDIEWMICKDIKKCNNETS-WTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAV 499
              | |:::| |||::| | |::| |  |  | ::|  |:     : :|  : |  :| |:||
Db        415 PFPEVDWYICKNLKHCANDSSQWMPLPINSTDITVELQMNVDNHIESHIIFHHLEGTVAV 474

Qy        500 RCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRW 559
              ||||:| :|  :||:||::    ||||||||||||||||||||:||||||||||||
Db        475 RCLARNDMGVVSREVKLMSSGPHSELTVAAAVLVLLVIVIISLIVLVIIWKQKPRYEIRW 534

Qy        560 RVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 619
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 RVIESVSPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 594

Qy        620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFY 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFY 654

Qy        680 GDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADT 739
              |||||||||||| ||| | || ||:|||||:||||||:|||||||  ||||||||||
Db        655 GDLVNYLHKNRDGFLSRHTEKGKKDLDIFGINPADESSRSYVILSFEGKGDYMDMKQADT 714

Qy        740 TQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFT 799
              |||||||  | |||| |||| || | |:::    : | ::|||||::|||| :||||||
Db        715 MQYVPMLEMNEASKYSPIQRSDYDHPPSHRQ---FNDEAESLLSDDSAEGLTTMDLLSFT 771

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
              |||||||||||||||||||||||||:||||||||||||||||:||||||||||||||||
Db        772 YQVARGMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPV 831

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
              |||||||||||||||||||||||||||||||||||||||||:|||:|||||||||||| ||:
Db        832 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMVVDSSFYNKIKSGYRMTKPE 891

Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
              ||:|:|||:|:|||||||||||||: ||: | :||| :|: ||::: |||||||||| |
Db        892 HASSDVYELMMKCWNSEPEKRPSFHSLSDTVASLLPSGFKRCYERVNHDFLKSDHPAVTR 951

Qy        980 MR-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRN 1038
              :: :|:|:||:|| ||| : |:|: | | |||||||:||||||||||:||:   ||  |||
Db        952 VQCIDNDDAYMGVLYKN-QGKMKNRESGFDEQRLSSDSGYIIPLPDLDPL-SNEDYSKRN 1009

Qy       1039 RHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLV 1084
              ||||||||||||:|||||||  ||| ||:||| ::|:: :|| |||
Db       1010 RHSSQTSEESAIDTGSSSST-TKREGETLEDITLLDEMCLDSGDLV 1054
```

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RESULT 14
Q8AXC8_FUGRU
ID   Q8AXC8_FUGRU PRELIMINARY;      PRT;  1078 AA.
AC   Q8AXC8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PDGFRalpha isoform 2.
GN   Name=PDGFRalpha;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22481137; PubMed=12592706; DOI=10.1080/1042517021000011627;
RA   Williams H., Brenner S., Venkatesh B.;
RT   "Characterization of the platelet-derived growth factor receptor alpha
RT   and c-kit genes in the pufferfish Fugu rubripes.";
RL   DNA Seq. 13:263-270(2002).
DR   EMBL; AF456419; AAN87556.1; -; Genomic_DNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q8AXC8; 781-934.
DR   Ensembl; SINFRUG00000126233; Fugu rubripes.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   1078 AA;  120388 MW;  45857F6DBD190BD0 CRC64;

  Query Match           58.3%;  Score 3296;  DB 2;  Length 1078;
  Best Local Similarity  60.2%;  Pred. No. 3.9e-168;
  Matches  662;  Conservative  148;  Mismatches  245;  Indels   44;  Gaps   16;

Qy          8 FLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESS 67
              ::| | :|  :  :   || |:|: || | ::  :|  :: | |:  | |  |:
Db          7 YVVFGVIL--VVSVTSGLSPPTIVSNEEEFILLPSSILNVSCTGKRNVVWAEPL------ 58

Qy         68 DVEIRNEENNS----GLFVTVLEVSSASAAHTGLYTCYYNHTQTEE-------NELEGRH 116
                        ||    | :   | : :|:  :|| ||| | | : |:       || |
Db         59 -------PTNSFVFPGYYTATLFIYNATVKNTGYYTCTYVHLEAEQEGQPQEANEAE--- 108

Qy        117 IYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN-SEG-VVPASYDS 174
              ||::|||  | |||    | ||:  |     | || :|| : ||| : | |  : | ||
Db        109 IYVFVPDAQVPFVP-ETPDNLVVTMDPSGVPISCRVSDPHSHVTLRSVSTGDEMSAFYDG 167

Qy        175 RQGFNGTFTVGPYICEATVKGKKFQTIPFNVYAL--KATSELDLEMEALKTVYKSGETIV 232
              | || |  : | | ||  | |: |::   ::| :  :  | | :|: |  ||   |:||
Db        168 RIGFFGMLSPGQYQCETFVNGRIFRS---DIYTVEDEGGSGLHVELTAKHTVLLVGDTIT 224

Qy        233 VTCAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
              | |    :|:::  | |||:|  : |  : | |    :::||||||:|:|||:| | |:

Db        225 VNCLAQGSEILEDHWKYPGKVANRAIKTVHENKKDQ-EILYTLTVPQASVKDTGIYSCSI 283

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKN 352
                    : : |:: | |:   |: |:| | : |:  | ||  |  |: ::|   ::| |:
Db        284 TDVVTNMSQTKQIAIRVYASEFMSIQPKFGEYESAELDEVCEFRAEITSFPTASVTWFKD 343

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412
              :: |      ||:| ::|: |  | | | ||||||||||:||:  :| |  :: :  | :
Db        344 SVPLSNVTAEISTSLQKLSETSYMSVLTLIRAKEEDSGNYTMRVKNGDQSRTVSLILEVK 403

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVSN 471
              ||: |:||:| ||||  ||:| |   | | | :|| :||:|| | |:| ||  |  | :
Db        404 VPAVIVDLMDIHHGSATGQSVVCITRGQPTPLVEWFVCKNIKHCANDTSSWVPLPVNSTE 463

Qy        472 IITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAV 531
              :  :    : : :| :| |  :| |:||||||:| : | :||:|||:     ||||||||
Db        464 VTMDSRFDEDNNLETQVIFGHLENTLAVRCLARNEMAAVSREIKLVSNGPHPELTVAAAV 523

Qy        532 LVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRD 591
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        524 LVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESVSPDGHEYIYVDPMQLPYDSRWEFPRD 583

Qy        592 GLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHL 651
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 RLVLGRILGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHL 643

Qy        652 GPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKP-KKELDIFGL 710
              |||||||||||||||||||||||||||||||||||||||:|||:  |||  ||||||||:
Db        644 GPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRESFLNPKPEKSNKKELDIFGI 703

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
              ||||||:|||||||||: |||||||||| ||||||||     |||||:| | || | | |
Db        704 NPADESSRSYVILSFESKGDYMDMKQADNTQYVPMLEISNASKYSDLQGSNYDHPPSQKG 763

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
              :  | |:  ||||: |||||  ||||||||||:|||||||||||||||||||||:|||
Db        764 SN--DGEMDQLLSDNMSEGLTTNDLLSFTYQVAKGMEFLASKNCVHRDLAARNVLLSQGK 821

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        822 IVKICDFGLARDIMHDNNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 881

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
              |||||||||:|||:|||||||||||:||:||  :||::|:|||||||||||||  ||: :
Db        882 LGGTPYPGMIVDSSFYNKIKSGYRMSKPEHAPQDVYDMMMKCWNSEPEKRPSFLGLSDTI 941

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
              :|||  ||: ||::: :||||||||| |: ||:|:||||:|||| : |||| | | |||
Db        942 ASLLPSSYKRHYERVNHEFLKSDHPAVTRVCVDNDDAYIGITYKN-QGKLKDRESGFDEQ 1000

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
              |||:|||||||||:||: :||  |||||||||||||||||||||||| ||| ||:|||
Db       1001 RLSSDSGYIIPLPDLDPISDEE-YGKRNRHSSQTSEESAIETGSSSSTFAKREGETLEDI 1059

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
                ::|:: :| |||||||||
Db       1060 TLLDEMCLDCSDLVEDSFL 1078


RESULT 15
Q4RKW0_TETNG
ID   Q4RKW0_TETNG PRELIMINARY;      PRT;  1337 AA.
AC   Q4RKW0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 1 SCAF15025, whole genome shotgun sequence.
GN   ORFNames=GSTENG00032764001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
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OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015025; CAG10972.1; -; Genomic_DNA.
SQ   SEQUENCE   1337 AA;  149726 MW;  FB23964C6B27FAFC CRC64;

  Query Match             57.5%;  Score 3250.5;  DB 2;  Length 1337;
  Best Local Similarity   54.3%;  Pred. No. 1.4e-165;
  Matches  657;  Conservative  160;  Mismatches  235;  Indels  157;  Gaps   16;

Qy         20 LILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSG 79
              |:    : |    :  | || |:::|:| | ||: ::|  |:       ||  : :|:|||
Db        147 LLYSHQNQPPRRKSSEELVVPLHTAFTLTCQGEATIAWDTPL------DVPEKTQEDNSG 200

Qy         80 LFVTVLEVSSASAAHTGLYTCYYNHTQTE-ENELEGRHIYIYVPDPDVAFVPLGMTDYLV 138
              |||| : | :|:| |:| |||:|:   |: |:::   ||:|||||: ||| :
Db        201 LFVTTISVDTATAMHSGYYTCFYSRNDTDREDDMMQSAIYVYVPDPDMPFVPSVVPFGNH 260

Qy        139 IVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPASYDSRQGFNGTFTVGPYICEATVKGK 196
              :: | :   | || :||   ||| |  ::  ||  |||::|  | || | |:|:| : |:
Db        261 VLSDHEEMEIQCRVSDPSANVTLINVDTQQPVPCVYDSKRGALGIFTAGTYVCKALINGE 320

Qy        197 KFQT----IPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGE 252
              :  :     |         | | :|: | :||   |:|| | |    :|::: | |||:
Db        321 EHYSEDGCCP------SGGSGLHVELTAKRTVLLVGDTITVNCLARGSEILEDHWKYPGK 374

Qy        253 VKGKGIT----------MLEEIKVPSI----------------KLVYTLTVPEATVKDS 285
              |    :           :   :||:                  :::|||||:|:|||:
Db        375 VVRTRVAAQFHPDFVKFKVSVTHLPSVSQTNRAVKNVHENKKDQEILYTLTVPQASVKDT 434

Qy        286 GDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPP 345
              | | |:          : |:: | |:   |: |:| | :  |:  | ||  |   : ::|
Db        435 GIYSCSITDIVTNKSQTKQIAIRVYASEFMSIQPEFREYESAELDEVSEFRAYISSFPTA 494

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
              |::|||: : | :   ||:: : :: |  | | | ||||||||||:||:  :| |  :|
Db        495 RVTWLKDGVPLSDVTAEISSSLRQLNETSYISVLTLIRAKEEDSGNYTMRVENGD--QSR 552

Qy        406 TFELLTQ------------------VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIE 446
              | |: :                  ||: |:||:| |||   ||:| |   | | | :|
Db        553 TVGLILELPRLVHVAPLTHTILDSVAVPAVIVDLLDIHHGSATGQSVVCITRGQPTPLVE 612

Qy        447 WMICKDIKKCNNET-SWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKN 505
              | :||:|| | |:| ||   |  | : :  :    : : :| :| |  :| |:||||:|
Db        613 WFVCKNIKSCTNDTSSWVPLPVNATEVTMDSRFDEDNNLETQVMFGHLESTLAVRCLARN 672

Qy        506 LLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESI 565
               : | :||:|||:     |||||||||||||||||||||||||||||||||||||||:
Db        673 EMAAVSREIKLVSTGPHPELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESV 732

Qy        566 SPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVA 625
              |||||||||||||||||||||||| |||||:|||||||||||||||||||||||||||||
Db        733 SPDGHEYIYVDPMQLPYDSRWEFPRDRLVLGRILGSGAFGKVVEGTAYGLSRSQPVMKVA 792

Qy        626 VKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNY 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 VKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNY 852

Qy        686 LHKNRDSFLSHHPEK-PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVP 744
              |||||::||:   ||  |||||||:||||||:|||||||: |||||||||  |||||
Db        853 LHKNRENFLNPKAEKNNKKELDIFGINPADESSRSYVILSFESKGDYMDMKQADNTQYVP 912

Qy        745 MLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVAR 804
              ||||   |||||:| | || | | |  :  | |:  ||||: :|||| ||||||||||:
Db        913 MLERSNTSKYSDLQGSNYDHPPSQKGSN--DGEMDELLSDNVNEGLTTKDLLSFTYQVAK 970

Qy        805 GMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGS---------- 854
              |||||||||||||||||||:|||||||||||||||||||:|||||||
Db        971 GMEFLASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSVSCPWAHTAI 1030

Qy        855 --------------------TFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGT 894
                                  |||||||||||||||||:|||||||||||||||||||||
Db       1031 TVEQKATVSRRMNTFSFVPQTFLPVKWMAPESIFDNLYTSLSDVWSYGILLWEIFSLGGT 1090

Qy        895 PYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLL 954
              |||||:|||:||||||||||:||:||  :||::|::|||||||||||  ||: | :||
Db       1091 PYPGMIVDSSFYNKIKSGYRMSKPEHAPQDVYDMMMRCWNSEPEKRPSFLGLSDTVASLL 1150

Qy        955 PGQYKK---------------------------------------------------- 960
              |  ||:
Db       1151 PSSYKRFELRQDDELALLLAIRRIFSLDCTVQLATPPGTTRFVTTWLLAFLKSNRSLLLQ 1210

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
               ||::: :|||||||| |: :|:|:||||:|||| : |||| | | ||||||:||||||
Db       1211 HYERVNQEFLKSDHPAVTRVCMDNDDAYIGITYKN-QGKLKDRESGFDEQRLSSDSGYII 1269

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||:||: :||  |||||||||||||||||||||: ||| ||:||| ::|:: :|
Db       1270 PLPDLDPISDEE-YGKRNRHSSQTSEESAIETGSSSSTYAKREGETLEDITLLDEMCLDC 1328

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1329 SDLVEDSFL 1337


RESULT 16
Q7Z608_HUMAN
ID   Q7Z608_HUMAN PRELIMINARY;      PRT;   849 AA.
AC   Q7Z608;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   FIP1L1/PDGFRA fusion protein.
GN   Name=FIP1L1/PDGFRA fusion;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22709183; PubMed=12808148; DOI=10.1073/pnas.0932698100;
RA   Griffin J.H., Leung J., Bruner R.J., Caligiuri M.A., Briesewitz R.;
RT   "Discovery of a fusion kinase in EOL-1 cells and idiopathic
RT   hypereosinophilic syndrome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7830-7835(2003).
DR   EMBL; AY229892; AAP69563.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007854; Fip1.
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DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF05182; Fip1; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   849 AA;  94704 MW;  597527ED06A129FF CRC64;

  Query Match             47.6%;  Score 2692;  DB 2;  Length 849;
  Best Local Similarity   74.6%;  Pred. No. 7.2e-136;
  Matches  551;  Conservative   28;  Mismatches   61;  Indels   99;  Gaps   12;

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
              | :|  :   |:|   | ||: |:     | : ::  :|:    :: | |: |   | |
Db        209 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRTGN----SEKETALPSTKAE-FT 258

Qy        412 QVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVS 470
                ||     :     ||  |:   ||                :| |:    |
Db        259 SPPSLFKTGLPPSRNSTSSQSQTSTAS--------------RKANSSVGKW-------- 295

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
                  :||       : : |                    :| ||    :  |
Db        296 --------QDR--------YGRAE----------------------SPDLR---RLPGA 313

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
              : |:   : ||            | | | |  |: :           :||||||||||||
Db        314 IDVIGQTITIS------------RVEGRRRANENSN-----------IQLPYDSRWEFPR 350

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 410

Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 470

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 530

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 590

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 650

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 710

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 770

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 830

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
              ||||||||||||||||||
Db        831 DMMDDIGIDSSDLVEDSFL 849


RESULT 17
PGFRB_HUMAN
ID   PGFRB_HUMAN     STANDARD;      PRT;  1106 AA.
AC   P09619; Q8N5L4;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-beta) (CD140b antigen).
GN   Name=PDGFRB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217915; PubMed=2835772;
RA   Gronwald R.G.K., Grant F.J., Haldeman B.A., Hart C.E., O'Hara P.J.,
RA   Hagen F.S., Ross R., Bowen-Pope D.F., Murray M.J.;
RT   "Cloning and expression of a cDNA coding for the human platelet-
RT   derived growth factor receptor: evidence for more than one receptor
RT   class.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:3435-3439(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89096941; PubMed=2850496;
RA   Claesson-Welsh L., Eriksson A., Moren A., Severinsson L., Ek B.,
RA   Oestman A., Betsholtz C., Heldin C.-H.;
RT   "cDNA cloning and expression of a human platelet-derived growth factor
RT   (PDGF) receptor specific for B-chain-containing PDGF molecules.";
RL   Mol. Cell. Biol. 8:3476-3486(1988).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 548-569.
RX   MEDLINE=97429921; PubMed=9285559; DOI=10.1038/sj.onc.1201267;
RA   Chi K.D., McPhee R.A., Wagner A.S., Dietz J.J., Pantazis P.,
RA   Goustin A.S.;
RT   "Integration of proviral DNA into the PDGF beta-receptor gene in HTLV-
RT   I-infected T-cells results in a novel tyrosine kinase product with
RT   transforming activity.";
RL   Oncogene 15:1051-1057(1997).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 1046-1106.
RX   MEDLINE=89028677; PubMed=2846185; DOI=10.1016/0092-8674(88)90224-3;
RA   Roberts W.M., Look A.T., Roussel M.F., Sherr C.J.;
RT   "Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor
RT   genes.";
RL   Cell 55:655-661(1988).
RN   [6]
RP   PROTEIN SEQUENCE OF 33-47.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
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RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [7]
RP   AUTOPHOSPHORYLATION SITES.
RX   MEDLINE=89376563; PubMed=2550144; DOI=10.1016/0092-8674(89)90510-2;
RA   Kazlauskas A., Cooper J.A.;
RT   "Autophosphorylation of the PDGF receptor in the kinase insert region
RT   regulates interactions with cell proteins.";
RL   Cell 58:1121-1133(1989).
RN   [8]
RP   CHROMOSOMAL TRANSLOCATION WITH TRIP11.
RX   MEDLINE=98043615; PubMed=9373237;
RA   Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.;
RT   "Fusion of the platelet-derived growth factor receptor beta to a novel
RT   gene CEV14 in acute myelogenous leukemia after clonal evolution.";
RL   Blood 90:4271-4277(1997).
RN   [9]
RP   INTERACTION WITH APS.
RX   MEDLINE=99142932; PubMed=9989826; DOI=10.1038/sj.onc.1202326;
RA   Yokouchi M., Wakioka T., Sakamoto H., Yasukawa H., Ohtsuka S.,
RA   Sasaki A., Ohtsubo M., Valius M., Inoue A., Komiya S., Yoshimura A.;
RT   "APS, an adaptor protein containing PH and SH2 domains, is associated
RT   with the PDGF receptor and c-Cbl and inhibits PDGF-induced
RT   mitogenesis.";
RL   Oncogene 18:759-767(1999).
RN   [10]
RP   INTERACTION WITH PIK3C2B.
RX   PubMed=10805725;
RA   Arcaro A., Zvelebil M.J., Wallasch C., Ullrich A., Waterfield M.D.,
RA   Domin J.;
RT   "Class II phosphoinositide 3-kinases are downstream targets of
RT   activated polypeptide growth factor receptors.";
RL   Mol. Cell. Biol. 20:3817-3830(2000).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (1.79 ANGSTROMS) OF 751-755 IN COMPLEX WITH
RP   PIK3R1, AND COMPARISON WITH NMR ANALYSIS.
RX   MEDLINE=21450159; PubMed=11567151; DOI=10.1107/S0907444901012434;
RA   Pauptit R.A., Dennis C.A., Derbyshire D.J., Breeze A.L., Weston S.A.,
RA   Rowsell S., Murshudov G.N.;
RT   "NMR trial models: experiences with the colicin immunity protein Im7
RT   and the p85alpha C-terminal SH2-peptide complex.";
RL   Acta Crystallogr. D 57:1397-1404(2001).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1102-1106 IN COMPLEX WITH
RP   SLC9A3R1 AND PDGFRA.
RX   MEDLINE=22013966; PubMed=11882663; DOI=10.1074/jbc.M201507200;
RA   Karthikeyan S., Leung T., Ladias J.A.A.;
RT   "Structural determinants of the Na+/H+ exchanger regulatory factor
RT   interaction with the beta 2 adrenergic and platelet-derived growth
RT   factor receptors.";
RL   J. Biol. Chem. 277:18973-18978(2002).
CC   -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
CC       tyrosine-protein kinase activity. Phosphorylates Tyr residues at
CC       the C-terminus of PTPN11 creating a binding site for the SH2
CC       domain of GRB2.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with
CC       APS. The autophoshorylated form interacts with PIK3C2B, maybe
CC       indirectly.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DISEASE: A chromosomal aberration involving PDGFRB is found in a
CC       form of chronic myelomonocytic leukemia (CMML). Translocation
CC       t(5;12)(q33;p13) with EVT6/TEL. It is characterized by abnormal
CC       clonal myeloid proliferation and by progression to acute
CC       myelogenous leukemia (AML).
CC   -!- DISEASE: A chromosomal aberration involving PDGFRB may be a cause
CC       of acute myelogenous leukemia. Translocation t(5;14)(q33;q32) with
CC       TRIP11. The fusion protein may be involved in clonal evolution of
CC       leukemia and eosinophilia.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 4 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J03278; AAA60049.1; -; mRNA.
DR   EMBL; M21616; AAA36427.1; -; mRNA.
DR   EMBL; U33172; AAC51675.1; -; Genomic_DNA.
DR   EMBL; BC032224; AAH32224.1; -; mRNA.
DR   PIR; A28206; PFHUGB.
DR   PDB; 1GQ5; X-ray; A=-.
DR   PDB; 1H9O; X-ray; B=751-755.
DR   PDB; 1LWP; Model; A=600-962.
DR   Ensembl; ENSG00000113721; Homo sapiens.
DR   HGNC; HGNC:8804; PDGFRB.
DR   H-InvDB; HIX0005310; -.
DR   MIM; 173410; -.
DR   GO; GO:0004992; F:platelet activating factor receptor activity; TAS.
DR   GO; GO:0005017; F:platelet-derived growth factor receptor act. . .; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; ReceptTyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   3D-structure; ATP-binding; Chromosomal translocation;
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW   Kinase; Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor;
KW   Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL       1     32
FT   CHAIN       33   1106       Beta platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM     33    531       Extracellular (Potential).
FT   TRANSMEM    532    556       Potential.
FT   TOPO_DOM    557   1106       Cytoplasmic (Potential).
FT   DOMAIN      600    962       Protein kinase.
FT   NP_BIND     606    614       ATP (By similarity).

  Query Match             41.7%;  Score 2354.5;  DB 1;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 1.3e-117;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :      |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239
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Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
                : :: | : |:| | |:: :      |:   || :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| | ::|||| : |:|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:              |:  ::||| :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:|||||| : ::  ||| || ||||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
               :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :    ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 18
PGFRB_MOUSE
ID   PGFRB_MOUSE     STANDARD;      PRT;  1098 AA.
AC   P05622;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-beta).
GN   Name=Pdgfrb; Synonyms=Pdgfr;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=87014762; PubMed=3020426;
RA   Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O.,
RA   Tremble P.M., Chen E.Y., Ando M.E., Harkins R.N., Francke U.,
RA   Fried V.A., Ullrich A., Williams L.T.;
RT   "Structure of the receptor for platelet-derived growth factor helps
RT   define a family of closely related growth factor receptors.";
RL   Nature 323:226-232(1986).
CC   -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
CC       tyrosine-protein kinase activity. Phosphorylates Tyr residues at
CC       the C-terminus of PTPN11 creating a binding site for the SH2
CC       domain of GRB2 (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. Interacts with
CC       APS. The autophoshorylated form interacts with PIK3C2B, maybe
CC       indirectly (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 4 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X04367; CAA27882.1; -; mRNA.
DR   PIR; A25742; PFMSRB.
DR   PDB; 1AYA; X-ray; P/Q=1005-1015.
DR   PDB; 1AYC; X-ray; P=736-744.
DR   Ensembl; ENSMUSG00000024620; Mus musculus.
DR   MGI; MGI:97531; Pdgfrb.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0016301; F:kinase activity; IMP.
DR   GO; GO:0004871; F:signal transducer activity; IDA.
DR   GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.
DR   GO; GO:0007165; P:signal transduction; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   3D-structure; ATP-binding; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation;
KW   Receptor; Repeat; Signal; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
FT   SIGNAL       1     31
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FT   CHAIN        32   1098       Beta platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM     32    530       Extracellular (Potential).
FT   TRANSMEM    531    555       Potential.
FT   TOPO_DOM    556   1098       Cytoplasmic (Potential).
FT   DOMAIN       33    119       Ig-like C2-type 1.
FT   DOMAIN      128    209       Ig-like C2-type 2.
FT   DOMAIN      213    308       Ig-like C2-type 3.
FT   DOMAIN      415    523       Ig-like C2-type 4.
FT   DOMAIN      599    961       Protein kinase.
FT   NP_BIND     605    613       ATP (By similarity).
FT   ACT_SITE    825    825       By similarity.
FT   BINDING     633    633       ATP (By similarity).
FT   MOD_RES     750    750       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     856    856       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    214    214       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    353    353       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    370    370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    444    444       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    467    467       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    478    478       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     53     99       Potential.
FT   DISULFID    148    189       Potential.
FT   DISULFID    234    290       Potential.
FT   DISULFID    435    507       Potential.
SQ   SEQUENCE   1098 AA;  122806 MW;  8D391CAFAC3FC31D CRC64;

  Query Match             41.3%;  Score 2336.5;  DB 1;  Length 1098;
  Best Local Similarity   44.1%;  Pred. No. 1.2e-116;
  Matches  498;  Conservative  192;  Mismatches  356;  Indels   83;  Gaps   21;

Qy          6 PAFLVLG-CLLTGLSLILCQLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPMSE 63
              || :: |  ||: | |:  | |    :: |    | |: ::|:| | | | : | |
Db          8 PALVLRGQLLLSVLWLLGPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPVMW------ 61

Qy         64 EESSDVEIRNEE-NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122
              |: | |  :    |  | | :|| ::: :   || | | ||::    |   | : |||:||
Db         62 EQMSQVPWQEAAMNQDGTFSSVLTLTNVTGGDTGEYFCVYNNSLGPELS-ERKRIYIFVP 120

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVP--ASYDSRQGFNG 180
              || : |:|:   |  : | |      |||| |||:  ||||  :  :|    || ::|| |
Db        121 DPTMGFLPMDSEDLFIFVTDVTETTIPCRVTDPQLEVTLHEKKVDIPLHVPYDHQRGFTG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||    |||: |:  ::   :  : ||:|: :| ::: : |::|| : ||:| : | |  |
Db        181 TFEDKTYICKTTIGDREVDSDTYYVYSLQVSS-INVSVNAVQTVVRQGESITIRCIVMGN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEE--IKVPSIKLVYTLTVPEATVKDSGDYECAARQATRE 298
              :||: |||||    |: :  : :    ||| ::   | :| | : ||| | |    :  :
Db        240 DVVNFQWTYPRMKSGRLVEPVTDYLFGVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

Qy        299 VKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIE 358
              : | : ||| | |:: :  |   :|   || :   |   ||| | : |||:| || :
Db        299 HGDEKAINISVIENGYVRLLETLGDVEIAELHRSRTLRVVFEAYPMPSVLWLKDNRTLGD 358

Qy        359 N-LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSI 417
              :   |:      : | || |:| |:| |  ::|:||: | :||     :|:|   ||  :
Db        359 SGAGELVLSTRNMSETRYVSELILVRVKVSEAGYYTMRAFHEDDEVQLSFKLQVNVPVRV 418

Qy        418 LDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIH 477
              |:|  : | : | ||:||   | | |:: |  |:|:|:|  : | | | |:
Db        419 LEL-SESHPANGEQTIRCRGRGMPQPNVTWSTCRDLKRCPRKLSPTPLGNS--------- 468

Qy        478 SRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAPTLR 522
              |:: | :|  |||                |:: ::|||: :| :| :::|: :|  :|
Db        469 SKEESQLETNVTFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGGDSQEVTVVPHSLP 528

Qy        523 SELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPY 582
              :: | :|:| |:|: :||||:|:::|::|||||||:||||:| ||||||||||:||||
Db        529 FKVVVISAILALVVLTVISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPVQLPY 588

Qy        583 DSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALM 642
              || || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||||
Db        589 DSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALM 648

Qy        643 SELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK-- 700
              ||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :||  |  |
Db        649 SELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKHC 708

Qy        701 -PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
               |  ||     | |    |  |:: |: |::| |||| : ::  |||||: |   ||:||:
Db        709 PPSAELYSNAL-PVGFSLPSHLNLTGESDGGYMDMSKDESIDYVPMLDMKGDIKYADIES 767

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
              |  |       |  :   :  | :| |  |:  ||: |:|||| ||:||||||||||||
Db        768 PSYMAPYDNYVPSAPERTYRATLIND-SPVLSYTDLVGFSYQVANGMDFLASKNCVHRDL 826

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
              ||||||: :||:|||||||||||||| ||||:|||||:||:|||||||||::|||||||||
Db        827 AARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTYLPLKWMAPESIFNSLYTTLSDVW 886

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
              |:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  : |
Db        887 SFGILLWEIFTLGGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFET 946

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDSDNA 987
              || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|: :
Db        947 RPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARFPGIHSLRSPLDTSSV 1006

Qy        988 YIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDL--GKRNRHSSQTS 1045
                          ||                :|: |||||||  |   :| |  |  :  ||  :
Db       1007 LYTAVQPNE----------------SDNDYIIPLPDPKPDVADEGLPEGSPSLASSTLN 1049

Qy       1046 EESAIETGSSSSTFIKRED----ETIEDIDMMDDIGIDSS-DLVEDSFL 1089
              | :   | |  |    :|:   |   ::   | |        |||||
Db       1050 EVNTSSTISCDSPLELQEEPQQAEPEAQLEQPQDSGCPGPLAEAEDSFL 1098


RESULT 19
Q7TMR8_MOUSE
ID   Q7TMR8_MOUSE PRELIMINARY;      PRT;  1099 AA.
AC   Q7TMR8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Platelet derived growth factor receptor, beta polypeptide.
GN   Name=Pdgfrb;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He; TISSUE=Mesenchymal Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055311; AAH55311.1; -; mRNA.
DR   HSSP; P11362; 1FGI.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0016301; F:kinase activity; IMP.
DR   GO; GO:0004871; F:signal transducer activity; IDA.
DR   GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.
DR   GO; GO:0007165; P:signal transduction; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   1099 AA;  122934 MW;  BCE126ACC116F740 CRC64;

  Query Match             41.2%;  Score 2327;  DB 2;  Length 1099;
  Best Local Similarity   44.2%;  Pred. No. 3.9e-116;
  Matches  499;  Conservative  191;  Mismatches  356;  Indels   84;  Gaps   22;

Qy          6 PAFLVLG-CLLTGLSLILCQLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPMSE 63
              || :: |  ||: | |:  | |   :: |   | |: ::|:| | | | : | |
Db          8 PALVLRGQLLLSVLWLLGPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPVMW------ 61

Qy         64 EESSDVEIRNEE-NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122
              |: | |  :    |  | | :|| ::: :   || | | ||::   |   | : |||:||
Db         62 EQMSQVPWQEAAMNQDGTFSSVLTLTNVTGGDTGEYFCVYNNSLGPELS-ERKRIYIFVP 120

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVP--ASYDSRQGFNG 180
              || : |:|:   |  : | |     |||| |||:  ||||  :  :|   || ::|| |
Db        121 DPTMDFLPMDSEDLFIFVTDVTETTIPCRVTDPQLEVTLHEKKVDIPLHVPYDHQRGFTG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||    |||: |:  ::  :  : ||:|: :| ::: : |::|| : ||:| : | |  |
Db        181 TFEDKTYICKTTIGDREVDSDTYYVYSLQVSS-INVSVNAVQTVVRQGESITIRCIVMGN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEE--IKVPSIKLVYTLTVPEATVKDSGDYECAARQATRE 298
              :||: |||||    |: :  : :    ||| ::   | :| | : ||| | |    :  :
Db        240 DVVNFQWTYPRMKSGRLVEPVTDYLFGVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

Qy        299 VKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIE 358
              : | : ||| | |:: :  |   :|   ||  :   |   ||| | : |||:| || :
Db        299 HGDEKAINISVIENGYVRLLETLGDVEIAELHRSRTLRVVFEAYPMPSVLWLKDNRTLGD 358

Qy        359 N-LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSI 417
              :   |:      : | || |:| |:| |  ::|:||: | :||     :|:|   ||  :
Db        359 SGAGELVLSTRNMSETRYVSELILVRVKVSEAGYYTMRAFHEDDEVQLSFKLQVNVPVRV 418

Qy        418 LDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIK-KCNNETSWTILANNVSNIITEI 476
              |:|  : | : | ||:||   | | |:: |  |:|:| :|  : | | | |:
Db        419 LEL-SESHPANGEQTIRCRGRGMPQPNVTWSTCRDLKSRCPRKLSPTPLGNS-------- 469

Qy        477 HSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAPTL 521
              |:: | :|  |||                |:: ::||: :| :|  :::|: :|  :|
Db        470 -SKEESQLETNVTFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGGDSQEVTVVPHSL 528

Qy        522 RSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLP 581
              :: | :|:|  |:|: :|||:|:::|::|||||||:||||:| ||||||||||:|||
Db        529 PFKVVVISAILALVVLTVISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPVQLP 588

Qy        582 YDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQAL 641
              ||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||||
Db        589 YDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQAL 648

Qy        642 MSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK- 700
              |||||||:|||||||:||||||||| |||||||||| ||||:|||:|: :||  |  |
Db        649 MSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKH 708

Qy        701 --PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
                |  ||    | |   |  |:: |: |::| |||| : ::  |||||: |   ||:||:
Db        709 CPPSAELYSNAL-PVGFSLPSHLNLTGESDGGYMDMSKDESIDYVPMLDMKGDIKYADIE 767

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
              | |       | :   :  | :| |  |:  ||: |:|||| ||:|||||||||||
Db        768 SPSYMAPYDNYVPSAPERTYRATLIND-SPVLSYTDLVGFSYQVANGMDFLASKNCVHRD 826

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
              |||||||: :||:|||||||||||| ||||:|||||||||:|||||||::|||||||||
Db        827 LAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDV 886

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
              ||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  : |
Db        887 WSFGILLWEIFTLGGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFE 946

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDSDN 986
              || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|: :
Db        947 TRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARFPGIHSLRSPLDTSS 1006

Qy        987 AYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDL--GKRNRHSSQT 1044
                          ||                :|: |||||||  |   :| |  |  :  ||
Db       1007 VLYTAVQPNE----------------SDNDYIIPLPDPKPDVADEGLPEGSPSLASSTL 1049

Qy       1045 SEESAIETGSSSSTFIKRED----ETIEDIDMMDDIGIDSS-DLVEDSFL 1089
              :| :   | |  |    :|:    |   ::   | |        |||||
Db       1050 NEVNTSSTISCDSPLELQEEPQQAEPEAQLEQPQDSGCPGPLAEAEDSFL 1099
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RESULT 20
PGFRB_RAT
ID   PGFRB_RAT      STANDARD;      PRT;  1097 AA.
AC   Q05030; Q8R406; Q925F7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Beta platelet-derived growth factor receptor precursor (EC 2.7.1.112)
DE   (PDGF-R-beta).
GN   Name=Pdgfrb;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Wang Y., Culty M.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 35-533.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=93305723; PubMed=8318539; DOI=10.1016/0167-4781(93)90127-Y;
RA   Herren B., Weyer K.A., Rouge M., Loetscher P., Pech M.;
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RT   "Conservation in sequence and affinity of human and rodent PDGF
RT   ligands and receptors.";
RL   Biochim. Biophys. Acta 1173:294-302(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 528-1090.
RC   STRAIN=Wistar;
RX   MEDLINE=21359359; PubMed=11346654; DOI=10.1074/jbc.M102995200;
RA   Okuyama H., Shimahara Y., Kawada N., Seki S., Kristensen D.B.,
RA   Yoshizato K., Uyama N., Yamaoka Y.;
RT   "Regulation of cell growth by redox-mediated extracellular proteolysis
RT   of platelet-derived growth factor receptor beta.";
RL   J. Biol. Chem. 276:28274-28280(2001).
CC   -!- FUNCTION: Receptor that binds specifically to PDGFB and has a
CC       tyrosine-protein kinase activity. Phosphorylates Tyr residues at
CC       the C-terminus of PTPN11 creating a binding site for the SH2
CC       domain of GRB2 (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Homodimer, and heterodimer with PDGFRA. The
CC       autophoshorylated form interacts with PIK3C2B, maybe indirectly
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 4 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY090783; AAM09098.1; -; mRNA.
DR   EMBL; Z14119; CAA78489.1; -; mRNA.
DR   EMBL; AF359356; AAK43716.1; -; mRNA.
DR   PIR; S33766; S33766.
DR   HSSP; P17948; 1QSV.
DR   Ensembl; ENSRNOG00000018461; Rattus norvegicus.
DR   GO; GO:0005017; F:platelet-derived growth factor receptor act. . .; IDA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Receptor; Repeat; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     31       Potential.
FT   CHAIN        32   1097       Beta platelet-derived growth factor
FT                                receptor.
FT   TOPO_DOM      32    532       Extracellular (Potential).
FT   TRANSMEM     533    555       Potential.
FT   DOMAIN        32    119       Ig-like C2-type 1.
FT   DOMAIN       128    209       Ig-like C2-type 2.
FT   DOMAIN       213    308       Ig-like C2-type 3.
FT   DOMAIN       415    523       Ig-like C2-type 4.
FT   DOMAIN       599    961       Protein kinase.
FT   NP_BIND      605    613       ATP (By similarity).
FT   ACT_SITE     825    825       By similarity.
FT   BINDING      633    633       ATP (By similarity).
FT   MOD_RES      750    750       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES      856    856       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD      44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD      88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     102    102       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     214    214       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     291    291       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     353    353       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     370    370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     444    444       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     467    467       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     478    478       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID      53     99       Potential.
FT   DISULFID     148    189       Potential.
FT   DISULFID     234    290       Potential.
FT   DISULFID     435    507       Potential.
SQ   SEQUENCE   1097 AA;  122828 MW;  5E6540FA0C5CF22B CRC64;
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  Query Match             41.2%;  Score 2326;  DB 1;  Length 1097;
  Best Local Similarity   43.8%;  Pred. No. 4.4e-116;
  Matches  494;  Conservative  193;  Mismatches  359;  Indels   82;  Gaps   21;

Qy          6 PAFLVLGCLLTGLSLIL-CQLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPMSE 63
              || :: | ||  : |:|  |:|   ::  |   | |: ::|:| | |   : | |
Db          8 PASVLRGQLLLFVLLLLGPQISQGLVITPPGPEFVLNISSTFVLTCSSSAPVMW------ 61

Qy         64 EESSDVEIRNEE-NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122
              |: | |  :    |  | | :|| ::: :   || | | ||::   |   | : |||:||
Db         62 EQMSQVPWQEAAMNQDGTFSSVLTLTNVTGGDTGEYFCVYNNSLGPELS-ERKRIYIFVP 120

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVP--ASYDSRQGFNG 180
              || : |:|:   |  : | |     |||| |||:  ||||  :  :|    || ::|| |
Db        121 DPTMGFLPMDSEDLFIFVTDVTETTIPCRVTDPQLEVTLHEKKVDIPLHVPYDHQRGFIG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||    |||: |:  ::  :  : ||:|: :| ::: : |::|| : ||:| : | |  |
Db        181 TFEDKTYICKTTIGDREVDSDTYYVYSLQVSS-INVSVNAVQTVVRQGESITIRCIVMGN 239

Qy        241 EVVDLQWTYPGEVKGKGITMLEE--IKVPSIKLVYTLTVPEATVKDSGDYECAARQATRE 298
              :||: |||||    |: :  : :    ||| ::   | :| | : ||| | |     : :
Db        240 DVVNFQWTYPRMKSGRLVEPVTDYLFGVPS-RIGSILHIPTAELSDSGTYTCNVSVSVND 298

Qy        299 VKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIE 358
              : | : ::| | |:: :  |   ::   ||  :   |   ||| | : | |:| || :
Db        299 HGDEKAINVTVIENGYVRLLETLEDVQIAELHRSRTLQVVFEAYPTPSVLWFKDNRTLGD 358

Qy        359 NLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSI 417
              :   |:      : | || |:| |:| |  ::|:||: | : |     :|:|   ||  :
Db        359 SSAGELVLSTRNVSETRYVSELTLVRVKVSEAGYYTMRAFHADDQVQLSFKLQVNVPVRV 418

Qy        418 LDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIH 477
              |:|  : | : | | :||    | | |:: |  |:|:|:|  : | | | |:
Db        419 LEL-SESHPANGEQILRCRGRGMPQPNVTWSTCRDLKRCPRKLSPTPLGNS--------- 468

Qy        478 SRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAPTLR 522
              |:: | :|  |||                 |:: ::|||: :| :| :::|: :|  :|
Db        469 SKEESQLETNVTFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGRDSQEVTVVPHSLP 528

Qy        523 SELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPY 582
              :: | :|:| |:|: :||||:|:::|:::|||||||:||||:| ||||||||||:||||
Db        529 FKVVVISAILALVVLTVISLIILIMLWQRKPRYEIRWKVIESVSSDGHEYIYVDPVQLPY 588

Qy        583 DSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALM 642
              || || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||||
Db        589 DSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALM 648

Qy        643 SELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK-- 700
              ||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :||  |  |
Db        649 SELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKHC 708
```

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Qy        701 -PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
Db        709 PPSTELYSNAL-PVGLSLPSHLNLTGESDGGYMDMSKDESVDYVPMLDMKGHIKYADIES 767

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
Db        768 SSYMAPYDNYVPSAPERTYRATLIND-SPVLSYTDLVGFSYQVANGMEFLASKNCVHRDL 826

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
Db        827 AARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVW 886

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
Db        887 SFGILLWEIFTLGGTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFET 946

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDSDNA 987
Db        947 RPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGLHSLRSPLDTSSV 1006

Qy        988 YIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDL--GKRNRHSSQTS 1045
Db       1007 LYTAVQPNE----------------TDNDYIIPLPDPKPDAADEGLLEGSPSLASSTLN 1049

Qy       1046 EESAIETGSSSSTFIKREDETIE---DIDMMDDIGIDSS-DLVEDSFL 1089
Db       1050 EVNTSSTISCDSPLELQEEPQAEPEAQLEQPQDSGCPGPLAEAEDSFL 1097
```

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RESULT 21
Q6QNF3_CANFA
ID   Q6QNF3_CANFA PRELIMINARY;      PRT;  1103 AA.
AC   Q6QNF3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Platelet-derived growth factor receptor beta.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Liao A.T., Chien M.B., London C.A.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY532634; AAS48371.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   Ensembl; ENSCAFG00000018214; Canis familiaris.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; Recepttyrkinsiii.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   1103 AA;  123021 MW;  A3D66E78A34C5FE0 CRC64;
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  Query Match             40.4%;  Score 2285.5;  DB 2;  Length 1103;
  Best Local Similarity   44.1%;  Pred. No. 6.6e-114;
  Matches  489;  Conservative  182;  Mismatches  348;  Indels   91;  Gaps   20;

Qy         30 ILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEVSS 89
Db         35 ITPPGPELVLNISSTFVLTCSGPAPVVW-----ERLSQEPLQKMARTQDGTFSSTLTLTN 89

Qy         90 ASAAHTGLYTCYYNHTQTEENELEGR-HIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAII 148
Db         90 VTGLDTGEYFCTYKGSHGLEP--DGRKRLYIFVPDPTMGFLPVDPEELFIFLTEITEITI 147

Qy        149 PCRTTDPETPVTLHNSEGVV--PASYDSRQGFNGTFTVGPYICEATVKGKKFQTIPFNVY 206
Db        148 PCRVTDPRLVVTLHEKKVDIPLPIPYDHQRGFSGTFEDKTYVCKTTIGDKEVDSEAYYVY 207

Qy        207 ALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITMLEE--I 264
Db        208 SLQVSS-INVSVNAVQTVVRQGENITIMCIVTGNEVVNFEWTYPRMESGRLVEPVTDFLF 266

Qy        265 KVPS-IKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQ 323
Db        267 NVPSHIRSI--LHIPSAELGDSGTYICNVSESVNDHRDEKSINVTVVESGYVRLLGELDA 324

Qy        324 LEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLT-EITTDVEKIQEIRYRSKLKLI 382
Db        325 VQFAELHRSRALQVVFEAYPPPTVVWFKDNRTLGDSSAGEIALSTRNVSETRYVSELTLV 384

Qy        383 RAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPL 442
Db        385 RVKVAEAGYYTMRAFHEDAEAQLSFQLQVNVPVRVLELSESHPAS-GEQTVRCRGRGMPQ 443

Qy        443 PDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTF------------ 490
Db        444 PHLTWSTCSDLKRCPRELPPTPLGNS---------SEEESQLETNVTYWPEDQEFEVVST 494

Qy        491 ---AKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVV 547
Db        495 LRLRRVDQPLSVRCTLHNLLGHDMQEVTVVPHSLPFKVVVISAILALVVLTIISLIILIM 554

Qy        548 IWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKV 607
Db        555 LWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQLVLGRTLGSGAFGQV 614

Qy        608 VEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKS 667
Db        615 VEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSELKIMSHLGPHLNVVNLLGACTKG 674

Qy        668 GPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK---PKKELDIFGLNPADESTRSYVILS 724
Db        675 GPIYIITEYCRYGDLVDYLHRNKHTFLQLCSDKRRPPSAELYSNAL-PAGLPLPSHVSLP 733

Qy        725 FENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSD 784
Db        734 GESDGGYMDMSKDESVDYVPMLDMKGGVKYADIESSSYMAPYDNYVPTAPERTCRATLIN 793

Qy        785 DNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIM 844
Db        794 E-SPVLSYTDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLVKICDFGLARDIM 852

Qy        845 HDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDST 904
Db        853 RDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTPYPELPMNEQ 912

Qy        905 FYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEK 964
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Db        913 FYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLLERLLGEGYKKKYQQ 972

Qy        965 IHLDFLKSDHPAVARMR-----------VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRL 1012
Db        973 VDEEFLRSDHPAVLRSQARLPGFPGLRSPLDTSSVLYTAVQPNE---------------- 1016

Qy       1013 SADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFI--------KRED 1064
Db       1017 -GDNDYIIPLP--DPKPEVADGPLESSPSLASSTLNEVNTSSTISCDSPLEPQEEPEPEP 1073

Qy       1065 ETIEDIDMMDDIGIDSS-----DLVEDSFL 1089
Db       1074 EPQPEPQVVPEPPLDSSCPGPRAEAEDSFL 1103


RESULT 22
P79749_FUGRU
ID   P79749_FUGRU PRELIMINARY;      PRT;  1048 AA.
AC   P79749;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Platelet-derived growth factor receptor beta.
GN   Name=PDGFRbeta;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97129405; PubMed=8973913;
RA   How G.F., Venkatesh B., Brenner S.;
RT   "Conserved linkage between the puffer fish (Fugu rubripes) and human
RT   genes for platelet-derived growth factor receptor and macrophage
RT   colony-stimulating factor receptor.";
RL   Genome Res. 6:1185-1191(1996).
DR   EMBL; U63926; AAC60062.1; -; Genomic_DNA.
DR   PIR; T30815; T30815.
DR   HSSP; P35968; 1VR2.
DR   Ensembl; SINFRUG00000146041; Fugu rubripes.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Receptor.
SQ   SEQUENCE   1048 AA;  117867 MW;  7363EFD38D9B913C CRC64;

  Query Match           38.6%;  Score 2182.5;  DB 2;  Length 1048;
  Best Local Similarity  43.9%;  Pred. No. 2.1e-108;
  Matches  472;  Conservative  175;  Mismatches  334;  Indels   93;  Gaps   25;

Qy          9 LVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQ-------YPM 61
Db         16 VALAALLSSCTTVSCL----KIVPEEKQLILAEGSSLSLTCAGSSETTWDLKSDDVPFFQ 71

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db         72 MKAESSDLNYKIVQSNS--TASVLTLWHVDWKNTAVYQC------REQLTGEIKEVAVFV 123

Qy        122 PDPDVAFVPLGM----TDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPAS--YDSR 175
Db        124 PD---RFSPQTLRFIESSHGMVTKTSGESTVPCVVTNPNITVTLYDKDTDLPVNGVYVPS 180

Qy        176 QGFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTC 235
Db        181 EGFKAYLDYRTYVCRGELNGEVKESQAFNVYSIHVPEDIDAYVNASQTVLKQGEPLTVNC 240

Qy        236 AVFNNEVVDLQWTYPGE--VKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
Db        241 TVQGVELVLFSWDIPNRDIVKHKP----ETVVLSATTMRSCLVFPHATVAHSGTYVCHAH 296

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNN 353
Db        297 ESTQDQKAFASVNITVLERGFVAVKSTRKQNITAELQENVELRVEIEAYPPPQIRWKKDG 356

Qy        354 LTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQV 413
Db        357 APVRGDKTII---IRQEHEIRYVTILTLVRVRTEQKGLYTALITNEDDVKEVTFALEVQV 413

Qy        414 PSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETS-WTILAN----- 467
Db        414 LARIKDLT-DHHLPGKKQLVTCVAEGVPTPTIQWYSCDSMLKCNNQTSLWQQLKADPELL 472

Qy        468 NVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLG-AENRELKLVAPTLRSELT 526
Db        473 SIHTSVTE--ARQTNQVRSQVTFFKPQHT-TVRCETTNQEGLIDFRDVKLVSSSLFSQVV 529

Qy        527 VAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRW 586
Db        530 LLAVVLTLVPIIIMSIIILIAVWKKKPRYEIRWKVIESVSQDGHEYIYVDPIHLPYDLAW 589

Qy        587 EFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELK 646
Db        590 EMPRDNLVLGRTLGSGAFGRVVEATAHGLSHSQSSIKVAVKMLKATARRSETQALMSELK 649

Qy        647 IMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELD 706
Db        650 IMSHLGPHLNIVNLLAACTKHGPLYLVTEYCRYGDLVDYLHRNKHTFLQYYLDKNQDDGS 709

Qy        707 IF--GLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDR 764
Db        710 LISGGSTPLSQ-RKGYVSFGSESDGGYMDMSKDEPAVYVPMQEQMDTIKYADIQPSPYES 768

Qy        765 PAS---YKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAA 821
Db        769 PYQQDLYQEQG--GGRVDLVISD--SPALTYDDLLGFSYQVAKGMEFLASKNCVHRDLAA 824

Qy        822 RNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSY 881
Db        825 RNVLICEGKLVKICDFGLARDIMHDSNYISKGSTFLPLKWMAPESIFHNLYTTLSDVWSY 884

Qy        882 GILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRP 941
Db        885 GILLWEIFTLGGTPYPDLPMNELFYSPLKRGYRMAKPAHASDEVYEIMKRCWDETFEKRP 944

Qy        942 SFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAY------------I 989
Db        945 DFSFLVHCVGDMLTDSYKKKYSQVNETFLKSDHPAVARTKPRLSSPFPIANPAFGSPSLV 1004

Qy        990 GVT------------YKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEE 1031
Db       1005 GLSDFPDPYNQNTRRFRNEAEV---------QEGVTSFNEYIIPIP--DPKPEK 1047


RESULT 23
Q75WK5_ORYLA
ID   Q75WK5_ORYLA PRELIMINARY;      PRT;  686 AA.
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AC   Q75WK5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   PDGFR (Fragment).
GN   Name=pdgfr;
OS   Oryzias latipes (Medaka fish) (Japanese ricefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
OX   NCBI_TaxID=8090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kawamura T., Yamashita I.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
DR   EMBL; AB121073; BAD05034.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00047; ig; 2.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Immunoglobulin domain; Nucleotide-binding; Receptor;
KW   Transmembrane.
FT   NON_TER       1      1
FT   NON_TER     686    686
SQ   SEQUENCE   686 AA;  76477 MW;  F1DC86A1DF9A476F CRC64;

  Query Match             37.7%;  Score 2132.5;  DB 2;  Length 686;
  Best Local Similarity   61.4%;  Pred. No. 5.7e-106;
  Matches  423;  Conservative   89;  Mismatches  168;  Indels    9;  Gaps    6;

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              |  |  | |:|:| : | :: :  : |:     : | :|::| :|    |||| |||
Db          2 GVFLAGTYVCKALINGHEYYSEEYIVHGWPGGTALHVELKAKRTALLVGETITVTCLARG 61

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREV 299
                |::  | |||:   :|   : | |    :::||||:|:|:|||| | |:
Db         62 PEILEDNWKYPGKAANRGTKTVRENKKDQ-EILYTLTIPQASVKDSGSYSCSIVDIANNE 120

Qy        300 KEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIEN 359
               : |:  | |    |: | | | : |:  | ||: |   | ::|  |::|:|: : | :
Db        121 IQTKEQEIQVFAGEFVSIDPEFGEHESAELDEVREFRANVHSFPNARVTWIKDGIPLSDV 180

Qy        360 LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 419
                ||:| : :  |  | | | ||||| ||||:||:  :| :  :  :  |  :||: |:|

Db        181 TAEISTSLRQTSETSYMSVLTLIRAKGEDSGNYTMRVENGNQSRHVSLILEVKVPAVIVD 240

Qy        420 LVDDHHGSTGGQTVRCTAEGTPLPDIEW--MICKDIKKC-NNETSWTILANNVSNIITEI 476
              |:| ||||  ||:| |   |   | : |    || || | || : |  || | :||: :
Db        241 LMDIHHGSAIGQSVVCITRGR--PHLRWSGSSCKSIKHCGNNSSFWVPLATNSTNIVFDS 298

Qy        477 HSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLV 536
              |  : : :| :| |  :| |:||||||:| :   :||:|||:     ||||||||||||
Db        299 HF-EGNNLESQVVFGHLESTLAVRCLARNEMATVSREVKLVSSGPHPELTVAAAVLVLLV 357

Qy        537 IVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLG 596
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||| ||||
Db        358 IVIISLIVLVVIWKQKPRYEIRWRVIESVSPDGHEYIYVDPMQLPYDSRWEFPRDRLVLG 417

Qy        597 RVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLN 656
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        418 RVLGSGAFGKVVEGTAYGPSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLN 477

Qy        657 IVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADES 716
              ||||||||||||||||||||||||||||||||||::|||  ||| :||:||||:||||||
Db        478 IVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRENFLSLSPEKNRKEMDIFGINPADES 537

Qy        717 TRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDS 776
              :|||||||||: |||||||||| ||||||||     ||:||:||| || | | |  | :
Db        538 SRSYVILSFESKGDYMDMKQADNTQYVPMLEMNNASKHSDVQRSNYDHPPSQKGSS--EC 595

Qy        777 EVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICD 836
              |::|||||| :|||| ||||||||||:|||||:||| ||||||||||||:|||||||||
Db        596 EMENLLSDDTTEGLTTTDLLSFTYQVAKGMEFLSSKNSVHRDLAARNVLLSQGKIVKICD 655

Qy        837 FGLARDIMHDSNYVSKGSTFLPVKWMAPE 865
              |||||||||||| |||||||:||: ||
Db        656 FGLARDIMHDSNYCSKGSTFLPLKWIGPE 684


RESULT 24
Q4RZA4_TETNG
ID   Q4RZA4_TETNG PRELIMINARY;      PRT;  1094 AA.
AC   Q4RZA4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 1 SCAF14944, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00026578001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
```

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CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
DR   EMBL; CAAE01014944; CAG06278.1; -; Genomic_DNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW   Receptor; Transferase; Transmembrane.
FT   NON_TER    1094   1094
SQ   SEQUENCE   1094 AA;  123161 MW;  8E9C68FA1D4A6CCE CRC64;

  Query Match             37.2%;  Score 2104;  DB 2;  Length 1094;
  Best Local Similarity   41.1%;  Pred. No. 3.6e-104;
  Matches  466;  Conservative  168;  Mismatches  349;  Indels  150;  Gaps   25;

Qy          7 AFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQY-----PM 61
              | | |    || |        :   ::|::   ::    || |: | |   | :| :     |
Db          4 AVLHLTVTLTALLYSCTPANCLRMVPDDRRHILAEGSSLSITCSGSGETTWDFKSEDAPF 63

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
               : |:    :  :   |    :|| :   :  :||:| |       |:| |     : |:|
Db         64 FQMEAKSGGLNYKIVQSNRTTSVLTLWHVNWKYTGVYQC--KDVLTKEME----EVAIFV 117

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNS------EGVVPASYDSR 175
              |||:| |:    :|: ::  : : : :||  |:|   ||||:       |||    |
Db        118 PDPEVWFI---RSDHGMVPMNREESTVPCLVTNPNIRVTLHDKDTGLSIEGV----YVPG 170

Qy        176 QGFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTC 235
              :||        |:|   : |:  :: |:|||::    ::|  : | ||| | || : | |
Db        171 EGFKAYLEYRTYVCRGELNGEVKESQPYNVYSVHVPEDIDAYVNASKTVLKQGEPLTVNC 230

Qy        236 AVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQA 295
              |   |:|:  | |           : |   :::     | | |||  || | | | :
Db        231 TVQGVELVNFSWVIPNRDSVGAQPQTDIISATTMR--SCLVFPHATVAHSGTYVCRAVEG 288

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              :       : ||| ||||: :| |  |         |      ||: |||||:| |  |:  |
Db        289 IQNQATNASINISVLEKGFVAVKSTQKQNITAKHQENVELRVEMEAYPPPQILWKKDGAT 348

Qy        356 LIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPS 415
              :  : | :   : :  |||| : | :| : |  | ||::  |||  |   | |  |:|:
Db        349 VKADRTIV---IRQEHEIRYVTILTLVRVRSEQKGLYTVLITNEDDRKEVAFALEVQIPA 405

Qy        416 SILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETS-WTILAN-----NV 469
              : ||  |||       | | ||| | | |:|  |  : ||:|::: | :|       ::
Db        406 QVKDLT-DHHLPGNKHLVTCVAEGVPTPVIQWRSCDRMLKCSNQSALWQLLTADPELLSI 464

Qy        470 SNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLG-AENRELKLVAPTLRSELTVA 528
              :||   |    |  :||| | :  : ||| | |   |  : |::|||: || |:: :
Db        465 QTNVTE--PRGTKQVRSQVTFFKPQH-VTVRCEASNQDGLIDRRDIKLVSSTLFSQVALL 521

Qy        529 AAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEF 588
              ||:| |: |:|:|:|:|: :|::|||||||:||||:| ||||||||||: ||||  ||
Db        522 AALLTLVPIIIMSIIILIAVWRKKPRYEIRWKVIESVSQDGHEYIYVDPIHLPYDLAWEM 581

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
              || ||||| ||||||:||| ||||  ||  :||||||||  :| || ||||||||||
Db        582 SRDNLVLGRTLGSGAFGRVVEATAYGLMHSQSSIKVAVKMLK--SRESETQALMSELKIM 639

Qy        649 THLGPHLNIVNLLGACTK--------------------------SGPIYIITEYCFYG 680
              :|||||||||||| ||||                          |||:|::|||| ||
Db        640 SHLGPHLNIVNLLAACTKHGEVKNLHQLCQYHVHEYSHNTIVSPNQSGPLYLVTEYCRYG 699

Qy        681 DLVNYLHKNRDSFLSHHPEKPKK--ELDIFGLNPADESTRSYVILSFENNGDYMDMKQAD 738
              |||:|||:|: :|| :: :| :     |   |  |  :  : ||    |::| |||| : :
Db        700 DLVDYLHRNKHTFLQYYLDKNQDGGSLISGGSTPLSQ-RKGYVSFGSESDGGYMDMSKDE 758

Qy        739 TTQYVPMLERKEVSKYSDIQRSLYDRPAS---YKKKSMLDSEVKNLLSDDNSEGLTLLDL 795
              |||| |: :  ||:||| | || |     |:::       |  ::||  |  ||  ||
Db        759 PAVYVPMQEQTDAIKYADIQPSPYDSPYQQDIYQEQG--GGRVDLVISD--SPALTYDDL 814

Qy        796 LSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGS- 854
              | |:||||:|||||||||||||||||||||: :||:|||||||||||||||||:||||
Db        815 LGFSYQVAKGMEFLASKNCVHRDLAARNVLICEGKLVKICDFGLARDIMHDSNYISKGSV 874

Qy        855 ------------------------------TFLPVKWMAPESIFDNLYTTLSDVWSYGI 883
                                           ||||:|||||||| ||||||||||||||
Db        875 SVPISVMAPTWDAEQEIHESVNTFEQHSLLQTFLPLKWMAPESIFHNLYTTLSDVWSYGI 934

Qy        884 LLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSF 943
              ||||||:|||||||  : ::  ||: :| |||||||  ||: ||||||  :||:   |||| |
Db        935 LLWEIFTLGGTPYPDLPMNELFYSALKRGYRMAKPAHASDEVYEIMKRCWDETFEKRPDF 994

Qy        944 YHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR---------------------- 981
                |   | |:|   ||| | :::  ||||:|||||| :
Db        995 SFLVHCVGNMLTDGYKKKYREVNETFLKSNHPAVARTKPRLSSPFPIANPAFGSPSQVGL 1054

Qy        982 ---VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEE 1031
                  |  :   |||: :  ::           ::: : ||||:|  || |||
Db       1055 SNFPDPYSQNTNVTYEADAQEV----------MTSFNEYIIPIP--DPKPEE 1094


RESULT 25
Q8CGH8_MOUSE
ID   Q8CGH8_MOUSE PRELIMINARY;      PRT;   486 AA.
AC   Q8CGH8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Pdgfra protein (Fragment).
GN   Name=Pdgfra;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC037467; AAH37467.1; -; mRNA.
DR   HSSP; P17948; 1QSV.
DR   MGI; MGI:97530; Pdgfra.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0048407; F:platelet-derived growth factor binding; IDA.
DR   GO; GO:0030539; P:male genitalia morphogenesis; IMP.
DR   GO; GO:0009887; P:organogenesis; IMP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
FT   NON_TER     486    486
SQ   SEQUENCE   486 AA;  54569 MW;  2BA1DE55490720B6 CRC64;

  Query Match             36.1%;  Score 2043;  DB 2;  Length 486;
  Best Local Similarity   84.3%;  Pred. No. 2.3e-101;
  Matches  387;  Conservative   38;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| |||||  || ||| ||||||||||:|||||||||| ||||||||:|
Db          1 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:|||||||||||||| :|||||| ||||||||||:|:|:|||||||
Db         61 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:||||||||||||| |||||:  :|||||||||||||
Db        121 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:|||||||||||: |:|  ||||||||||||:|||:| :||||:|||||||||||||
Db        181 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:|||||||||||||:|||||||:|||||||||:|||
Db        241 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:||||||||||:||:|||  |||||||||| |||||:||| ||||||||:||||||||
Db        301 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:|||||||||||||||: |||| |||||||| | ||:|||||
Db        361 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNE 459
              ||||||| |||||||||||||:|:||||| |||  |:
Db        421 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKYGNQ 459


RESULT 26
Q90269_BRARE
ID   Q90269_BRARE PRELIMINARY;      PRT;   457 AA.
AC   Q90269;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Partial intracellular tyrosine kinase domains of platelet-derived
DE   growth factor receptor subtype alpha (Fragment).
GN   Name=pdgfra;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu W., Richardson W.D.;
RL   Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z32814; CAA83675.1; -; mRNA.
DR   PIR; S44269; S44269.
DR   HSSP; P36888; 1RJB.
DR   Ensembl; ENSDARG00000030379; Danio rerio.
DR   ZFIN; ZDB-GENE-990415-208; pdgfra.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Kinase; Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   457 AA;  51738 MW;  292B4F252725BCC8 CRC64;

  Query Match             33.9%;  Score 1914.5;  DB 2;  Length 457;
  Best Local Similarity   79.2%;  Pred. No. 1.6e-94;
  Matches  365;  Conservative   48;  Mismatches   41;  Indels    7;  Gaps    5;

Qy        630 KPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKN 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 KPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKN 62

Qy        690 RDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERK 749
              || ||| | || ||:|||||:||||||:|||||||||  |||||||||| |||||||
Db         63 RDGFLSRHTEKGKKDLDIFGINPADESSRSYVILSFEGKGDYMDMKQADTMQYVPMLEMN 122

Qy        750 EVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFL 809
              | |||| |||| || | |:::    : | ::|||||::|||| :|||||||||||||||
Db        123 EASKYSPIQRSDYDHPPSHRQ---FNDEAESLLSDDSAEGLTTMDLLSFTYQVARGMEFL 179

Qy        810 ASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFD 869
              ||||||||||||||||:||||||||||||||||||:||||||||||||||||||||||||
Db        180 ASKNCVHRDLAARNVLLSQGKIVKICDFGLARDIMHDNNYVSKGSTFLPVKWMAPESIFD 239

Qy        870 NLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIM 929
              |||||||||||||||||||||||||||:|||:||||||||||| ||:||:|:|||:|
Db        240 NLYTTLSDVWSYGILLWEIFSLGGTPYPGMVVDSSFYNKIKSGYRMTKPEHASSDVYELM 299

Qy        930 VKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-VDSDNAY 988
              :|||||||||||||: ||: | :|||  :|: ||::: |||||||||| |:: :|:|:||
Db        300 MKCWNSEPEKRPSFHSLSDTVASLLPSGFKRCYERVNHDFLKSDHPAVTRVQCIDNDDAY 359

Qy        989 IGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEES 1048
              :|| ||| : |:|: | | |||||:|||||||||:||:   ||  ||||||||||||
Db        360 MGVLYKN-QGKMKNRESGFDEQRLSSDSGYIIPLPDLDPL-SNEDYSKRNRHSSQTSEES 417

Qy       1049 AIETGSSSSTFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              ||:|||||||  ||| ||:||| ::|:: :|| ||||||||
Db        418 AIDTGSSSST-TKREGETLEDITLLDEMCLDSGDLVEDSFL 457
```

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RESULT 27
Q59F04_HUMAN
ID   Q59F04_HUMAN PRELIMINARY;      PRT;   777 AA.
AC   Q59F04;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Platelet-derived growth factor receptor beta variant (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA   Ohara O., Nagase T., Kikuno F.R.;
RT   "None Title.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB209657; BAD92894.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   777 AA;  86905 MW;  D9865277C3839F9C CRC64;

  Query Match             33.0%;  Score 1863;  DB 2;  Length 777;
  Best Local Similarity   49.1%;  Pred. No. 1.9e-91;
  Matches  393;  Conservative  118;  Mismatches  207;  Indels   82;  Gaps   15;

Qy        339 VRAYPPPRISWLKNNLTLIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQ 397
              ||  |      :::| || ::   ||      : | || |:| |:| |  ::||||: |
Db         11 VRGLPTAHCPVVQDNRTLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAF 70

Qy        398 NEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCN 457
              :|||    :|:|   ||  :|:| : |  | | ||||   | | |:| |  |:|:|:|
Db         71 HEDAEVQLSFQLQINVPVRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCP 129

Qy        458 NETSWTILANNVSNIITEIHSRDRSTVEGRVTF--------------AKVEETIAVRCL 502
              |   |:| |:         | : | :|  ||:                 |:  ::|||
Db        130 RELPPTLLGNS---------SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCT 180

Qy        503 AKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVI 562
              :| :| : :|: :|  :|  :: | :|:| |:|: |||||:|:::|::|||||||:||
Db        181 LRNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVI 240

Qy        563 ESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVM 622
              ||:| |||||||||||||||| || ||| ||||| |||||||:||| ||:||| ||  |
Db        241 ESVSSDGHEYIYVDPMQLPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATM 300

Qy        623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL 682
              |||||||| |||||||||||||||||:|||||||:|||||||| ||||||||| ||||
Db        301 KVAVKMLKSTARSSEKQALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDL 360

Qy        683 VNYLHKNRDSFLSHHPEK---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADT 739
              |:|||:|: :|| || :|    |  ||     | |       |:| |: |::| |||| : ::
Db        361 VDYLHRNKHTFLQHHSDKRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDES 419

Qy        740 TQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFT 799
              |||||: |   ||:||: | | |       | :   :  | :: |  |: :||: |:
Db        420 VDYVPMLDMKGDVKYADIESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFS 478

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
              |||| |||||||||||||||||||: :||:||||||||||||| |||||||||||||:
Db        479 YQVANGMEFLASKNCVHRDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPL 538

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
              |||||||||::|||||||||:|||||||:|||||| : ::  ||| || |||||:|
Db        539 KWMAPESIFNSLYTTLSDVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPA 598

Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
              ||: |:|||| |||  : | || |  |  ::| ||   ||| |::  :||:|||||: |
Db        599 HASDEIYEIMQKCWEEKFEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILR 658

Qy        980 MR------------VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDP 1027
               :            :|: :        ||                |: ||||||  ||
Db        659 SQARLPGFHGLRSPLDTSSVLYTAVQPNE----------------GDNDYIIPLP--DP 699

Qy       1028 VPEEEDLGKRNRHSSQTSEESAIETGSSSSTF-----IKREDE---------TIE---DI 1070
              ||  | |       | | | :   ::|||      :: :||          :|   ::
Db        700 KPEVADEGPLEGSPSLAS--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPEL 757

Qy       1071 DMMDDIGIDSSDL-VEDSFL 1089
              : : | |  :     |||||
Db        758 EQLPDSGCPAPRAEAEDSFL 777


RESULT 28
Q8UVR9_FUGRU
ID   Q8UVR9_FUGRU PRELIMINARY;      PRT;   986 AA.
AC   Q8UVR9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Platelet-derived growth factor receptor beta 2 (Fragment).
GN   Name=PDGFRbeta2;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22241651; PubMed=12354661; DOI=10.1016/S0378-1119(02)00736-9;
RA   Williams H., Brenner S., Venkatesh B.;
RT   "Identification and analysis of additional copies of the platelet-
RT   derived growth factor receptor and colony stimulating factor 1
RT   receptor genes in fugu.";
RL   Gene 295:255-264(2002).
DR   EMBL; AF411927; AAL50567.1; -; Genomic_DNA.
DR   HSSP; P35968; 1VR2.
DR   Ensembl; SINFRUG00000128914; Fugu rubripes.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000005; HTHAraC.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
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DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 3.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
FT   NON_TER     986     986
SQ   SEQUENCE   986 AA;  110504 MW;  0FC38815AB635EB3 CRC64;

  Query Match             32.5%;  Score 1835.5;  DB 2;  Length 986;
  Best Local Similarity   38.3%;  Pred. No. 8e-90;
  Matches  377;  Conservative  213;  Mismatches  316;  Indels   79;  Gaps   20;

Qy         15 LTGLSLILCQ--LSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIR 72
              |  |: |:| :  |||  :||:  | ::: | :|:: | | |:||| :|   :::    :
Db         17 LLGVFLVLPEAFLSL-ELLPSSTEVLLRSNENFTVVCSGWSQVSWLFP---QDALVDGVA 72

Qy         73 NEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP--DPDVAFVP 130
               |:  |   :::| : :|:  |:| |||       |    : : : |::|   |:  |:
Db         73 VEDQGS---ISILNIFNATWKHSGRYTC------EEGLSSQSKSVDIFIPGQGPEEWFL- 122

Qy        131 LGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFNGTFTVGPYI 188
                ::|  |:::: :   |||  :||:  |:|:       |    |:  :|| |       |:
Db        123 --LSDLGVVMKEKEEGTIPCLVSDPQLNVSLYERPDIPVTGLMYEPGRGFTGPLNDTSYL 180

Qy        189 CEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNNEVVDLQWT 248
              | |:   :| ::  : |:::     :::::      | | || : | | | : |:|   |
Db        181 CVASNGRQKIESQVYYVFSVIVPKVMEVDLTVSSRVLKQGEVLTVNCTVKDTEMVYFFWD 240

Qy        249 YPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTIS 308
              :| : : : :|     :: |      : : :||| ||| | |  ::  :    |: :|::
Db        241 FPRKQEIEPLTEFLPNRIRSF-----VNISKATVADSGVYACTVQETMKGQTVMENITVT 295

Qy        309 VHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVE 368
              | ::|:: : |:     :  ||    | :|| |:| | : |  ::| |: :: | :||
Db        296 VLDQGYVYLWPSGETNVSSLLHHTVEFSIEVDAHPAPTVRWTRDNQTVDKDTTSVTT--T 353

Qy        369 KIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGST 428
              ::   || | |||:| : : :|:|    | |||| :   | |  : |   | |  |
Db        354 RLTGSRYMSTLKLVRVRMDQTGNYAATAYNEDAEEEVVFHLEIKAPPKITSL-----SEI 408

Qy        429 GGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVSNI-----ITEIHSRDRS 482
              : : | :|| | | : |  | :  :| | | ||  : :     :     :|:: ::  :
Db        409 SNKVMLCVSEGAPPPSVTWYGCHNSHRCINMTDSWRRVPSAPEGVAVRENVTKLENKGVT 468

Qy        483 TVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISL 542
              |   :|   :    |||| | |  |   |:|::   :| |:: | ||||||: | :: |
Db        469 QVHSVLTLQSLSSLSAVRCEATNSAGRRARDLRIQTTSLYSQVAVLAAVLVLVFITVVFL 528

Qy        543 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 602
              |||:::|::|||||:||:||||:|||| :| |:||  |||:| || ||| : || |||||
Db        529 IVLILLWRKKPRYEVRWKVIESVSPDGQQYTYLDPTHLPYNSTWEVPRDNISLGPVLGSG 588

Qy        603 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 662
              |||:|||    ||  |   |||:||:|  : |   |:||||||:: ||||||||||||
Db        589 AFGRVVEANVSGLLHSHSTTKVAIKMVK--SNSGAVQSLMSELKVLVHLGPHLNIVNLLG 646

Qy        663 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 722
              |||: ||:|:|||:| :||||:|| :|| :||    :| ||
Db        647 ACTRGGPVYLITEFCRHGDLVSYLERNRHTFLQR--DKQKKS------------------ 686

Qy        723 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRP--ASYKKKSMLDSEVKN 780
                : :| |||| : :: :|| | :       |:||: ::|: |   : ::::||
Db        687 ---DADGGYMDMNKEESVEYVTMTK----LSYADIEPAVYETPYTPADQQEAML------ 733

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||  |  ||| |||||::|||: |:||:|:||:|||||||||: :||:||:|||||
Db        734 LLSD--SPLLTLHDLLSFSFQVAQAMDFLSSRNCLHRDLAARNVLVCEGKLVKVCDFGLA 791

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||:  | :||:||::|||||||:||||| |:|:  |||||||||||||||:||| :
Db        792 RDLTKDQDYVAKGTSFLPVKWMSPESIFQNIYSCQSDVWSYGILLWEIFSLGGSPYPDVP 851

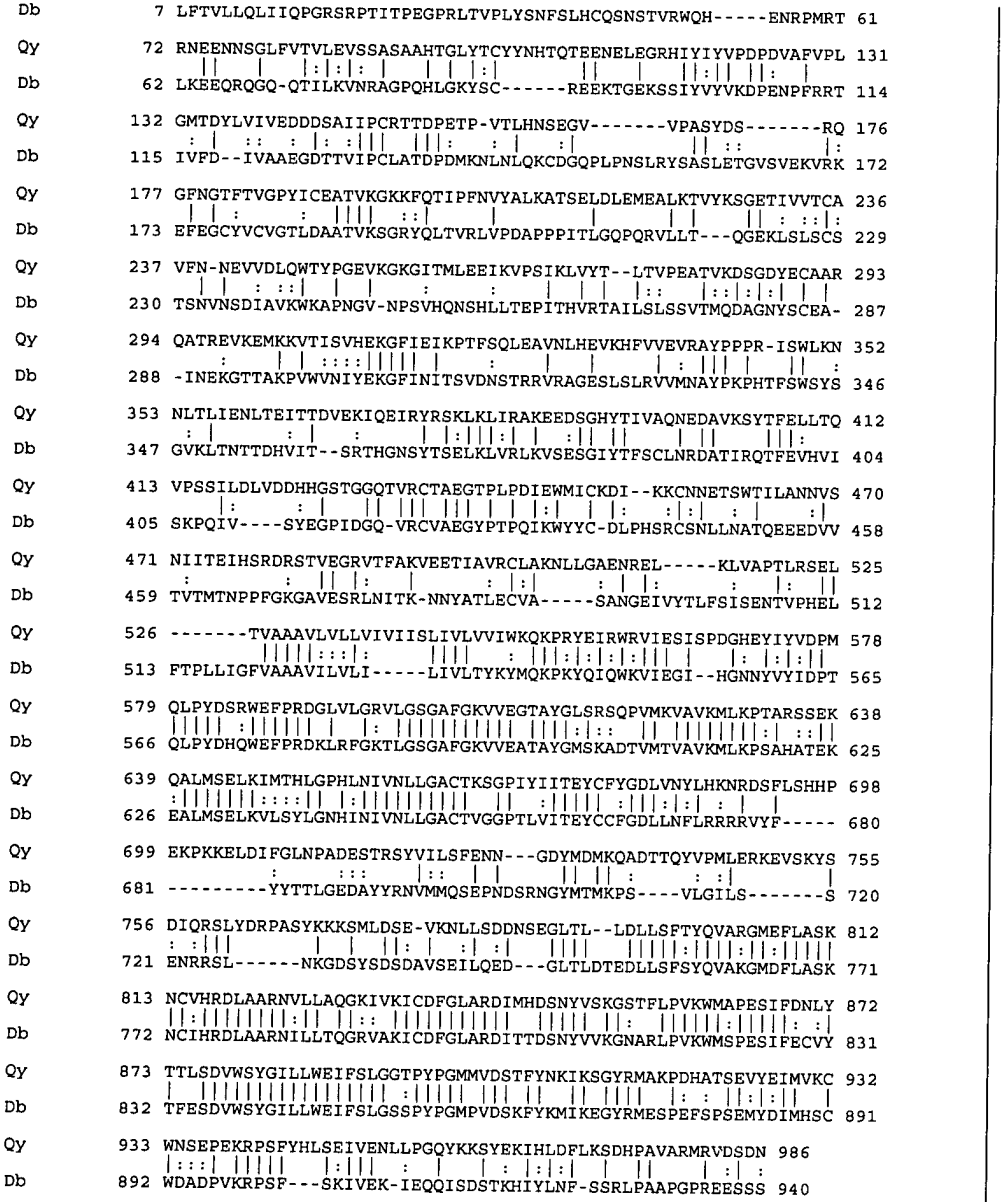
Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              :   ||: :| |||| :|:||   ::::| :||  :|: ||:|  |   | |:|   |||
Db        852 LTQEFYSALKRGYRMNRPEHAPQSIFDLMKQCWEEKPQSRPTFSSLVVSVGNMLTDDYKK 911

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSD 985
                |  :  :||| : ||| | |   |
Db        912 RYHNLAENFLKGEQPAVLRSRAAGD 936


RESULT 29
Q5RID5_BRARE
ID   Q5RID5_BRARE PRELIMINARY;      PRT;   976 AA.
AC   Q5RID5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Kit receptor.
GN   Name=kit; ORFNames=CH211-176L11.1-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hunter G.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX276114; CAI11666.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   976 AA;  109279 MW;  A56921FA4ED2A90D CRC64;

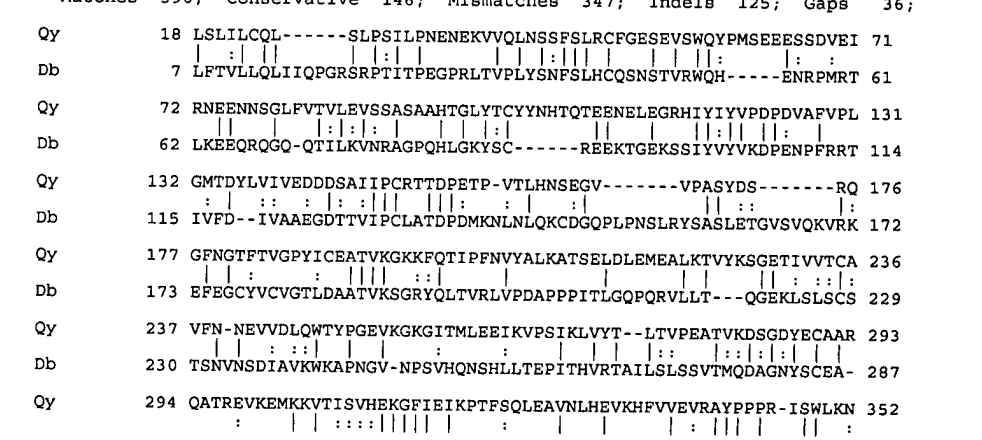
  Query Match             27.5%;  Score 1554.5;  DB 2;  Length 976;
  Best Local Similarity   39.1%;  Pred. No. 9.4e-75;
  Matches  396;  Conservative  146;  Mismatches  347;  Indels  125;  Gaps   36;

Qy         18 LSLILCQL------SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEI 71
              |  :| ||      | |:| |      | | |:||| |   | | ||:     |:  :
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RESULT 30
Q9W755_BRARE
ID Q9W755_BRARE PRELIMINARY; PRT; 976 AA.
AC Q9W755;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kit receptor tyrosine kinase.
GN Name=kit;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99396707; PubMed=10393121;
RA Parichy D.M., Rawls J.F., Pratt S.J., Whitfield T.T., Johnson S.L.;
RT "Zebrafish sparse corresponds to an orthologue of c-kit and is
RT required for the morphogenesis of a subpopulation of melanocytes, but
RT is not essential for hematopoiesis or primordial germ cell
RT development.";
RL Development 126:3425-3436(1999).
DR EMBL; AF153446; AAD41890.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q9W755; 538-920.
DR ZFIN; ZDB-GENE-980526-464; kit.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR009134; VEGFR.
DR Pfam; PF00047; ig; 2.
DR PRINTS; PR01832; VEGFRECEPTOR.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Kinase; Receptor.
SQ SEQUENCE 976 AA; 109278 MW; A80AA01658C1A2DA CRC64;

Query Match 27.5%; Score 1554.5; DB 2; Length 976;
Best Local Similarity 39.1%; Pred. No. 9.4e-75;
Matches 396; Conservative 146; Mismatches 347; Indels 125; Gaps 36;



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Db        288 -INEKGTTAKPVWVNIYEKGFINITSVDNSTRRVRAGESLSLRVVMNAYPKPHTFSWSYS 346

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412

Db        347 GVKLTNTTDHVIT--SRTHGNSYTSELKLVRLKVSESGIYTFSCLNRDATIRQTFEVHVI 404

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI--KKCNNETSWTILANNVS 470

Db        405 SKPQIV----SYEGPIDGQ-VRCVAEGYPTPQIKWYYC-DLPHSRCSNLLNATQEEEDVV 458

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENREL-----KLVAPTLRSEL 525

Db        459 TVTMTNPPFGKGAVESRLNITK-NNYATLECVA-----SANGEIVYTLFSISENTVPHEL 512

Qy        526 -------TVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578

Db        513 FTPLLIGFVAAAVILVLI-----LIVLTYKYMQKPKYQIQWKVIEGI--HGNNYVYIDPT 565

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638

Db        566 QLPYDHQWEFPRDKLRFGKTLGSGAFGKVVEATAYGMSKADTVMTVAVKMLKPSAHATEK 625

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698

Db        626 EALMSELKVLSYLGNHINIVNLLGACTVGGPTLVITEYCCFGDLLNFLRRRRVYF----- 680

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENN---GDYMDMKQADTTQYVPMLERKEVSKYS 755

Db        681 ---------YYTTLGEDAYYRNVMMQSEPNDSRNGYMTMKPS----VLGILS-------S 720

Qy        756 DIQRSLYDRPASYKKKSMLDSE-VKNLLSDDNSEGLTL--LDLLSFTYQVARGMEFLASK 812

Db        721 ENRRSL------NKGDSYSDSDAVSEILQED---GLTLDTEDLLSFSYQVAKGMDFLASK 771

Qy        813 NCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLY 872

Db        772 NCIHRDLAARNILLTQGRVAKICDFGLARDITTDSNYVVKGNARLPVKWMSPESIFECVY 831

Qy        873 TTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKC 932

Db        832 TFESDVWSYGILLWEIFSLGSSPYPGMPVDSKFYKMIKEGYRMESPEFSPSEMYDIMHSC 891

Qy        933 WNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDN 986

Db        892 WDADPVKRPSF---SKIVEK-IEQQISDSTKHIYLNF-SSRLPAAPGPREESSS 940


RESULT 31
Q8JFR5_BRARE
ID   Q8JFR5_BRARE PRELIMINARY;      PRT;   976 AA.
AC   Q8JFR5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Kit receptor.
GN   Name=kit; ORFNames=BUSM1-116L04.1-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pandian R.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Holt K.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL691516; CAD43458.1; -; Genomic_DNA.
DR   EMBL; BX248242; CAI11525.1; -; Genomic_DNA.
DR   EMBL; BX248242; CAD43458.1; JOINED; Genomic_DNA.
DR   EMBL; AL691516; CAI11525.1; JOINED; Genomic_DNA.
DR   HSSP; P35968; 1VR2.
DR   SMR; Q8JFR5; 538-920.
DR   ZFIN; ZDB-GENE-980526-464; kit.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 2.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
SQ   SEQUENCE   976 AA;  109293 MW;  A56921FA48DE58ED CRC64;

  Query Match             27.5%;  Score 1553.5;  DB 2;  Length 976;
  Best Local Similarity   39.1%;  Pred. No. 1.1e-74;
  Matches  396;  Conservative  146;  Mismatches  347;  Indels  125;  Gaps   36;

Qy         18 LSLILCQL------SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEI 71

Db          7 LFTVLLQLIIQPGRSRPTITPEGPRLTVPLYSNFSLHCQSNSTVRWQH-----ENRPMRT 61

Qy         72 RNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPL 131

Db         62 LKEEQRQGQ-QTILKVNRAGPQHLGKYSC------REEKTGEKSSIYVYVKDPENPFRRT 114

Qy        132 GMTDYLVIVEDDDSAIIPCRTTDPETP-VTLHNSEGV-------VPASYDS-------RQ 176

Db        115 IVFD--IVAAEGDTTVIPCLATDPDMKNLNLQKCDGQPLPNSLRYSASLETGVSVEKVRK 172

Qy        177 GFNGTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCA 236

Db        173 EFEGCYVCVGTLDAATVKSGRYQLTVRLVPDAPPPITLGQPQRVLLT---QGEKLSLSCS 229

Qy        237 VFN-NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYT--LTVPEATVKDSGDYECAAR 293

Db        230 TSNVNSDIAVKWKAPNGV-NPSVHQNSHLLTEPITHVRTAILSLSSVTMQDAGNYSCEA- 287

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPR-ISWLKN 352

Db        288 -INEKGTTAKPVWVNIYEKGFINITSVDNSTRRVRAGESLSLRVVMNAYPKPHTFSWSYS 346

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412

Db        347 GVKLTNTTDHVIT--SRTHGNSYTSELKLVRLKVSESGIYTFSCLNRDATIRQTFEVHVI 404

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI--KKCNNETSWTILANNVS 470

Db        405 SKPQIV----SYEGPIDGQ-VRCVAEGYPTPQIKWYYC-DLPHSRCSNLLNATQEEEDVV 458

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENREL-----KLVAPTLRSEL 525

Db        459 TLTMTNPPFGKGAVESRLNITK-NNYATLECVA-----SANGEIVYTLFSISENTVPHEL 512

Qy        526 -------TVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578

Db        513 FTPLLIGFVAAAVILVLI-----LIVLTYKYMQKPKYQIQWKVIEGI--HGNNYVYIDPT 565
```

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Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
              |||||| :|||||| |  |: |||||||||||| ||||:|::  || ||||||||:| ::||
Db        566 QLPYDHQWEFPRDKLRFGKTLGSGAFGKVVEATAYGMSKADTVMTVAVKMLKPSAHATEK 625

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
              :|||||||:::||  |:||||||||||  ||  :|||||  :|||:|:|  :  |  |
Db        626 EALMSELKVLSYLGNHINIVNLLGACTVGGPTLVITEYCCFGDLLNFLRRRRVYF----- 680

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENN---GDYMDMKQADTTQYVPMLERKEVSKYS 755
                        :    :::   |::  | |     || || :     : :|        |
Db        681 ---------YYTTLGEDAYYRNVMMQSEPNDSRNGYMTMKPS----VLGILS-------S 720

Qy        756 DIQRSLYDRPASYKKKSMLDSE-VKNLLSDDNSEGLTL--LDLLSFTYQVARGMEFLASK 812
              : :|||       |  |  ||: |  :| :|   ||||   |||||:||||:||:|||||
Db        721 ENRRSL------NKGDSYSDSDAVSEILQED---GLTLDTEDLLSFSYQVAKGMDFLASK 771

Qy        813 NCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLY 872
              ||:|||||||:|| ||:: |||||||||||  |||||  ||:  ||||||:|||||: :|
Db        772 NCIHRDLAARNILLTQGRVAKICDFGLARDITTDSNYVVKGNARLPVKWMSPESIFECVY 831

Qy        873 TTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKC 932
              |  |||||||||||||||| :|||||  ||| ||  ||  |||||  |: : ||:|:||  |
Db        832 TFESDVWSYGILLWEIFSLGSSPYPGMPVDSKFYKMIKEGYRMESPEFSPSEMYDIMHSC 891

Qy        933 WNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDN 986
              |:::| |||||   |:|||  :  |  | : |:|:|  |  ||    | :| :
Db        892 WDADPVKRPSF---SKIVEK-IEQQISDSTKHIYLNF-SSRLPAAPGPREESSS 940
```

RESULT 32
Q8AXC6_FUGRU
ID   Q8AXC6_FUGRU PRELIMINARY;   PRT;   984 AA.
AC   Q8AXC6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Kinase receptor c-kit.
GN   Name=c-kit;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22481137; PubMed=12592706; DOI=10.1080/1042517021000011627;
RA   Williams H., Brenner S., Venkatesh B.;
RT   "Characterization of the platelet-derived growth factor receptor alpha
RT   and c-kit genes in the pufferfish Fugu rubripes.";
RL   DNA Seq. 13:263-270(2002).
DR   EMBL; AF456419; AAN87555.1; -; Genomic_DNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q8AXC6; 537-924.
DR   Ensembl; SINFRUG00000126238; Fugu rubripes.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000169; Pept_cys_AS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR   PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
KW   Kinase; Receptor.
SQ   SEQUENCE   984 AA; 110731 MW; 27D1EDC837CE8295 CRC64;

  Query Match   27.0%; Score 1527; DB 2; Length 984;
  Best Local Similarity   37.3%; Pred. No. 2.8e-73;
  Matches 389; Conservative 141; Mismatches 329; Indels 184; Gaps   36;

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Qy         20 LILCQLSL----------PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDV 69
              ::|| :||           |:| |     || ||:   |:| ||  : ||     ||
Db          6 ILLC-VSLCFTFHPGDTKPTITPAGTYVVVSLNAPLELQCQGEKAMQWQ----REERP-- 58

Qy         70 EIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFV 129
              ::| |     |  : | :  |  || | | |        ||   |   |||| |||  |
Db         59 KVRGETKVDG--KSTLYIPKAHPAHMGRYIC------LEETSQERASIYIYVKDPDNPFR 110

Qy        130 PLGMTDYLVIVEDDDSAIIPCRTTDP------------------------ETPVTLHNS 164
                 :::  ::  : ||| |||  |||                        |  : :||:
Db        111 KSMVSN--ILSREGDSASIPCLATDPSLENLQLKTCSSKALASGLHFSPSLEQGIIIHNT 168

Qy        165 EGVVPASYDSRQGFNGTFTVGPYICEATVKGKKFQTIPFN--VYALKATSELDLEMEALK 222
              :    ||:          | |:|   :|     ::  ::  |  :      : :     :
Db        169 Q----KSYE----------GCYVCTGRLKETNVRSHDYHLTVRPVPVAPPVIMMQAPKR 213

Qy        223 TVYKSGETIVVTCAVFN-NEVVDLQW-----TYPGEVKGKGITMLEEIKVPSIKLVYTLT 276
              :    |:: :||   | |  : |:|     : | :| |     : |           ||
Db        214 VILIRDESLYLTCNTTNVNGNIKLKWVAPLGSQPAKVDGSSRILTENFTQARSA---TLH 270

Qy        277 VPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFV 336
              :    ::|:| |:| |     :    : | : ||||:   |  :    |   |
Db        271 IAAVRIQDTGRYQCEAE--NEKGVSTQSVWLDVFEKGFMYSNPVNNGTIQVRAGESLLLS 328

Qy        337 VEVRAYPPPR-ISW------LKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDS 389
              | : ||| ||  ||      | |    :     |||   :  |  | |:|||:| |  :
Db        329 VSIEAYPMPRSASWSFMGRGLHNTSDHV-----ITT---RSHEYTYSSELKLVRLKMSEG 380

Qy        390 GHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMI 449
              | ||  | | ||  ::|| :      |:     | |   || ||| ||| | | | |
Db        381 GVYTFQASNGDASVNHTFTIFVISKPEIV----SHEGPVDGQ-VRCVAEGFPAPQITWYY 435

Qy        450 CKD-IKKCNNETSWTILANNVSNII--------TEIHSRDR-----------STVEGR- 487
              |:    :|: : : |    ||  :          ||: ||                :|||
Db        436 CEQPYARCSQQVNATQEEQNVITVTLFSPLFGKTEVESRVNISRGRFSTLECVATVEGEQ 495

Qy        488 --VTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVL 545
                 |:  | ||:    :  |:|                    :|:|| :: |:     ||||
Db        496 AFTLFSISERTISHDLFSPLLIG----------------SVSAACILCLI-----LIVL 533

Qy        546 VVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFG 605
              : |||:|:|:|:||| |    |: |:|:|| ||||| :|||||   |  |: |||||||
Db        534 FYKYMQKPKYQIQWKVIEGI--HGNNYVYIDPTQLPYDHQWEFPRKNLRFGKTLGSGAFG 591

Qy        606 KVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACT 665
              |||| |||||:    :| |||||| :| |:|||:||||||:: :|| |:||||||||||
Db        592 KVVEATAYGLANEDSMMTVAVKMLKSSAHSTEKEALMSELKVLIYLGNHINIVNLLGACT 651

Qy        666 KSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSF 725
                 ||  :||||| :|||:|:| : |:||:       | | |    |          ::|
Db        652 VGGPTLVITEYCCFGDLLNFLRRKRESFICF-----KLEEDCHYRN---------IMLQR 697

Qy        726 ENNGD----YMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNL 781
              |  ||    || |:          |  |  |  :|       : | ::   ||| :
Db        698 EMAGDSLNGYMTMR--------PSAAGKPSSSSSSEKRRSLREGSPYVEE---DSESE-- 744

Qy        782 LSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLAR 841
              : |::|  |   |||||:||||:||||| |||||:||||||||:|| ||:: |||||||||
Db        745 MFDEDSLSLDTEDLLSFSYQVAKGMEFLTSKNCIHRDLAARNILLTQGRVAKICDFGLAR 804
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Qy        842 DIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMV 901
              ||  ||||| ||:  ||||||:|||||: :||  ||||||||||||||||| :||||| |
Db        805 DINTDSNYVVKGNARLPVKWMSPESIFECVYTFESDVWSYGILLWEIFSLGNSPYPGMPV 864

Qy        902 DSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKS 961
              |: ||  || |||| |: | ||:|:||  ||:::|  || |  : | :|     |   :
Db        865 DAKFYKLIKEGYRMDAPEFAPSEMYQIMRSCWDADPLNRPPFRKVVERIEQ----QLSDT 920

Qy        962 YEKIHLDFLKSDHPAVARMRVDS 984
                : |:|:|  |  | : | | :|
Db        921 TKHIYLNF-SSRVPVMPRGREES 942


RESULT 33
Q4RKW2_TETNG
ID   Q4RKW2_TETNG PRELIMINARY;      PRT;   966 AA.
AC   Q4RKW2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 1 SCAF15025, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00032762001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC       cycle. It is required in higher cells for entry into S-phase and
CC       mitosis. Component of the kinase complex that phosphorylates the
CC       repetitive C-terminus of RNA polymerase II. Catalytic component of
CC       MPF (By similarity).
CC   -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC       mature oocytes (By similarity).
DR   EMBL; CAAE01015025; CAG10970.1; -; Genomic_DNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000169; Pept_cys_AS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR   PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
KW   ATP-binding; Immunoglobulin domain; Kinase; Nucleotide-binding;
KW   Receptor; Transferase; Transmembrane.
FT   NON_TER     966    966
SQ   SEQUENCE   966 AA;  108354 MW;  1F89440507CF5CE1 CRC64;

  Query Match             26.6%;  Score 1501;  DB 2;  Length 966;
  Best Local Similarity   36.4%;  Pred. No. 6.9e-72;
  Matches  383;  Conservative  141;  Mismatches  319;  Indels  210;  Gaps   33;

Qy         14 LLTGLSLILCQL---SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVE 70
              |:   :| |  |   : ||| |     || ||: | |:| ||  : ||         ::
Db         12 LMQQFTLTLWHLGGDTKPSITPAGPYVVVLLNAPFELQCLGEKAMQWQ-------RERLK 64

Qy         71 IRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVP 130
              :| |:   |   : |     |  || | | |        ||   |   ||:|| ||:  |
Db         65 VRGEKKVDG--KSTLYFPKAQPAHMGRYIC------LEEASQETASIYVYVKDPNNPFRK 116

Qy        131 LGMTDYLVIVEDDDSAIIPCRTTDP------------------------ETPVTLHNSE 165
              :::  :|  :     |||  |||                          |  : :||::
Db        117 PMVSN--IISGEGSITFIPCLATDPSLENLQLKTCSSKALAPGLEFSSSLEQGIIIHNTQ 174

Qy        166 GVVPASYDSRQGFNGTFTVGPYICEATVK--------------GKKFQT--IPFNVYAL 208
                ||:           | |:|   :|                |||  ||   | ::
Db        175 ----KSYE----------GCYVCTGRLKETNVRSHDYFLTVRPGKKLQTAATPPSIIFF 219

Qy        209 KATSELD--------------LEMEALKTVYK-SGETIVVTCAVFN-NEVVDLQWT--- 248
              |   :|                : ::| | |     |:: :||   | |  : |:|
Db        220 FAGQRVDHDPLYFLPVPVAPPAIMLQAPKRVILICNESLYLTCNTTNVNGNIKLKWVTPL 279

Qy        249 ---------YPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREV 299
                      | :| |    : |     :     || :    ::|:| |:| |:|    :
Db        280 GSGAVWYPQQPAKVDGSSRILTENF---THACSATLHITAVQIQDTGRYQCEAQ--NEKG 334

Qy        300 KEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPR-ISW------LKN 352
              : | : |:||||:   |  :    |   |     | : ||| |  |||      |:|
Db        335 VSTQSVWLDVYEKGFMYSSPVNNGTIQVRAGESLSLSVSLEAYPKPHTISWSFMGRGLRN 394

Qy        353 NLTLIENLTEITTD---VEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFEL 409
                        |||         :  | |:|||:| |  :  | ||  | | ||  ::|| :
Db        395 -----------TTDHVITTHSHDYTYSSELKLVRLKMTEGGVYTFQASNGDASVNHTFTI 443

Qy        410 LTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKD-IKKCNNETSWTILANN 468
                    |:     | |   || ||| ||| | | | |  |:    :|: : : |   :|
Db        444 FVISKPEIV----SHEGPVDGQ-VRCVAEGFPAPQITWYYCEQPYARCSQQVNATQEEHN 498

Qy        469 VSNII--------TEIHSRDR-----------STVEGR---VTFAKVEETIAVRCLAKN 505
              |  :          ||: ||                :||||       |:  | :::    :
Db        499 VITVTLFSPLFGKTEVESRVNVSRGRFSTLECVATVEGEQAYTLFSISERSVSHDLFSPL 558

Qy        506 LLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESI 565
              |:|                :|:|| :: ||      ||||   : |||:|:|:|:||| |
Db        559 LIG----------------SVSAAGILCLV-----LIVLFYKYMQKPKYQIQWKVIEGI 596

Qy        566 SPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVA 625
                |: |:|:|| ||||| :|||||   |  |: |||||||||| |||||: :    | ||
Db        597 --HGNNYVYIDPTQLPYDHQWEFPRKNLRFGKTLGSGAFGKVVEATAYGLASADSTMTVA 654

Qy        626 VKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNY 685
              ||||| :| |:|||:|||||||:: :|| |:|||||||||  ||  :||||| :|||:|:
Db        655 VKMLKSSAHSTEKEALMSELKVLIYLGNHINIVNLLGACTVGGPTLVITEYCCFGDLLNF 714

Qy        686 LHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGD----YMDMKQADTTQ 741
              | : |:||:       | | |     |          |:|  |  ||    || |: :
Db        715 LRRKRESFICF-----KLEEDCHYRN---------VMLQREMAGDSLNGYMTMRPSAAGT 760
```

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Qy        742 YVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQ 801
Db        761 LSP-------SFSSEKKRSLRKGKHASHCSQYVEADSESEMFDEDSLSLDTEDLLSFSYQ 813

Qy        802 VARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKW 861
Db        814 VAKGMEFLTSKNCIHRDLAARNILLTQGRVAKICDFGLARDINTDSNYVVKGNARLPVKW 873

Qy        862 MAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHA 921
Db        874 MSPESIFECVYTFESDVWSYGILLWEIFSLGNSPYPGMPVDAKFYKLIKEGYRMDAPEFA 933

Qy        922 TSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLL 954
Db        934 PSEMYQIMRSCWDADPLNRPPFRKVVERIEQQL 966
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RESULT 34
KIT_CAPHI
ID KIT_CAPHI STANDARD; PRT; 978 AA.
AC Q28317;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN Name=KIT;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Shiba; TISSUE=Cerebellum;
RX MEDLINE=97342548; PubMed=9199245; DOI=10.1016/S0167-4781(97)00055-9;
RA Tanaka S., Yanagisawa N., Tojo H., Kim Y.-J., Tsujimura T.,
RA Kitamura Y., Sawasaki T., Tachi C.;
RT "Molecular cloning of cDNA encoding the c-kit receptor of Shiba goats
RT and a novel alanine insertion specific to goats and sheep in the
RT kinase insert region.";
RL Biochim. Biophys. Acta 1352:151-155(1997).
CC -!- FUNCTION: This is the receptor for stem cell factor (mast cell
CC growth factor). It has a tyrosine-protein kinase activity. Binding
CC of the ligands leads to the autophosphorylation of KIT and its
CC association with substrates such as phosphatidylinositol 3-kinase
CC (Pi3K).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Interacts with APS and MPDZ (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC receptor subfamily.
CC -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC domains.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR EMBL; D45168; BAA08116.1; -; mRNA.
DR HSSP; P35968; 1VR2.
DR SMR; Q28317; 548-694, 761-935.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; ReceptTyrkinsIII.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; ig; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.

FT	SIGNAL	1	22	Potential.
FT	CHAIN	23	978	Mast/stem cell growth factor receptor.
FT	TOPO_DOM	23	521	Extracellular (Potential).
FT	TRANSMEM	522	544	Potential.
FT	TOPO_DOM	545	978	Cytoplasmic (Potential).
FT	DOMAIN	590	939	Protein kinase.
FT	NP_BIND	596	604	ATP (By similarity).
FT	ACT_SITE	794	794	By similarity.
FT	BINDING	624	624	ATP (By similarity).
FT	SITE	569	569	APS-binding (By similarity).
FT	SITE	938	938	APS-binding (By similarity).
FT	MOD_RES	825	825	Phosphotyrosine (by autocatalysis) (By similarity).
FT	CARBOHYD	94	94	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	130	130	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	145	145	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	284	284	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	294	294	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	301	301	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	321	321	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	353	353	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	368	368	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	401	401	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	464	464	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	487	487	N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 978 AA; 109722 MW; CA4D663F98205CA9 CRC64;

Query Match 26.3%; Score 1489; DB 1; Length 978;
Best Local Similarity 36.5%; Pred. No. 3.1e-71;
Matches 367; Conservative 151; Mismatches 367; Indels 120; Gaps 30;

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Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
Db         33 ELSLPSIHPAKSELIVSVGDEIRLLCTDPGFVKWTFEILGQLS--------EKTNPEWIT 84

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
Db         85 ----EKAEATNTGNYTC------TNKGGLSS-SIYVFVRDPEKLF----LIDLPLYGKEE 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
Db        130 NDTLVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNV---YALKATSELDLEMEALKTVY--KSGETIVVTCAVFN- 239
Db        183 CLHCSANQKGKSMLSKKFTLKVRAAIKAVPVVSVS----KTSYLLREGEEFAVTCLIKDV 238

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLV--YTLTVPEATVKDSGDYECAARQATR 297
Db        239 SSSVDSMWIKENSQQSKAQTKKNSWHQGDFSYLRQERLTISSARVNDSGVFMCYANNTFG 298

Qy        298 EVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKNNLTL 356
Db        299 SAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGENVDLVVEYEAYPKPEHRQWIYMNRTS 356

Qy        357 IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSS 416
Db        357 TDKWDDYPKS-ENESNIRYVNELHLTRLKGTEGGTYTFHVSNSDVNSSVTFNVNVNTKPE 415

Qy        417 ILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTILANNVSNIITE 475
Db        416 ILT-----HDRLVNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP---------VGPVDVQ 461
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Qy        476 IHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE----------NRELKLVAPT 520
              |  :   |      | :: ::::       | | | | :|            | : :: | |
Db        462 IQNSSVSPFGKLVVYSTIDDSTFKHNGTVECRAYNDVGKSSASFNFAFKGNNKEQIHAHT 521

Qy        521 LRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQL 580
              | : | :   :   |: : :  ::|   : ||| ||::|:|:| |  :|: |:|:|| ||
Db        522 LFTPLLIGFVIAAGLMCIFV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQL 577

Qy        581 PYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQA 640
              ||| :|||||: |  |: ||:|||||||| ||||| :|   | ||||||||:|  :|::|
Db        578 PYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREA 637

Qy        641 LMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK 700
              ||||||::::|| |:|||||||||| ||  :||||| ||||:|:| : ||||:    |
Db        638 LMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQED 697

Qy        701 PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRS 760
                :      |  : ||: :      ::  :|||||    :  ||       :| :| :||
Db        698 HAEVALYKNLLHSKESSCN------DSTNEYMDMKPG-VSYVVP-------TKAADKRRS 743

Qy        761 LYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLA 820
                |  ||     :: :|   : :|:   | | |||||:||||:|| ||||||||:|||||
Db        744 A--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLA 796

Qy        821 ARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWS 880
              |||:||  :| |||||||||| :||||| ||:  |||||||||||: :||  |||||
Db        797 ARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWS 856

Qy        881 YGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKR 940
              ||| |||:|||| :||||| ||| ||  || |:||  |:|| :|:|:||  ||:::| ||
Db        857 YGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKR 916

Qy        941 PSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
              |:|  : :::|  :       |  :       ::|||   :|::|
Db        917 PTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 961
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RESULT 35
KIT_BOVIN
ID   KIT_BOVIN      STANDARD;      PRT;   977 AA.
AC   P43481;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE   (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN   Name=KIT;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94215924; PubMed=7512939; DOI=10.1016/0378-1119(94)90592-4;
RA   Kubota T., Hikono H., Sasaki E., Sakurai M.;
RT   "Sequence of a bovine c-kit proto-oncogene cDNA.";
RL   Gene 141:305-306(1994).
CC   -!- FUNCTION: This is the receptor for stem cell factor (mast cell
CC       growth factor). It has a tyrosine-protein kinase activity. Binding
CC       of the ligands leads to the autophosphorylation of KIT and its
CC       association with substrates such as phosphatidylinositol 3-kinase
CC       (Pi3K).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with APS and MPDZ (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; D16680; BAA04084.1; -; mRNA.
DR   HSSP; P35968; 1VR2.
DR   SMR; P43481; 548-694, 760-934.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     22       Potential.
FT   CHAIN        23    977       Mast/stem cell growth factor receptor.
FT   TOPO_DOM     23    521       Extracellular (Potential).
FT   TRANSMEM    522    544       Potential.
FT   TOPO_DOM    545    977       Cytoplasmic (Potential).
FT   DOMAIN      590    938       Protein kinase.
FT   NP_BIND     596    604       ATP (By similarity).
FT   ACT_SITE    793    793       By similarity.
FT   BINDING     624    624       ATP (By similarity).
FT   SITE        569    569       APS-binding (By similarity).
FT   SITE        937    937       APS-binding (By similarity).
FT   MOD_RES     824    824       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     94     94       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    130    130       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    145    145       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    294    294       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    301    301       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    321    321       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    353    353       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    368    368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    401    401       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    464    464       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    487    487       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   977 AA;  109685 MW;  4B2719050883B7EF CRC64;
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  Query Match             26.2%;  Score 1481.5;  DB 1;  Length 977;
  Best Local Similarity   36.4%;  Pred. No. 7.7e-71;
  Matches  366;  Conservative  150;  Mismatches  368;  Indels  121;  Gaps   30;

Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
              :|||||| | ::| :| :      | |      | | : :  : |        |  :  ::|
Db         33 ELSLPSIHPAKSELIVSVGDEIRLLCTDPGFVKWTFEILGQLS--------EKTNPEWIT 84

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPPDVAFVPLGMTDYLVIVEDD 143
                 | | :|| |||      | :  |    ||::| ||:  |    : |  :  :::
Db         85 ----EKAEATNTGNYTC------TNKGGLSS-SIYVFVRDPEKLF----LIDLPLYGKEE 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
              :  :: |  |||| |  :|   ||  |   |       ||   |
Db        130 NDTLVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNV---YALKATSELDLEMEALKTVY--KSGETIVVTCAVFN- 239
                 | |  :||   :  | :    |:||   : :     || |  : ||   ||| : :
Db        183 CLHCSANQRGKSMLSKKFTLKVRAAIKAVPVVSVS----KTSYLLREGEEFAVTCLIKDV 238
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Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLV--YTLTVPEATVKDSGDYECAARQATR 297
Db        239 SSSVDSMWIKENSQQTKAQTKKNSWHQGDFSYLRQERLTISSARVNDSGVFMCYANNTFG 298

Qy        298 EVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPP-RISWLKNNLTL 356
Db        299 SAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGENVDLVVEYEAYPKPVHRQWIYMNRTS 356

Qy        357 IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSS 416
Db        357 TDKWDDYPKS-ENESNIRYVNELHLTRLKGTEGGTYTFHVSNSDVNSSVTFNVYVNTKPE 415

Qy        417 ILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTILANNVSNIITE 475
Db        416 ILT-----HDRLVNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP---------VGPVDVQ 461

Qy        476 IHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE----------NRELKLVAPT 520
Db        462 IQNSSVSPFGKLVVYSTIDDSTFKHNGTVECRAYNDVGKSSASFNFAFKGNSKEQIHAHT 521

Qy        521 LRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQL 580
Db        522 LFTPLLIGFVIAAGLMCIFV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQL 577

Qy        581 PYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQA 640
Db        578 PYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREA 637

Qy        641 LMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK 700
Db        638 LMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQED 697

Qy        701 PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRS 760
Db        698 HAEVALYKNLLHSKESSCN------DSTNEYMDMKPG--VSYV-------VPTKADKRRS 742

Qy        761 LYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLA 820
Db        743 A--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLA 795

Qy        821 ARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWS 880
Db        796 ARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWS 855

Qy        881 YGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKR 940
Db        856 YGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKR 915

Qy        941 PSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
Db        916 PTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 960
```

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RESULT 36
O97744_PIG
ID   O97744_PIG  PRELIMINARY;      PRT;   964 AA.
AC   O97744;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mast/stem cell growth factor receptor (Fragment).
GN   Name=KIT1*0101;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Hampshire breed; TISSUE=Leukocyte;
RX   MEDLINE=98391767; PubMed=9724328;
RA   Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA   Moller M., Edfors-Lilja I., Andersson L.;
RT   "Molecular evolution of the dominant white phenotype in the domestic
RT   pig.";
RL   Genome Res. 8:826-833(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Hampshire breed; TISSUE=Leukocyte;
RA   Marklund S.;
RL   Thesis (1997), Department of Animal Breeding and Genetics, Swedish
RL   University of Agricultural Sciences, Uppsala, SWEDEN.
DR   EMBL; AJ223228; CAA11196.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; O97744; 543-689, 755-929.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
FT   NON_TER     964    964
SQ   SEQUENCE   964 AA;  108288 MW;  90E72EDFAB1358B7 CRC64;
```

Query Match 26.0%; Score 1472; DB 2; Length 964;
Best Local Similarity 36.2%; Pred. No. 2.5e-70;
Matches 366; Conservative 147; Mismatches 359; Indels 140; Gaps 31;

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Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
Db         33 ELSPPSIHPAKSELIVSAGDEIRLFCTDPGSVKWTFETLGQLS--------ENTHAEWI- 83

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
Db         84 ---VEKAEAMNTGNYTC------TNEGGLSS-SIYVFVRDPEKLF----LVDPPLYGKED 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
Db        130 NDALVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNVYALKATSELDLEMEALKTV--------YKSGETIVVTCAV 237
Db        183 CLHCSANQGGK-------SVLSKKFTLKVRAAIRAVPVVAVSKASYLLREGEEFAVMCLI 235

Qy        238 FN-NEVVDLQW-----TYPGEVKGKG-----ITMLEEIKVPSIKLVYTLTVPEATVKDSG 286
Db        236 KDVSSSVDSMWIRENSQTKAQVKRNSWHQGDFNFLRQER---------LTISSARVNDSG 286

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
Db        287 VFMCYANNTFGSAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGEDVDLIVEYEAYPKPE 344

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
Db        345 HRQWIYMNRTATDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNADVNSSV 403

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTI 464
```

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Db        404 TFNVYVNTKPEILT-----HDRLMNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP----- 453

Qy        465 LANNVSNIITEIHSRDRS-----TVEGRVTFAKVEETIAVRCLAKNLLGAENR------E 513
                  |  :  :| :   |       :   : ::  :    | | | | :|  :       :
Db        454 ----VGPVDVQIQNSSVSPFGKLVIHSSIDYSAFKHNGTVECRAYNDVGKSSAFFNFAFK 509

Qy        514 LKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYI 573
               :: | || : | :   :   :: :|:  ::|   : ||| ||::|:|:| |  :|: |:
Db        510 EQIHAHTLFTPLLIGFVIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYV 565

Qy        574 YVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTA 633
               |:|| ||||| :|||||: |  |: ||:||||||| ||||| :|   | ||||||||:|
Db        566 YIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSA 625

Qy        634 RSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSF 693
                 :|::|||||||::::|| |:||||||||||  ||  :||||| ||||:|:| : ||||
Db        626 HLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSF 685

Qy        694 LSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSK 753
               :   |   :      |  : ||: |      ::  :|||||      ||        |
Db        686 ICSKQEDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPT 730

Qy        754 YSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN 813
               :| :||   |  ||     :: :|   : :|:   | | |||||:||||:|| ||||||
Db        731 KADKRRSA--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKN 783

Qy        814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYT 873
               |:|||||||:||  |:| |||||||||| :|||| ||:  ||||||||||||: :||
Db        784 CIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYT 843

Qy        874 TLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCW 933
               |||||||| |||:|||| :||||| ||| ||  || |:||  |:|| :|:|:||  ||
Db        844 FESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCW 903

Qy        934 NSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
               :::| |||:|  : :::|  :       |  :       ::|||   :|::|
Db        904 DADPLKRPTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 955


RESULT 37
Q9TQQ0_PIG
ID   Q9TQQ0_PIG  PRELIMINARY;      PRT;   964 AA.
AC   Q9TQQ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mast/stem cell growth factor receptor (Fragment).
GN   Name=KIT1*0202;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RX   MEDLINE=98391767; PubMed=9724328;
RA   Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA   Moller M., Edfors-Lilja I., Andersson L.;
RT   "Molecular evolution of the dominant white phenotype in the domestic
RT   pig.";
RL   Genome Res. 8:826-833(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RA   Marklund S.;
RL   Thesis (1997), Department of Animal Breeding and Genetics, Swedish
RL   University of Agricultural Sciences, Uppsala, SWEDEN.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RA   Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA   Moller M., Edfors-Lilja I., Andersson L.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ223230; CAA11198.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q9TQQ0; 543-689, 755-929.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; ReceptTyrKinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
FT   NON_TER     964     964
SQ   SEQUENCE   964 AA;  108288 MW;  1B21292A962E9191 CRC64;

  Query Match             26.0%;  Score 1472;  DB 2;  Length 964;
  Best Local Similarity   36.3%;  Pred. No. 2.5e-70;
  Matches  367;  Conservative  145;  Mismatches  360;  Indels  140;  Gaps   31;

Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
              :|| ||| | ::| :|       | |     | | :    : |        ||    ::
Db         33 ELSPPSIHPAKSELIVSAGDEIRLFCTDPGSVKWTFETLGQLS--------ENTHAEWI- 83

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
                 |  | | :|| |||      | |  |    ||::| ||:  |    : |  :  ::|
Db         84 ---VEKAEAMNTGNYTC------TNEGGLSS-SIYVFVRDPEKLF----LVDPPLYGKED 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
               : |:: |  |||| |  :|   ||  |   |       ||   |
Db        130 NDALVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNVYALKATSELDLEMEALKTV--------YKSGETIVVTCAV 237
                 | |   ||       :| : | | ::   : |:  |          : ||   | | :
Db        183 CLHCSANQGGK-------SVLSKKFTLKVRAAIRAVPVVAVSKASYLLREGEEFAVMCLI 235

Qy        238 FN-NEVVDLQW-----TYPGEVKGKG-----ITMLEEIKVPSIKLVYTLTVPEATVKDSG 286
               : :  ||  |          :||           | : |          ||:  | | |||
Db        236 KDVSSSVDSMWIRENSQTKAQVKRNSWHQGDFNFLRQEK---------LTISSARVNDSG 286

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
               : | |             |: | :|||| | |  :    ||  |    :||  ||| |
Db        287 VFMCYANNTFGSAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGEDVDLIVEYEAYPKPE 344

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
               |:  | |  :   :     |    ||| |:| | | |  : | || :  | |   |
Db        345 HRQWIYMNRTATDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNADVNSSV 403

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTI 464
               || :       ||       |       ::| | | | | |:|  |    ::|:
Db        404 TFNVYVNTKPEILT-----HDRLMNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP----- 453

Qy        465 LANNVSNIITEIHSRDRS-----TVEGRVTFAKVEETIAVRCLAKNLLGAENR------E 513
                  |  :  :| :   |       :   : ::  :    | | | | :|  :       :
Db        454 ----VGPVDVQIQNSSVSPFGKLVIHSSIDYSAFKHNGTVECRAYNDVGKSSAFFNFAFK 509

Qy        514 LKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYI 573
               :: | || : | :   :   :: :|:  ::|   : ||| ||::|:|:| |  :|: |:
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Db        510 EQIHAHTLFTPLLIGFVIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYV 565

Qy        574 YVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTA 633

Db        566 YIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSA 625

Qy        634 RSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSF 693

Db        626 HLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSF 685

Qy        694 LSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSK 753

Db        686 ICSKQEDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPT 730

Qy        754 YSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN 813

Db        731 KADKRRSA--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKN 783

Qy        814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYT 873

Db        784 CIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYT 843

Qy        874 TLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCW 933

Db        844 FESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPVEMYDIMKTCW 903

Qy        934 NSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984

Db        904 DADPLKRPTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 955
```

```
RESULT 38
Q7YRV7_CANFA
ID   Q7YRV7_CANFA PRELIMINARY;      PRT;   975 AA.
AC   Q7YRV7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tyrosine kinase receptor.
GN   Name=c-kit;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tsai K.L., Guyon R., Murphy K.E.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY313776; AAP76390.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q7YRV7; 564-695, 758-932.
DR   Ensembl; ENSCAFG00000002065; Canis familiaris.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
```

```
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   975 AA;  109366 MW;  D845FADB06231FD9 CRC64;

  Query Match           26.0%;  Score 1470.5;  DB 2;  Length 975;
  Best Local Similarity  36.4%;  Pred. No. 3e-70;
  Matches  360;  Conservative  145;  Mismatches  386;  Indels   99;  Gaps   28;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85

Db         37 SLPSIHPAKSELIVSVGDELRLSCTDPGFVKWTFETLGQLN--------ENTHNEWIT-- 86

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145

Db         87 --EKAEAGHTGNYTC------TNRDGL-SRSIYVFVRDPAKLF----LVDLPLYGKEGND 133

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188

Db        134 TLVRCPLTDPEVTNYSLRGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRLCL 186

Qy        189 -CEATVKGKKFQTIPFNVYALKATSELD----LEMEALKTVYKSGETIVVTCAVFN-NEV 242

Db        187 HCSADQKGR---TVLSKKFTLKVRAAIRAVPVVSVSKTSSLLKEGEAFSVMCFIKDVSSF 243

Qy        243 VDLQWTYPGEVKGKGITMLEEIKVP--SIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Db        244 VDSMWIKENSQQTNAQTQSNSWHHGDFNFERQEKLIISSARVNDSGVFMCYANNTFGSAN 303

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKNNLTLIEN 359

Db        304 --VTTTLEVVDKGFINIFPMMSTTIFVNDGENVDLIVEYEAYPKPEHQQWIYMNRTFTDK 361

Qy        360 LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 419

Db        362 WEDYPKS-DNESNIRYVSELHLTRLKGNEGGTYTFQVSNSDVNSSVTFNVYVNTKPEIL- 419

Qy        420 LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSR 479

Db        420 ---THESLTNGM-LQCVVAGFPEPAVDWYFCPGAEQ---RCSVPIGPMDVQMQNSSLSPS 472

Qy        480 DRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIV- 538

Db        473 GKLVVQSSIDYSAFKHNGTVECRAYNNVGRSSAFFNFAFKEQIHPHTLFTPLLIGFVIAA 532

Qy        539 -IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVL 595

Db        533 GMMCIIVMILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDHKWEFPRNRLSF 590

Qy        596 GRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHL 655

Db        591 GKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHM 650

Qy        656 NIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADE 715

Db        651 NIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHGEVALYKNLLHSKE 710

Qy        716 STRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLD 775

Db        711 SSCS------DSTNEYMDMKPG--VSYV-------VPTKADKRRSA--RIGSY-----IE 748

Qy        776 SEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKIC 835

Db        749 RDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKIC 808

Qy        836 DFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTP 895

Db        809 DFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLGSSP 868

Qy        896 YPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLP 955

Db        869 YPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFKQIVQLIEKQIS 928
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Qy        956 GQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
Db        929 DSTNHIYSNLANCSPNPERPVVDHSVRINS 958


RESULT 39
Q8WN23_CANFA
ID   Q8WN23_CANFA PRELIMINARY;      PRT;   979 AA.
AC   Q8WN23;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Tyrosine kinase receptor c-KIT.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Zemke D., Yuzbasiyan-Gurkan V.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Tsai K.L., Guyon R., Murphy K.E.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF448148; AAL40833.1; -; mRNA.
DR   EMBL; AY296484; AAP51178.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q8WN23; 568-699, 762-936.
DR   Ensembl; ENSCAFG00000002065; Canis familiaris.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   979 AA;  109752 MW;  46C30D5DEB8E33D3 CRC64;

  Query Match             26.0%;  Score 1469.5;  DB 2;  Length 979;
  Best Local Similarity   36.0%;  Pred. No. 3.4e-70;
  Matches  359;  Conservative  147;  Mismatches  383;  Indels  107;  Gaps   28;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         37 SLPSIHPAKSELIVSVGDELRLSCTDPGFVKWTFETLGQLN--------ENTHNEWIT-- 86

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         87 --EKAEAGHTGNYTC------TNRDGL-SRSIYVFVRDPAKLF----LVDLPLYGKEGND 133

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        134 TLVRCPLTDPEVTNYSLRGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRLCL 186

Qy        189 -CEATVKGKKFQTIPFNVYALKATSELD----LEMEALKTVYKSGETIVVTCAVFN-NEV 242
Db        187 HCSADQKGR---TVLSKKFTLKVRAAIRAVPVVSVSKTSSLLKEGEAFSVMCFIKDVSSF 243

Qy        243 VDLQWTYPGEVKGKGITMLEEIKVP--SIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db        244 VDSMWIKENSQQTNAQTQSNSWHHGDFNFERQEKLIISSARVNDSGVFMCYANNTFGSAN 303

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKNNLTLIEN 359
Db        304 --VTTTLEVVDKGFINIFPMMSTTIFVNDGENVDLIVEYEAYPKPEHQQWIYMNRTFTDK 361

Qy        360 LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 419
Db        362 WEDYPKS-DNESNIRYVSELHLTRLKGNEGGTYTFQVSNSDVNSSVTFNVYVNTKPEIL- 419

Qy        420 LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSR 479
Db        420 ---THESLTNGM-LQCVVAGFPEPAVDWYFCPGAEQ---RCSVPIGPMDVQMQNSSLSPS 472

Qy        480 DRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVAPTLRSELTVAA 529
Db        473 GKLVVQSSIDYSAFKHNGTVECRAYNNVGRSSAFFNFAFKGNSKEQIHPHTLFTPLLIGF 532

Qy        530 AVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
Db        533 VIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDHKWEFP 588

Qy        590 RDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMT 649
Db        589 RNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLS 648

Qy        650 HLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFG 709
Db        649 YLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHGEVALYKN 708

Qy        710 LNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYK 769
Db        709 LLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKRRSA--RIGSY- 750

Qy        770 KKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQG 829
Db        751 ----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHG 806

Qy        830 KIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIF 889
Db        807 RITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELF 866

Qy        890 SLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEI 949
Db        867 SLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFKQIVQL 926

Qy        950 VENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
Db        927 IEKQISDSTNHIYSNLANCSPNPERPVVDHSVRINS 962


RESULT 40
Q9TQQ1_PIG
ID   Q9TQQ1_PIG  PRELIMINARY;      PRT;   964 AA.
AC   Q9TQQ1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mast/stem cell growth factor receptor (Fragment).
GN   Name=KIT1*0201;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
```

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RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RX   MEDLINE=98391767; PubMed=9724328;
RA   Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA   Moller M., Edfors-Lilja I., Andersson L.;
RT   "Molecular evolution of the dominant white phenotype in the domestic
RT   pig.";
RL   Genome Res. 8:826-833(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RA   Marklund S.;
RL   Thesis (1997), Department of Animal Breeding and Genetics, Swedish
RL   University of Agricultural Sciences, Uppsala, SWEDEN.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Yorkshire / Landrace cross; TISSUE=Leukocyte;
RA   Marklund S., Kijas J., Rodriguez-Martinez H., Roennstrand L., Funa K.,
RA   Moller M., Edfors-Lilja I., Andersson L.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ223229; CAA11197.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q9TQQ1; 543-689, 755-929.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Receptor.
FT   NON_TER     964     964
SQ   SEQUENCE   964 AA;  108316 MW;  996C3C46201358A8 CRC64;

  Query Match             26.0%;  Score 1469;  DB 2;  Length 964;
  Best Local Similarity   36.2%;  Pred. No. 3.6e-70;
  Matches  366;  Conservative  146;  Mismatches  360;  Indels  140;  Gaps   31;

Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
Db         33 ELSPPSIHPAKSELIVSAGDEIRLFCTDPGSVKWTFETLGQLS--------ENTHAEWI- 83

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
Db         84 ---VEKAEAMNTGNYTC------TNEGGLSS-SIYVFVRDPEKLF----LVDPPLYGKED 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
Db        130 NDALVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNVYALKATSELDLEMEALKTV--------YKSGETIVVTCAV 237
Db        183 CLHCSANQGGK-------SVLSKKFTLKVRAAIRAVPVVAVSKASYLLREGEEFAVMCLI 235

Qy        238 FN-NEVVDLQW-----TYPGEVKGKG-----ITMLEEIKVPSIKLVYTLTVPEATVKDSG 286
Db        236 KDVSSSVDSMWIRENSQTKAQVKRNSWHQGDFNFLRQER---------LTISSARVNDSG 286

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
Db        287 VFMCYANNTFGSAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGEDVDLIVEYEAYPKPE 344

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
Db        345 HRQWIYMNRTATDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNADVNSSV 403

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTI 464
Db        404 TFNVYVNTKPEILT-----HDRLMNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP----- 453

Qy        465 LANNVSNIITEIHSRDRS-----TVEGRVTFAKVEETIAVRCLAKNLLGAENR------E 513
Db        454 ----VGPVDVQIQNSSVSPFGKLVIHSSIDYSAFKHNGTVECRAYNDVGKSSAFFNFAFK 509

Qy        514 LKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYI 573
Db        510 EQIHAHTLFTPLLIGFVIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYV 565

Qy        574 YVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTA 633
Db        566 YIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSA 625

Qy        634 RSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSF 693
Db        626 HLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSF 685

Qy        694 LSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSK 753
Db        686 ICSKQEDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPT 730

Qy        754 YSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN 813
Db        731 KADKRRSA--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKN 783

Qy        814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYT 873
Db        784 CIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYT 843

Qy        874 TLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCW 933
Db        844 FESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPVEMYDIMKTCW 903

Qy        934 NSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
Db        904 DADPLKRPTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 955
```

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RESULT 41
Q9XS93_CANFA
ID   Q9XS93_CANFA PRELIMINARY;      PRT;   978 AA.
AC   Q9XS93;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   KIT.
GN   Name=c-kit;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Cerebellum;
RX   MEDLINE=99225052; PubMed=10210327; DOI=10.1016/S0301-472X(98)00075-7;
RA   London C.A., Galli S.J., Yuuki T., Hu Z.-Q., Helfand S.C.,
RA   Geissler E.N.;
RT   "Spontaneous canine mast cell tumors express tandem duplications in
RT   the proto-oncogene c-kit.";
RL   Exp. Hematol. 27:689-697(1999).
```

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DR   EMBL; AF099030; AAD28369.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q9XS93; 549-695, 761-935.
DR   Ensembl; ENSCAFG00000002065; Canis familiaris.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   978 AA;  109651 MW;  5AC31E5AC4E9910F CRC64;

  Query Match             26.0%;  Score 1469;  DB 2;  Length 978;
  Best Local Similarity   35.8%;  Pred. No. 3.6e-70;
  Matches  362;  Conservative  145;  Mismatches  366;  Indels  138;  Gaps   29;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              ||||| | ::| :| :     | |     | | :    : :         ||    ::|
Db         37 SLPSIHPAKSELIVSVGDELRLSCTDPGFVKWTFETLGQLN--------ENTHNEWIT-- 86

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                | | ||| |||       |  : |  | ||::| ||    |    : |  :  :: :
Db         87 --EKAEAGHTGNYTC------TNRDGL-SRSIYVFVRDPAKLF----LVDLPLYGKEGND 133

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               ::  |  |||| |  :|   || |   |        ||   |
Db        134 TLVRCPLTDPEVTNYSLRGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRLCL 186

Qy        189 -CEATVKGKKFQTIPFNVYALKATSELD----LEMEALKTVYKSGETIVVTCAVFN-NEV 242
               | |  ||:   |:    : ||  : :     : :    :: | ||   | | : : :
Db        187 HCSADQKGR---TVLSKKFTLKVRAAIRAVPVVSVSKTSSLLKEGEAFSVMCFIKDVSSF 243

Qy        243 VDLQWTYPGEVKGKGITMLEEIKVPSIKLVYT----------------LTVPEATVKDS 285
              ||  |                ||  |    |                | :  | | ||
Db        244 VDSMW----------------IKENSQTNAQTQSNSWHHGDFNFERQEKLIISSARVNDS 287

Qy        286 GDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-P 344
              | : | |             |: | :|||| | |  |    ||  |    :||  ||| |
Db        288 GVFMCYANNTFGSAN--VTTTLEVVDKGFINIFPMMSTTIFVNDGENVDLIVEYEAYPKP 345

Qy        345 PRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKS 404
                |:  | |  :    :    :    ||| |:| | | |  : | ||    | |   |
Db        346 EHQQWIYMNRTFTDKWEDYPKS-DNESNIRYVSELHLTRLKGNEGGTYTFQVSNSDVNSS 404

Qy        405 YTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTI 464
               || :      ||    |  | |  ::|   | | | ::|  | ::    |   | |
Db        405 VTFNVYVNTKPEIL----THESLTNGM-LQCVVAGFPEPAVDWYFCPGAEQ---RCSVPI 456

Qy        465 LANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NREL 514
                 :|    : :    :  |:  : ::  :    | | | | :|            | :
Db        457 GPMDVQMQNSSLSPSGKLVVQSSIDYSAFKHNGTVECRAYNNVGRSSAFFNFAFKGNSKE 516

Qy        515 KLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIY 574
              ::   || : | :   :   :: :|:  ::|   : ||| ||::|:|:| |  :|: |:|
Db        517 QIHPHTLFTPLLIGFVIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVY 572

Qy        575 VDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTAR 634
              :|| |||| :|||||: |  |: ||:|||||||| |||| :|   | ||||||||:|
Db        573 IDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAH 632

Qy        635 SSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFL 694
              :|::|||||||::::|| |:|||||||||  ||  :|||| ||||:|:| : ||||:
Db        633 LTEREALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFI 692

Qy        695 SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKY 754
                  |   :      |  : ||: |      ::  :|||||  |:  ||       |
Db        693 CSKQEDHGEVALYKNLLHSKESSCS------DSTNEYMDMKPGDS--YV-------VPTK 737

Qy        755 SDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNC 814
              :| :||   |  ||     :: :|   : :|:   | | |||||:||||:|| |||||||
Db        738 ADKRRS--RRIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNC 790

Qy        815 VHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTT 874
              :|||||||:||  |:| |||||||||| :|||| ||:  |||||||||||: :||
Db        791 IHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTF 850

Qy        875 LSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWN 934
              |||||||| |||:|||| :|||| ||| ||  || |:||  |:|| :|:|:||  ||:
Db        851 ESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWD 910

Qy        935 SEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
              ::| |||:   : :::|  :       |  :       : | |   :|::|
Db        911 ADPLKRPTSKQIVQLIEKQISDSTNHIYSNLANCSPNPERPVVDHSVRINS 961


RESULT 42
KIT_CANFA
ID   KIT_CANFA      STANDARD;      PRT;   975 AA.
AC   O97799;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE   (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN   Name=KIT;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99142897; PubMed=9989791;
RX   DOI=10.1046/j.1523-1747.1999.00488.x;
RA   Ma Y., Longley B.J., Wang X., Blount J.L., Langley K., Caughey G.H.;
RT   "Clustering of activating mutations in c-KIT's juxtamembrane coding
RT   region in canine mast cell neoplasms.";
RL   J. Invest. Dermatol. 112:165-170(1999).
CC   -!- FUNCTION: This is the receptor for stem cell factor (mast cell
CC       growth factor). It has a tyrosine-protein kinase activity. Binding
CC       of the ligands leads to the autophosphorylation of KIT and its
CC       association with substrates such as phosphatidylinositol 3-kinase
CC       (Pi3K).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with APS and MPDZ (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AF044249; AAD02327.1; -; mRNA.
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DR   HSSP; P35968; 1VR2.
DR   SMR; O97799; 564-695, 758-932.
DR   Ensembl; ENSCAFG00000002065; Canis familiaris.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    975       Mast/stem cell growth factor receptor.
FT   TOPO_DOM     25    519       Extracellular (Potential).
FT   TRANSMEM    520    542       Potential.
FT   TOPO_DOM    543    975       Cytoplasmic (Potential).
FT   DOMAIN      588    936       Protein kinase.
FT   NP_BIND     594    602       ATP (By similarity).
FT   ACT_SITE    791    791       By similarity.
FT   BINDING     622    622       ATP (By similarity).
FT   SITE        567    567       APS-binding (By similarity).
FT   SITE        935    935       APS-binding (By similarity).
FT   MOD_RES     822    822       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    132    132       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    147    147       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    286    286       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    303    303       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    355    355       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    370    370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    403    403       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    466    466       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    489    489       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   975 AA;  109336 MW;  8F570BDB9F05B1CB CRC64;

  Query Match           25.9%;  Score 1463.5;  DB 1;  Length 975;
  Best Local Similarity   36.3%;  Pred. No. 7.1e-70;
  Matches  359;  Conservative  145;  Mismatches  387;  Indels   99;  Gaps   28;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              ||||| | ::| :| :     | |     | | :    : :          ||    ::|
Db         37 SLPSIHPAKSELIVSVGDELRLSCTDPGFVKWTFETLGQLN--------ENTHNEWIT-- 86

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                 | | ||| |||       |  : |  | ||::| ||    |    : |  :  :: :
Db         87 --EKAEAGHTGNYTC------TNRDGL-SRSIYVFVRDPAKLF----LVDLPLYGKEGND 133

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               :: |  |||| |  :|   ||  |   |        ||   |
Db        134 TLVRCPLTDPEVTNYSLRGCEG-KPLPKDL------TFVADPKAGITIRNVKREYHRLCL 186

Qy        189 -CEATVKGKKFQTIPFNVYALKATSELD----LEMEALKTVYKSGETIVVTCAVFN-NEV 242
                | |  ||:   |:    : ||  : :     : :    :: | ||   | | : : :
Db        187 HCSADQKGR---TVLSKKFTLKVRAAIRAVPVVSVSKTSSLLKEGEAFSVMCFIKDVSSF 243

Qy        243 VDLQWTYPGEVKGKGITMLEEIKVP--SIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||  |       :   |           : :   | :  | | ||| : | |
Db        244 VDSMWIKENSQQTNAQTQSNSWHHGDFNFERQEKLIISSARVNDSGVFMCYANNTFGSAN 303

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKNNLTLIEN 359
                  |: | :|||| | |  |    ||  :    :||  ||| |    |:  | |  :

Db        304 --VTTTLEVVDKGFINIFPMMSTTIFVNDGQNVDLIVEYEAYPKPEHQQWIYMNRTFTDK 361

Qy        360 LTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILD 419
                :    :    ||| |:| | | |  : | ||    | |   | || :       ||
Db        362 WEDYPKS-DNESNIRYVSELHLTRLKGNEGGTYTFQVSNSDVNSSVTFNVYVNTKPEIL- 419

Qy        420 LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSR 479
                |   | |  ::|   | | | : |  |   ::     |  |   :|    : :
Db        420 ---THESLTNGM-LQCVVAGFPEPAVGWYFCPGAEQ---RCSVPIGPMDVQMQNSSLSPS 472

Qy        480 DRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIV- 538
                :  |:  : ::  :    | | | | :|  :                |:   :|:  ||
Db        473 GKLVVQSSIDYSAFKHNGTVECRAYNNVGRSSAFFNFAFKEQIHPHTLFTPLLIGFVIAA 532

Qy        539 -IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVL 595
                :: :||::: :|  ||| ||::|:|:|  |  :|: |:|:|| ||||| :|||||: |
Db        533 GMMCIIVMILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDHKWEFPRNRLSF 590

Qy        596 GRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHL 655
              |: ||:|||||||| ||||| :|   | ||||||||:|  :|::|||||||::::|| |:
Db        591 GKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHM 650

Qy        656 NIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADE 715
              ||||||||||   ||  :|||||  ||||:|:|  : ||||:     |   :       | : |
Db        651 NIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHGEVALYKNLLHSKE 710

Qy        716 STRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLD 775
              |: |       ::  :|||||       ||       |   :| :||   |  ||      ::
Db        711 SSCS------DSTNEYMDMKPG--VSYV-------VPTKADKRRSA--RIGSY-----IE 748

Qy        776 SEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKIC 835
                :|   : :|:   | | ||||||:||||:|| |||||||:||||||||:||   |:| |||
Db        749 RDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKIC 808

Qy        836 DFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTP 895
              |||||||| :||||| ||:  |||||||||||: :||  |||||||| |||:|||| :|
Db        809 DFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLGSSP 868

Qy        896 YPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLP 955
              |||| ||| ||  || |:||  |:|| :|:|:||  ||:::| |||:|  : :::|  :
Db        869 YPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFKQIVQLIEKQIS 928

Qy        956 GQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
                    |  :       : | |   :|::|
Db        929 DSTNHIYSNLANCSPNPERPVVDHSVRINS 958
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RESULT 43
KIT_CHICK
ID   KIT_CHICK      STANDARD;      PRT;   960 AA.
AC   Q08156;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE   (Proto-oncogene tyrosine-protein kinase Kit) (c-kit).
GN   Name=KIT;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=White leghorn; TISSUE=Brain;
RX   MEDLINE=93292995; PubMed=7685729; DOI=10.1016/0378-1119(93)90571-J;
RA   Sasaki E., Okamura H., Chikamune T., Kanai Y., Watanabe M., Naito M.,
RA   Sakurai M.;
RT   "Cloning and expression of the chicken c-kit proto-oncogene.";
RL   Gene 128:257-261(1993).
CC   -!- FUNCTION: This is the receptor for stem cell factor (mast cell
CC       growth factor). It has a tyrosine-protein kinase activity. Binding
CC       of the ligands leads to the autophosphorylation of KIT and its
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CC       association with substrates such as phosphatidylinositol 3-kinase
CC       (Pi3K).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: High in the brain and testes and also present
CC       in the bursa of Fabricus, heart, kidney, lung, spleen thymus and
CC       ovary.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; D13225; BAA02506.1; -; mRNA.
DR   PIR; JN0677; JN0677.
DR   HSSP; P35968; 1VR2.
DR   SMR; Q08156; 533-679, 744-916.
DR   Ensembl; ENSGALG00000013925; Gallus gallus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    960       Mast/stem cell growth factor receptor.
FT   TOPO_DOM     25    505       Extracellular (Potential).
FT   TRANSMEM    506    530       Potential.
FT   TOPO_DOM    531    960       Cytoplasmic (Potential).
FT   DOMAIN      575    913       Protein kinase.
FT   NP_BIND     581    589       ATP (By similarity).
FT   ACT_SITE    777    777       By similarity.
FT   BINDING     609    609       ATP (By similarity).
FT   MOD_RES     808    808       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     76     76       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    149    149       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    269    269       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    286    286       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    318    318       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    338    338       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    343    343       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    356    356       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    453    453       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    469    469       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   960 AA;  107312 MW;  0E93850527AB68F6 CRC64;

  Query Match           25.9%;  Score 1461.5;  DB 1;  Length 960;
  Best Local Similarity  36.1%;  Pred. No. 9e-70;
  Matches  365;  Conservative  148;  Mismatches  359;  Indels  139;  Gaps   30;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |  :| |: :   :|  ||||    |:|     |:  ||       |:|  |  |:| :

Db          1 MEGAHLAWELAHAVLL-LSLIPAGGSVPH---EESSLVVNKGEELRLKCNEEGPVTWNF- 55

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEG---RHI 117
               : : |:   | ||:          :|:    | | |          : :|

Db         56 QNSDPSAKTRISNEKE--------WHTKNATIRDIGRYEC----------KSKGSIVNSF 97

Qy        118 YIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPET-PVTLHNSEG-VVPASYDSR 175
              |::| ||:| |    : | |:  ::|   :: |  |||:    ||   :|  :|

Db         98 YVFVKDPNVLF----LVDSLIYGKEDSDILLVCPLTDPDVLNFTLRKCDGKPLPK----- 148

Qy        176 QGFNGTFTVGP----------------YICEATVKG--KKFQTIPFNVYAL-KATSELDL 216
                 ||   |                | | |   |  |  : |  ||  : ||   : |

Db        149 ---NMTFIPNPQKGIIIKNVQRSFKGCYQCLAKHNGVEKISEHIFLNVRPVHKALPVITL 205

Qy        217 EMEALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLV---- 272
                    : | ||   ||| : :   ||       ||   |:    |     : :

Db        206 SKS--YELLKEGEEFEVTCIITD---VD------SSVKASWISYKSAIVTSKSRNLGDYG 254

Qy        273 ----YTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVN 328
                  || :    | |||:: | |        |    ||:    |||: : | :    :|

Db        255 YERKLTLNIRSVGVNDSGEFTCQAENPFG--KTNATVTLKALAKGFVRLFATMNTTIDIN 312

Qy        329 LHEVKHFVVEVRAYPPPRIS-WLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEE 387
               :  :  ||  ||| |:   |:  | || :| ::     : :     | |:| | | |

Db        313 AGQNGNLTVEYEAYPKPKEEVWMYMNETL-QNSSDHYVKFKTVGNNSYTSELHLTRLKGT 371

Qy        388 DSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEW 447
               : | ||    | ||  | || :  :    || |       |   ::| | | | | | |

Db        372 EGGIYTFFVSNSDASSSVTFNVYVKTKPEILTL-----DMLGNDILQCVATGFPAPTIYW 426

Qy        448 MICKDI-KKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNL 506
                 |    ::| :  : : :   ||   : : | :|  ||  |  :  : |  : | |

Db        427 YFCPGTEQRCLDSPTISPMDVKVSYTNSSVPSFERILVESTVNASMFKSTGTICCEA--- 483

Qy        507 LGAENRELKLV-----------APTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRY 555
               : | :   |              || : | :|  |   |: :|:  ::|| |: |||:|

Db        484 --SSNGDKSSVFFNFAIKEQIRTHTLFTPLLIAFGVAAGLMCIIV--MILVYIYLQKPKY 539

Qy        556 EIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGL 615
              |::|:|:| |  :|: |:|:|| ||||| :|||||: |  |: ||:||||||| |||||

Db        540 EVQWKVVEEI--NGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGL 597

Qy        616 SRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITE 675
               :|   | |||||||:|  :|::|||||||:::|| |:||||||||||  ||  :|||

Db        598 FKSDAAMTVAVKMLKPSAHLTEREALMSELKVLSYLGNHINIVNLLGACTIGGPTLVITE 657

Qy        676 YCFYGDLVNYLHKNRDSFL----SHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDY 731
              || ||||:|:| : ||||:      | |    |  :    |  ::                :|

Db        658 YCCYGDLLNFLRRKRDSFICPKHEEHAEAAVYENLLHQAEPTADAV----------NEY 706

Qy        732 MDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLT 791
              ||||   :    | ::|              ||   |  |  | :|   : :|:   |

Db        707 MDMKPGVSYAVPPKADKK-------------RPV--KSGSYTDQDVTLSMLEDDELALD 750

Qy        792 LLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVS 851
              : |||||:||||:|| |||||||:|||||||:||  |:| |||||||||||| :|||||

Db        751 VEDLLSFSYQVAKGMSFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNYVV 810

Qy        852 KGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKS 911
              ||:  |||||||||||: :||  |||||||||||:|||| :|||| ||| ||  ||

Db        811 KGNARLPVKWMAPESIFNCVYTFESDVWSYGILLWELFSLGSSPYPGMPVDSKFYKMIKE 870

Qy        912 GYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962
              ||||  |: :  |:|:||  ||:::| :||:|  : :::|  |     : |

Db        871 GYRMFSPECSPPEMYDIMKSCWDADPLQRPTFKQIVQLIEQQLSDNAPRVY 921


RESULT 44
Q63702_RATRT
ID   Q63702_RATRT PRELIMINARY;      PRT;   974 AA.
AC   Q63702;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C-kit receptor tyrosine kinase isoform.
GN   Name=c-kit proto-oncogene;
OS   Rattus rattus (Black rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10117;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BN/fMai;
RA   Tsujimura T., Tono T., Yamazaki M., Nomura S., Kitamura Y.;
RT   "Two isoforms of rat c-kit receptor tyrosine kinase.";
RL   Nucleic Acids Res. 0:0-0(0).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BN/fMai;
RA   Tsujimura T.;
RL   Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X62491; CAA44354.1; -; mRNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q63702; 545-691, 756-929.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; ReceptTyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   974 AA;  108955 MW;  B9BFAD9BA0DA190D CRC64;

  Query Match             25.8%;  Score 1460;  DB 2;  Length 974;
  Best Local Similarity   35.9%;  Pred. No. 1.1e-69;
  Matches  363;  Conservative  153;  Mismatches  356;  Indels  138;  Gaps   30;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIQPAQSELIVEAGDTIRLTCTDPAFVKWTF-----EILDVRIENKQSE-----WIR 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEG----RHIYIYVPDPDVAFVPLGMTDYLVIVE 141
Db         85 E--KAEATHTGKYTC----------VSGSGLRSSIYVFVRDPAVLFL-VGLP---LFGK 127

Qy        142 DDDSAIIPCRTTDPE-TPVTLHNSEG--------VVPASYDSRQGFNGTFTVGPY----- 187
Db        128 EDNDALVRCPLTDPQVSNYSLIECDGKSLPTDLKFVP---NPKAGITIKNVKRAYHRLCI 184

Qy        188 ICEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVDL 245
Db        185 RCAAQREGKWMRSDKFTLKVRAAIKAIPVVSVPETSHLLKEGDTFTVICTIKDVSTSVDS 244

Qy        246 QWTYPGEVKGKGITMLEEIKV---PSIKLVY----------------TLTVPEATVKDSG 286
Db        245 MW----------------IKLNPQPQSKAQVKRNSWHQGDFNYERQETLTISSARVNDSG 288

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
Db        289 VFMCYANNTFGSAN--VTTTLKVVEKGFINIFPVKNTTVFVTDGENVDLVVEFEAYPKPE 346

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
Db        347 HQQWIYMNRT-PTNRGEDYVKSDNQSNIRYVNELRLTRLKGTEGGTYTFLVSNSDVSASV 405

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTIL 465
Db        406 TFDVYVNTKPEILTYDRLMNG-----RLQCVAAGFPEPTIDWYFC-----TGAEQRCTV- 454

Qy        466 ANNVSNIITEIHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAENRELKLVAPT 520
Db        455 --PVPPVDVQIQNASVSPFGKLVVQSSIDSSVFRHNGTVECKASNAVGKSSAFFNFAFKE 512

Qy        521 LRSELTVAAAVLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVD 576
Db        513 QIQPHTLFTPLLIGFVVTAGLMGIIVMVLAYKYLQKPMYEVQWKVVEEI--NGNNYVYID 570

Qy        577 PMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSS 636
Db        571 PTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLT 630

Qy        637 EKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSH 696
Db        631 EREALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFIFS 690

Qy        697 HPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        691 KQEEQADAALYKNLLHSKES-------SCDSSNEYMDMKPG-VSYVVP------------ 730

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        731 ---TKTDKRRSARIDSYIERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIH 787

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        788 RDLAARNILLTHGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFNCVYTFES 847

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        848 DVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAAMYEVMKTCWDAD 907

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984
Db        908 PLKRPTFKQVVQLIEKQISDSSKHIYSNLANCNPNPENPVVVDHSVRVNS 957
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RESULT 45
Q63116_RAT
ID   Q63116_RAT  PRELIMINARY;      PRT;   978 AA.
AC   Q63116;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C-kit receptor tyrosine kinase.
GN   Name=Kit;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=92003944; PubMed=1912577;
RA   Tsujimura T., Hirota S., Nomura S., Niwa Y., Yamazaki M., Tono T.,
RA   Morii E., Kim H., Kondo K., Nishimune Y., Kitamura Y.;
RT   "Characterization of Ws mutant allele of rats: a 12-base deletion in
RT   tyrosine kinase domain of c-kit gene.";
RL   Blood 78:1942-1946(1991).
DR   EMBL; D12524; BAA02094.1; -; mRNA.
DR   PIR; A49814; A49814.
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DR   HSSP; P36888; 1RJB.
DR   SMR; Q63116; 549-695, 760-933.
DR   Ensembl; ENSRNOG00000002227; Rattus norvegicus.
DR   RGD; 620568; Kit.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   Kinase; Receptor.
SQ   SEQUENCE   978 AA;  109341 MW;  0958C33F19889051 CRC64;

  Query Match           25.8%;  Score 1458;  DB 2;  Length 978;
  Best Local Similarity   35.9%;  Pred. No. 1.4e-69;
  Matches  365;  Conservative  152;  Mismatches  353;  Indels  146;  Gaps   30;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::| :|:   :  | |   : | | :     |  || | |:::      :
Db         35 SPPSIQPAQSELIVEAGDTIRLTCTDPAFVKWTF-----EILDVRIENKQSE-----WIR 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEG----RHIYIYVPDPDVAFVPLGMTDYLVIVE 141
              |   | | ||| |||           : |      ||::| || | |: :|:    :  :
Db         85 E--KAEATHTGKYTC-----------VSGSGLRSSIYVFVRDPAVLFL-VGLP---LFGK 127

Qy        142 DDDSAIIPCRTTDPE-TPVTLHNSEG--------VVPASYDSRQGFNGTFTVGPY----- 187
              :|: |:: |  |||: :  :|   :|         ||   : : |          |
Db        128 EDNDALVRCPLTDPQVSNYSLIECDGKSLPTDLKFVP---NPKAGITIKNVKRAYHRLCI 184

Qy        188 ICEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVDL 245
              | |  :||  ::  | :    |  :  : :     : | |:|  | | : : :  ||
Db        185 RCAAQREGKWMRSDKFTLKVRAAIKAIPVVSVPETSHLLKEGDTFTVICTIKDVSTSVDS 244

Qy        246 QWTYPGEVKGKGITMLEEIKV---PSIKLVY----------------TLTVPEATVKDSG 286
              |                ||:   |  |                  |||:  | | |||
Db        245 MW----------------IKLNPQPQSKAQVKRNSWHQGDFNYERQETLTISSARVNDSG 288

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
              : | |               |: | ||||| | |  :    |   |    |||  ||| |
Db        289 VFMCYANNTFGSAN--VTTTLKVVEKGFINIFPVKNTTVFVTDGENVDLVVEFEAYPKPE 346

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
              |:  | |   |  |     :   ||| ::|:| | |  : | || : | |   |
Db        347 HQQWIYMNRT-PTNRGEDYVKSDNQSNIRYVNELRLTRLKGTEGGTYTFLVSNSDVSASV 405

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTIL 465
              ||::       ||      :|      ::| | | | | |:|  |        |   |:
Db        406 TFDVYVNTKPEILTYDRLMNG-----RLQCVAAGFPEPTIDWYFC-----TGAEQRCTV- 454

Qy        466 ANNVSNIITEIHSRDRSTVEGRVTFAKVEETI-----AVRCLAKNLLGAE---------- 510
              |  :  :| :   |     |  : :: ::      | | | | :|
Db        455 --PVPPVDVQIQNASVSPFGKLVVQSSIDSSVFRHNGTVECKASNAVGKSSAFFNFAFKG 512

Qy        511 NRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGH 570
              | : ::   || : | :    |   |: :|:  :||   : ||| ||::|:|:| |  :|:
Db        513 NSKEQIQPHTLFTPLLIGFVVTAGLMGIIV--MVLAYKYLQKPMYEVQWKVVEEI--NGN 568

Qy        571 EYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLK 630
              |:|:|| ||||| :|||||: |  |: ||:|||||||| ||||| :|   | |||||||
Db        569 NYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLK 628

Qy        631 PTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNR 690
              |:|  :|::|||||||::::|| |:||||||||||  ||  :|||| ||||:|:| : |
Db        629 PSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKR 688

Qy        691 DSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKE 750
              |||:    |:         |  : ||       | ::: :|||||    :  ||
Db        689 DSFIFSKQEEQADAALYKNLLHSKES-------SCDSSNEYMDMKPG-VSYVVP------ 734

Qy        751 VSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLA 810
                       :  |:  | :  | :: :|   : :|:   | | |||||:||||:|| |||
Db        735 ---------TKTDKRRSARIDSYIERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLA 785

Qy        811 SKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDN 870
              ||||:||||||||:||  |:| ||||||||||| :||||| ||:  ||||||||||||:
Db        786 SKNCIHRDLAARNILLTHGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFNC 845

Qy        871 LYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMV 930
              :||  |||||||| |||:|||| :||||| ||| ||  || |:||  |:|| : :||:|
Db        846 VYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAAMYEVMK 905

Qy        931 KCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984
              ||:::| |||:|  : :::|  :    |  |  :       ::| |    :||:|
Db        906 TCWDADPLKRPTFKQVVQLIEKQISDSSKHIYSNLANCNPNPENPVVVDHSVRVNS 961


RESULT 46
Q99662_HUMAN
ID   Q99662_HUMAN PRELIMINARY;      PRT;   972 AA.
AC   Q99662;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KIT protein.
GN   Name=KIT;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92228497; PubMed=1373482;
RA   Andre C., Martin E., Cornu F., Hu W.X., Wang X.P., Galibert F.;
RT   "Genomic organization of the human c-kit gene: evolution of the
RT   receptor tyrosine kinase subclass III.";
RL   Oncogene 7:685-691(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97179223; PubMed=9027509; DOI=10.1006/geno.1996.4482;
RA   Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
RA   Hu W.X., Galibert F.;
RT   "Sequence analysis of two genomic regions containing the KIT and the
RT   FMS receptor tyrosine kinase genes.";
RL   Genomics 39:216-226(1997).
DR   EMBL; U63834; AAC50969.1; -; Genomic_DNA.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q99662; 543-689, 755-929.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
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DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   972 AA;  109450 MW;  D59DEFE9AF761FDA CRC64;

  Query Match           25.8%;  Score 1457.5;  DB 2;  Length 972;
  Best Local Similarity   36.1%;  Pred. No. 1.5e-69;
  Matches  354;  Conservative  147;  Mismatches  359;  Indels  121;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::: :|::     | |     | | : : :|          ||    ::|
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                | | :|| |||   |  :          ||::| ||   |    : |  :  ::|:
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               ::  |  |||| |  :|   :|  |   | |       |   |
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
               |    :||   :  | :    | ||   : :   :   : : ||   ||| : :
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
                    |   ||  |     |             : :   |||:  | | ||| : | |
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
                       |: | :|||| | |  :    ||  |    :||  |:| |    |:
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
               | |  :   :     |    ||| |:| | | |  : | || :  | |   :  | :
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
                 ||    ||:          ::| | | | | |:|  |   ::     | ::|  :
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVA 528
               |  : :      :  |:  :  :  :    | | | | :|  :             |:
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKEQIHPHTLF 518

Qy        529 AAVLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDS 584
              :|:  |||  :: :||::: :|  ||| ||::|:|:| |  :|: |:|:|| |||||
Db        519 TPLLIGFVIVAGMMCIIVMILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDH 576

Qy        585 RWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSE 644
              :|||||: |  |: ||:|||||||| ||||| :|   | |||||||:|  :|::|||||
Db        577 KWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSE 636

Qy        645 LKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKE 704
               ||:::|| |:|||||||||||  ||  :|||| ||||:|:| : ||||:    |   :
Db        637 LKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHAEA 696

Qy        705 LDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDR 764
                  | : ||: |       ::  :|||||       ||        |   :| :||:  |
Db        697 ALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKRRSV--R 739

Qy        765 PASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNV 824
                ||     :: :|   : :|:   | | |||||:||||:|| |||||||:||||||||:
Db        740 IGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNI 794

Qy        825 LLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGIL 884
              ||  |:| |||||||||| :|||| ||:  |||||||||||: :||  ||||||||
Db        795 LLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIF 854

Qy        885 LWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFY 944
              |||:|||| :|||| ||| ||  || |:||  |:|| :|:|:||  ||:::| |||:|
Db        855 LWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFK 914

Qy        945 HLSEIVENLLPGQYKKSYEKI 965
               : :::|  :       |  :
Db        915 QIVQLIEKQISESTNHIYSNL 935


RESULT 47
KIT_HUMAN
ID   KIT_HUMAN      STANDARD;      PRT;   976 AA.
AC   P10721; Q9UM99;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mast/stem cell growth factor receptor precursor (EC 2.7.1.112) (SCFR)
DE   (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen).
GN   Name=KIT;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Fetal brain, and Term placenta;
RX   MEDLINE=88111521; PubMed=2448137;
RA   Yarden Y., Kuang W.-J., Yang-Feng T., Coussens L., Munemitsu S.,
RA   Dull T.J., Chen E., Schlessinger J., Francke U., Ullrich A.;
RT   "Human proto-oncogene c-kit: a new cell surface receptor tyrosine
RT   kinase for an unidentified ligand.";
RL   EMBO J. 6:3341-3351(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93064697; PubMed=1279499;
RA   Giebel L.B., Strunk K.M., Holmes S.A., Spritz R.A.;
RT   "Organization and nucleotide sequence of the human KIT (mast/stem cell
RT   growth factor receptor) proto-oncogene.";
RL   Oncogene 7:2207-2217(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97179223; PubMed=9027509; DOI=10.1006/geno.1996.4482;
RA   Andre C., Hampe A., Lachaume P., Martin E., Wang X.P., Manus V.,
RA   Hu W.X., Galibert F.;
RT   "Sequence analysis of two genomic regions containing the KIT and the
RT   FMS receptor tyrosine kinase genes.";
RL   Genomics 39:216-226(1997).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 1-22.
RX   PubMed=7506248;
RA   Yamamoto K., Tojo A., Aoki N., Shibuya M.;
RT   "Characterization of the promoter region of the human c-kit proto-
RT   oncogene.";
RL   Jpn. J. Cancer Res. 84:1136-1144(1993).
RN   [5]
RP   INTERACTION WITH MPDZ, AND MUTAGENESIS OF LYS-623 AND ASP-816.
RX   MEDLINE=20472558; PubMed=11018522; DOI=10.1016/S0014-5793(00)02036-6;
RA   Mancini A., Koch A., Stefan M., Niemann H., Tamura T.;
RT   "The direct association of the multiple PDZ domain containing proteins
RT   (MUPP-1) with the human c-Kit C-terminus is regulated by tyrosine
RT   kinase activity.";
RL   FEBS Lett. 482:54-58(2000).
RN   [6]
RP   INTERACTION WITH APS, AND MUTAGENESIS OF ILE-571 AND LEU-939.
RX   MEDLINE=22510236; PubMed=12444928; DOI=10.1042/BJ20020716;
RA   Wollberg P., Lennartsson J., Gottfridsson E., Yoshimura A.,
RA   Ronnstrand L.;
RT   "The adapter protein APS associates with the multifunctional docking
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RT   sites Tyr-568 and Tyr-936 in c-Kit.";
RL   Biochem. J. 370:1033-1038(2003).
RN   [7]
RP   VARIANT LYS-583.
RX   MEDLINE=92291284; PubMed=1376329;
RA   Fleischman R.A.;
RT   "Human piebald trait resulting from a dominant negative mutant allele
RT   of the c-kit membrane receptor gene.";
RL   J. Clin. Invest. 89:1713-1717(1992).
RN   [8]
RP   VARIANT LEU-584.
RX   MEDLINE=92133600; PubMed=1370874;
RA   Spritz R.A., Giebel L.B., Holmes S.A.;
RT   "Dominant negative and loss of function mutations of the c-kit
RT   (mast/stem cell growth factor receptor) proto-oncogene in human
RT   piebaldism.";
RL   Am. J. Hum. Genet. 50:261-269(1992).
RN   [9]
RP   VARIANT ARG-664.
RX   MEDLINE=92020918; PubMed=1717985;
RA   Giebel L.B., Spritz R.A.;
RT   "Mutation of the KIT (mast/stem cell growth factor receptor)
RT   protooncogene in human piebaldism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:8696-8699(1991).
RN   [10]
RP   VARIANT VAL-816.
RX   MEDLINE=94013473; PubMed=7691885;
RA   Furitsu T., Tsujimura T., Tono T., Ikeda H., Kitayama H.,
RA   Koshimizu U., Sugahara H., Butterfield J.H., Ashman L.K., Kanayama Y.,
RA   Matsuzawa Y., Kitamura Y., Kanakura Y.;
RT   "Identification of mutations in the coding sequence of the proto-
RT   oncogene c-kit in a human mast cell leukemia cell line causing ligand-
RT   independent activation of c-kit product.";
RL   J. Clin. Invest. 92:1736-1744(1993).
RN   [11]
RP   VARIANTS PIEBALDISM GLY-791 AND VAL-812.
RX   MEDLINE=93322624; PubMed=7687267; DOI=10.1111/1523-1747.ep12358440;
RA   Spritz R.A., Holmes S.A., Itin P., Kuester W.;
RT   "Novel mutations of the KIT (mast/stem cell growth factor receptor)
RT   proto-oncogene in human piebaldism.";
RL   J. Invest. Dermatol. 101:22-25(1993).
RN   [12]
RP   VARIANT PIEBALDISM 893-GLU--PRO-896 DEL.
RX   MEDLINE=96287384; PubMed=8680409;
RA   Riva P., Milani N., Gandolfi P., Larizza L.;
RT   "A 12-bp deletion (7818del12) in the c-kit protooncogene in a large
RT   Italian kindred with piebaldism.";
RL   Hum. Mutat. 6:343-345(1995).
RN   [13]
RP   VARIANT GIST VAL-559 DEL.
RX   MEDLINE=98361155; PubMed=9697690; DOI=10.1038/1209;
RA   Nishida T., Hirota S., Taniguchi M., Hashimoto K., Isozaki K.,
RA   Nakamura H., Kanakura Y., Tanaka T., Takabayashi A., Matsuda H.,
RA   Kitamura Y.;
RT   "Familial gastrointestinal stromal tumours with germline mutation of
RT   the KIT gene.";
RL   Nat. Genet. 19:323-324(1998).
CC   -!- FUNCTION: This is the receptor for stem cell factor (mast cell
CC       growth factor). It has a tyrosine-protein kinase activity. Binding
CC       of the ligands leads to the autophosphorylation of KIT and its
CC       association with substrates such as phosphatidylinositol 3-kinase
CC       (Pi3K).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Interacts with APS. Interacts with the tenth PDZ domain
CC       of MPDZ.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DISEASE: Defects in KIT are a cause of piebaldism [MIM:172800].
CC       Piebaldism is an autosomal dominant genetic developmental
CC       abnormality of pigmentation characterized by congenital patches of
CC       white skin and hair that lack melanocytes.
CC   -!- DISEASE: Defects in KIT are a cause of gastrointestinal stromal
CC       tumor (GIST) [MIM:606764].
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 5 Ig-like C2-type (immunoglobulin-like)
CC       domains.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/KITID127.html".
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X06182; CAA29548.1; -; mRNA.
DR   EMBL; X69301; CAA49159.1; -; Genomic_DNA.
DR   EMBL; X69302; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69303; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69304; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69305; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69306; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69307; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69308; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69309; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69310; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69311; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69312; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69313; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69314; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69315; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; X69316; CAA49159.1; JOINED; Genomic_DNA.
DR   EMBL; U63834; AAC50968.1; -; Genomic_DNA.
DR   EMBL; S67773; AAB29529.1; -; Genomic_DNA.
DR   PIR; S01426; TVHUKT.
DR   PDB; 1PKG; X-ray; A/B=549-935.
DR   PDB; 1T45; X-ray; A=547-935.
DR   PDB; 1T46; X-ray; A=565-935.
DR   Ensembl; ENSG00000157404; Homo sapiens.
DR   HGNC; HGNC:6342; KIT.
DR   MIM; 164920; -.
DR   MIM; 172800; -.
DR   MIM; 606764; -.
DR   GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW   3D-structure; ATP-binding; Disease mutation; Glycoprotein;
KW   Immunoglobulin domain; Kinase; Nucleotide-binding; Phosphorylation;
KW   Proto-oncogene; Receptor; Signal; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
FT   SIGNAL       1     22
FT   CHAIN       23    976       Mast/stem cell growth factor receptor.
FT   TOPO_DOM     23    520       Extracellular (Potential).
FT   TRANSMEM    521    543       Potential.
FT   TOPO_DOM    544    976       Cytoplasmic (Potential).
FT   DOMAIN      589    937       Protein kinase.
FT   NP_BIND     595    603       ATP (By similarity).
FT   ACT_SITE    792    792       By similarity.
FT   BINDING     623    623       ATP (By similarity).

  Query Match             25.7%;  Score 1454.5;  DB 1;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 2.2e-69;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;
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Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939


RESULT 48
Q8C8K9_MOUSE
ID   Q8C8K9_MOUSE PRELIMINARY;      PRT;   979 AA.
AC   Q8C8K9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length
DE   enriched library, clone:B830009P17 product:kit oncogene, full insert
DE   sequence (Kit protein).
GN   Name=Kit;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1709486;
RA   Hayashi S., Kunisada T., Ogawa M., Yamaguchi K., Nishikawa S.;
RT   "Exon skipping by mutation of an authentic splice site of c-kit gene
RT   in W/W mouse.";
RL   Nucleic Acids Res. 19:1267-1271(1991).
DR   EMBL; AK046795; BAC32872.1; -; mRNA.
DR   EMBL; BC075716; AAH75716.1; -; mRNA.
DR   PIR; S34435; S34435.
DR   HSSP; P36888; 1RJB.
DR   SMR; Q8C8K9; 550-696, 761-934.
DR   MGI; MGI:96677; Kit.
DR   GO; GO:0009897; C:external side of plasma membrane; IDA.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0005020; F:stem cell factor receptor activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; TAS.
DR   GO; GO:0030154; P:cell differentiation; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0019221; P:cytokine and chemokine mediated signaling p. . .; IDA.
DR   GO; GO:0007281; P:germ cell development; TAS.
DR   GO; GO:0030097; P:hemopoiesis; IMP.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0048066; P:pigmentation; IMP.
DR   GO; GO:0007243; P:protein kinase cascade; IDA.
DR   GO; GO:0009314; P:response to radiation; IMP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   979 AA;  109343 MW;  03FB4D672248585E CRC64;

  Query Match             25.7%;  Score 1453.5;  DB 2;  Length 979;
  Best Local Similarity   35.8%;  Pred. No. 2.5e-69;
  Matches  361;  Conservative  151;  Mismatches  367;  Indels  129;  Gaps   30;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::| :|:   : || |     | | :     |     : |::|       :
Db         35 SPPSIHPAQSELIVEAGDTLSLTCIDPDFVRWTFKTYFNEM----VENKKNE-----WIQ 85

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
              |   | |  || ||| ::  |          ||::| ||   |: :|:    :  ::|
Db         86 E--KAEATRTGTYTCSNSNGLTSS-------IYVFVRDPAKLFL-VGLP---LFGKEDSD 132

Qy        146 AIIPCRTTDPE-TPVTLHNSEG-VVPASYDSRQGFNGTFTVGPYI--------------- 188
              |:: |  |||: :  :|  :|  :|            ||    |
Db        133 ALVRCPLTDPQVSNYSLIECDGKSLPTDL--------TFVPNPKAGITIKNVKRAYHRLC 184

Qy        189 --CEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVD 244
                | |   |    :  | :    |   :  : :     : | |:|  | | : : :  |:
Db        185 VRCAAQRDGTWLHSDKFTLKVRAAIKAIPVVSVPETSHLLKKGDTFTVVCTIKDVSTSVN 244

Qy        245 LQW-------TYPGEVK----GKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
                |       :  :||     :|    | :        |||:  | | ||| : | |
Db        245 SMWLKMNPQPQHIAQVKHNSWHRGDFNYERQE--------TLTISSARVDDSGVFMCYAN 296

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKN 352
                      |: | ||||| | |  :    |   |    |||  ||| |    |:
Db        297 NTFGSAN--VTTTLKVVEKGFINISPVKNTTVFVTDGENVDLVVEYEAYPKPEHQQWIYM 354

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412
              | |      :      |   ||| ::|:| | |  : | || :  | ||  | || :
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Db        355 NRTSANKGKDYVKSDNK-SNIRYVNQLRLTRLKGTEGGTYTFLVSNSDASASVTFNVYVN 413

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETS-WTILANNVS 470

Db        414 TKPEILTYDRLING-----MLQCVAEGFPEPTIDWYFCTGAEQRCTTPVSPVDVQVQNVS 468

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVAPT 520

Db        469 -----VSPFGKLVVQSSIDSSVFRHNGTVECKASNDVGKSSAFFNFAFKGNNKEQIQAHT 523

Qy        521 LRSELTVAAAVLVLLVIVIISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPM 578

Db        524 LFTPLLIGFVV----AAGAMGIIVMVLTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 577

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638

Db        578 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 637

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698

Db        638 EALMSELKVLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFIFSKQ 697

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758

Db        698 EEQAEAALYKNLLHSTEP-------SCDSSNEYMDMKPG-VSYVVP-------------- 735

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818

Db        736 -TKTDKRRSARIDSYIERDVTPAIMEDDELALDLDDLLSFSYQVAKGMAFLASKNCIHRD 794

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878

Db        795 LAARNILLTHGRITKICDFGLARDIRNDSNYVVKGNARLPVKWMAPESIFSCVYTFESDV 854

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938

Db        855 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMVSPEHAPAEMYDVMKTCWDADPL 914

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984

Db        915 KRPTFKQVVQLIEKQISDSTKHIYSNLANCNPNPENPVVVDHSVRVNS 962
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RESULT 49
Q76II0_CALJA
ID   Q76II0_CALJA PRELIMINARY;      PRT;   972 AA.
AC   Q76II0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-kit protein.
GN   Name=c-kit;
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC   Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Izawa K.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB097502; BAD04018.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   SMR; Q76II0; 543-689, 755-929.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR009134; VEGFR.
DR   Pfam; PF00047; ig; 1.
DR   PRINTS; PR01832; VEGFRECEPTOR.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   972 AA;  109680 MW;  5BC959312C3BB1FA CRC64;
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  Query Match             25.7%;  Score 1452;  DB 2;  Length 972;
  Best Local Similarity   35.8%;  Pred. No. 2.9e-69;
  Matches  362;  Conservative  144;  Mismatches  362;  Indels  144;  Gaps   29;

Qy         13 CLLTGLSLILCQLSLPSILPNE----------NEKVVQLNSSFSLRCFGESEVSWQYPMS 62

Db         12 CVLLLLLRVQTGSSQPSVSPEEASPPFIDPAKSELIVSVGDEIRLFCNDPGFVKWTFEVL 71

Qy         63 EEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVP 122

Db         72 DQMN--------ENKQKEWI----MQKAEATNTGKYTCTNKHGLSSS-------IYVFVR 112

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPE-TPVTLHNSEG--------VVPASYD 173

Db        113 DPDKLF----LVDRSLYGKEDNDTLVRCPLTDPEVTNYSLKGCQGKPIPKDLRFVP---D 165

Qy        174 SRQGFNGTFTVGPY-----ICEATVKGKK-------------FQTIPFNVYALKATSELD 215

Db        166 PKAGITIKNVKRAYHRLCLHCSADRKGQSKLSEKFILKVRPAFKAVP--VVSVSKASYL- 222

Qy        216 LEMEALKTVYKSGETIVVTCAVFN-NEVVDLQWTYPGEVKGKGITMLEEIKVPS------ 268

Db        223 ---------LREGEEFTVTCTIKDVSSSVYSSWK-----KENSPTKLQE-KYNSWHQGDF 267

Qy        269 -IKLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAV 327

Db        268 NYERQATLTISSVRVNDSGVFMCYASNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFV 325

Qy        328 NLHEVKHFVVEVRAYP-PPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKE 386

Db        326 NDGENVDLIVEYEAFPRPEHQQWIYMNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKD 384

Qy        387 EDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIE 446

Db        385 TEGGTYTFLVSNSDVSSSIAFTVYVNTKPEILTYDRLMNG-----MLQCVAAGFPEPTID 439

Qy        447 WMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNL 506

Db        440 WYFCPGTEQ---RCSAPVLPVDVQIQNTSGPPFGKLVVQSSIDSSAFKHNGTVECKAYND 496

Qy        507 LGAENRELKLVAPTLRSELTVAAAVLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVI 562

Db        497 VGKTSAYFNFAFKEQIQPHTLFTPLLIGFVVVAGMMCIIVMILTYKYLQKPMYEVQWKVV 556

Qy        563 ESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVM 622

Db        557 EEI--NGNNYVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDTAM 614

Qy        623 KVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL 682

Db        615 TVAVKMLKPSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDL 674

Qy        683 VNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQY 742
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           :|:| : ||||:    |   :      |  : ||: |      ::  :|||||    :
Db        675 LNFLRRKRDSFICSKQEDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG-VSYV 727

Qy        743 VPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQV 802
              ||    |  |           |  ||     :: :|   : :|:   | | |||||:|||
Db        728 VPTKAEKRRSA----------RVGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQV 772

Qy        803 ARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWM 862
              |:|| |||||||:||||||||:||  |:| ||||||||||| :||||| ||:  ||||||
Db        773 AKGMAFLASKNCIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWM 832

Qy        863 APESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHAT 922
              ||||||: :||  |||||||| |||:|||| :||||| ||| ||  || |:||  |:||
Db        833 APESIFNCVYTFESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAP 892

Qy        923 SEVYEIMVKCWNSEPEKRPSFYHLSEIVE--------------NLLPGQYK 959
              :|:|:||  ||:::| |||:|  : :::|              | | | |
Db        893 AEMYDIMKTCWDADPLKRPTFKQIVQLIEKQISESTNHIYSNLTNCSPSQQK 944


RESULT 50
Q6QJB8_MOUSE
ID   Q6QJB8_MOUSE PRELIMINARY;      PRT;   975 AA.
AC   Q6QJB8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Proto-oncogene c-kit.
GN   Name=Kit;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL6/J;
RX   PubMed=15731517; DOI=10.1534/genetics.104.027177;
RA   Ruan H.B., Zhang N., Gao X.;
RT   "Identification of a Novel Point Mutation of Mouse Proto-Oncogene c-
RT   kit Through N-Ethyl-N-nitrosourea Mutagenesis.";
RL   Genetics 169:819-831(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL6/J;
RA   Ruan H., Gao X.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY536430; AAS45606.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   SMR; Q6QJB8; 546-692, 757-930.
DR   GO; GO:0009897; C:external side of plasma membrane; IDA.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0005020; F:stem cell factor receptor activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; TAS.
DR   GO; GO:0030154; P:cell differentiation; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0019221; P:cytokine and chemokine mediated signaling p. . .; IDA.
DR   GO; GO:0007281; P:germ cell development; TAS.
DR   GO; GO:0030097; P:hemopoiesis; IMP.
DR   GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.
DR   GO; GO:0048066; P:pigmentation; IMP.
DR   GO; GO:0007243; P:protein kinase cascade; IDA.
DR   GO; GO:0009314; P:response to radiation; IMP.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001824; RecepttyrkinsIII.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   ProDom; PD000001; Prot_kinase; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00408; IGc2; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
SQ   SEQUENCE   975 AA;  108928 MW;  57BFE10AE456C145 CRC64;

  Query Match             25.7%;  Score 1450.5;  DB 2;  Length 975;
  Best Local Similarity   35.8%;  Pred. No. 3.6e-69;
  Matches  358;  Conservative  151;  Mismatches  374;  Indels  117;  Gaps   29;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::| :|:   : || |     | | :     |     : |::|       :
Db         35 SPPSIHPAQSELIVEAGDTLSLTCIDPDFVRWTFKTYFNEM----VENKKNE-----WIQ 85

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
              |   | |  || |||  ::  |          ||::| ||   |: :|:    :  ::|
Db         86 E--KAEATRTGTYTCSNSNGLTSS-------IYVFVRDPAKLFL-VGLP---LFGKEDSD 132

Qy        146 AIIPCRTTDPE-TPVTLHNSEG-VVPASYDSRQGFNGTFTVGPYI--------------- 188
              |:: |  |||: :  :|   :|  :|           ||   |
Db        133 ALVRCPLTDPQVSNYSLIECDGKSLPTDL--------TFVPNPKAGITIKNVKRAYHRLC 184

Qy        189 --CEATVKGKKFQTIPFNVYALKATSELD-LEMEALKTVYKSGETIVVTCAVFN-NEVVD 244
                | |   |    :  | :    |   :  : :     : | |:|  | | : : :  |:
Db        185 VRCAAQRDGTWLHSDKFTLKVRAAIKAIPVVSVPETSHLLKKGDTFTVVCTIKDVSTSVN 244

Qy        245 LQW-------TYPGEVK----GKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAAR 293
                |       :  :||     :|    | :        |||:  | | ||| : | |
Db        245 SMWLKMNPQPQHIAQVKHNSWHRGDFNYERQE--------TLTISSARVDDSGVFMCYAN 296

Qy        294 QATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLKN 352
                        |: | ||||| | |  :    |   |    |||  ||| |    |:
Db        297 NTFGSAN--VTTTLKVVEKGFINISPVKNTTVFVTDGENVDLVVEYEAYPKPEHQQWIYM 354

Qy        353 NLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQ 412
              | |      :      |   ||| ::|:| | |  : | || :  | ||  | || :
Db        355 NRTSANKGKDYVKSDNK-SNIRYVNQLRLTRLKGTEGGTYTFLVSNSDASASVTFNVYVN 413

Qy        413 VPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETS-WTILANNVS 470
                ||      :|      ::| ||| | | |:|  |    ::|    |  :   |||
Db        414 TKPEILTYDRLING-----MLQCVAEGFPEPTIDWYFCTGAEQRCTTPVSPVDVQVQNVS 468

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
                :   :  |:  :  :       | | | | :|  :              |:
Db        469 -----VSPFGKLVVQSSIDSSVFRHNGTVECKASNDVGKSSAFFNFAFKEQIQAHTLFTP 523

Qy        531 VLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRW 586
              :|:  |:    : :||:|: :|  ||| ||::|:|:| |  :|: |:|:|| ||||| :|
Db        524 LLIGFVVAAGAMGIIVMVLTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDHKW 581

Qy        587 EFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELK 646
              ||||: |  |: ||:|||||||| ||||| :|   | ||||||||:|  :|::|||||||
Db        582 EFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELK 641

Qy        647 IMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELD 706
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Db        642 VLSYLGNHMNIVNLLGACTVGGPTLVITEYCCYGDLLNFLRRKRDSFIFSKQEEQAEAAL 701

Qy        707 IFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPA 766
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Db        702 YKNLLHSTEP-------SCDSSNEYMDMKPG-VSYVVP--------------TKTDKRR 738

Qy        767 SYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLL 826
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Qy        827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLW 886
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Qy        947 SEIVENLLPGQYKKSYEKIHLDFLKSDHPAVA--RMRVDS 984
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Db        919 VQLIEKQISDSTKHIYSNLANCNPNPENPVVVDHSVRVNS 958


Search completed: May 15, 2006, 08:59:44
Job time : 280 secs
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OM protein - protein search, using sw model

Run on: May 15, 2006, 08:53:07 ; Search time 33 Seconds
(without alignments)
2728.297 Million cell updates/sec

Title: US-08-439-095-1
Perfect score: 5652
Sequence: 1 MGTSHPAFLVLGCLLTGLSL.....IDMMDDIGIDSSDLVEDSFL 1089

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5652	100.0	1089	1	US-08-168-917-4	Sequence 4, Appli
2	5652	100.0	1089	1	US-08-460-510-4	Sequence 4, Appli
3	5652	100.0	1089	1	US-08-460-490-4	Sequence 4, Appli
4	5652	100.0	1089	2	US-08-462-728-2	Sequence 2, Appli
5	5652	100.0	1089	2	US-08-461-917-2	Sequence 2, Appli
6	5652	100.0	1089	2	US-08-464-436-2	Sequence 2, Appli
7	5652	100.0	1089	2	US-08-464-436-2	Sequence 2, Appli
8	5652	100.0	1089	2	US-09-769-987-2	Sequence 2, Appli
9	5652	100.0	1089	2	US-09-866-510-2	Sequence 2, Appli
10	5652	100.0	1089	2	US-09-919-497-90	Sequence 90, Appl
11	5652	100.0	1089	2	US-09-949-016-6703	Sequence 6703, Ap
12	5652	100.0	1089	4	PCT-US92-00730-4	Sequence 4, Appli
13	5652	100.0	1089	4	PCT-US92-00862-4	Sequence 4, Appli
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16	5648	99.9	1089	1	US-08-477-329-36	Sequence 36, Appl
17	5648	99.9	1089	1	US-08-475-458-36	Sequence 36, Appl
18	5648	99.9	1089	2	US-08-980-400-36	Sequence 36, Appl
19	5648	99.9	1089	2	US-09-583-459A-36	Sequence 36, Appl
20	5648	99.9	1089	2	US-09-583-210-36	Sequence 36, Appl
21	5648	99.9	1089	2	US-09-583-449A-36	Sequence 36, Appl
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77	1214	21.5	1362	2	US-10-105-901A-33	Sequence 33, Appl
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167	859.5	15.2	270	1	US-07-857-224B-78	Sequence 78, Appl
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195	830.5	14.7	733	2	US-08-439-992A-4	Sequence 4, Appli
196	830.5	14.7	733	2	US-09-620-561-4	Sequence 4, Appli
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213	765.5	13.5	891	2	US-09-345-473E-25	Sequence 25, Appl
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217	761.5	13.5	351	1	US-08-701-191A-3	Sequence 3, Appli
218	761.5	13.5	351	2	US-09-664-526-3	Sequence 3, Appli
219	760	13.4	1072	2	US-09-949-016-6973	Sequence 6973, Ap
220	760	13.4	1085	2	US-09-949-016-8762	Sequence 8762, Ap
221	760	13.4	1085	2	US-09-949-016-8763	Sequence 8763, Ap
222	760	13.4	1085	2	US-09-949-016-8764	Sequence 8764, Ap
223	760	13.4	1085	2	US-09-949-016-8765	Sequence 8765, Ap
224	760	13.4	1106	2	US-09-949-016-6972	Sequence 6972, Ap
225	760	13.4	1114	2	US-09-949-016-5925	Sequence 5925, Ap
226	760	13.4	1114	2	US-09-949-016-6975	Sequence 6975, Ap
227	760	13.4	1127	2	US-09-949-016-7671	Sequence 7671, Ap
228	760	13.4	1127	2	US-09-949-016-7672	Sequence 7672, Ap
229	760	13.4	1127	2	US-09-949-016-7673	Sequence 7673, Ap
230	760	13.4	1127	2	US-09-949-016-7674	Sequence 7674, Ap
231	760	13.4	1127	2	US-09-949-016-8766	Sequence 8766, Ap
232	760	13.4	1127	2	US-09-949-016-8767	Sequence 8767, Ap
233	760	13.4	1127	2	US-09-949-016-8768	Sequence 8768, Ap
234	760	13.4	1127	2	US-09-949-016-8769	Sequence 8769, Ap
235	758	13.4	388	1	US-08-070-165F-4	Sequence 4, Appli
236	758	13.4	388	1	US-08-885-418-4	Sequence 4, Appli
237	757.5	13.4	310	1	US-08-701-191A-1	Sequence 1, Appli
238	757.5	13.4	310	1	US-08-701-191A-6	Sequence 6, Appli
239	757.5	13.4	310	2	US-09-390-326-7	Sequence 7, Appli
240	757.5	13.4	310	2	US-09-664-526-1	Sequence 1, Appli
241	757.5	13.4	310	2	US-09-664-526-6	Sequence 6, Appli
242	757.5	13.4	310	2	US-09-939-833-7	Sequence 7, Appli
243	757.5	13.4	310	2	US-09-506-906-7	Sequence 7, Appli
244	757.5	13.4	310	2	US-09-939-832-7	Sequence 7, Appli
245	757.5	13.4	310	2	US-09-939-754-7	Sequence 7, Appli
246	753.5	13.3	299	1	US-08-701-191A-13	Sequence 13, Appl

247	753.5	13.3	299	2	US-09-664-526-13	Sequence 13, Appl
248	753.5	13.3	300	1	US-08-701-191A-31	Sequence 31, Appl
249	753.5	13.3	300	2	US-09-664-526-31	Sequence 31, Appl
250	748	13.2	816	2	US-09-949-016-10904	Sequence 10904, A
251	744	13.2	802	2	US-09-173-151A-33	Sequence 33, Appl
252	731.5	12.9	310	1	US-08-701-191A-7	Sequence 7, Appli
253	731.5	12.9	310	2	US-09-664-526-7	Sequence 7, Appli
254	724	12.8	378	1	US-08-070-165F-8	Sequence 8, Appli
255	724	12.8	378	1	US-08-885-418-8	Sequence 8, Appli
256	705.5	12.5	309	1	US-08-701-191A-9	Sequence 9, Appli
257	705.5	12.5	309	2	US-09-664-526-9	Sequence 9, Appli
258	702.5	12.4	310	1	US-08-701-191A-8	Sequence 8, Appli
259	702.5	12.4	310	2	US-09-664-526-8	Sequence 8, Appli
260	702.5	12.4	313	1	US-08-278-089A-17	Sequence 17, Appl
261	702.5	12.4	313	1	US-08-838-957A-16	Sequence 16, Appl
262	697	12.3	304	1	US-08-701-191A-27	Sequence 27, Appl
263	697	12.3	304	2	US-09-664-526-27	Sequence 27, Appl
264	669.5	11.8	318	1	US-08-701-191A-10	Sequence 10, Appl
265	669.5	11.8	318	2	US-09-664-526-10	Sequence 10, Appl
266	654	11.6	316	1	US-08-278-089A-16	Sequence 16, Appl
267	654	11.6	316	1	US-08-838-957A-15	Sequence 15, Appl
268	648	11.5	269	1	US-07-857-224B-79	Sequence 79, Appl
269	622.5	11.0	258	2	US-09-964-956-75	Sequence 75, Appl
270	614.5	10.9	322	1	US-08-701-191A-11	Sequence 11, Appl
271	614.5	10.9	322	2	US-09-664-526-11	Sequence 11, Appl
272	605.5	10.7	860	4	PCT-US95-08493-19	Sequence 19, Appl
273	601.5	10.6	868	1	US-08-374-834-1	Sequence 1, Appli
274	601.5	10.6	868	1	US-08-644-271-1	Sequence 1, Appli
275	601.5	10.6	868	2	US-09-077-955-1	Sequence 1, Appli
276	601.5	10.6	868	2	US-10-016-283-1	Sequence 1, Appli
277	601.5	10.6	868	4	PCT-US95-08493-21	Sequence 21, Appl
278	590.5	10.4	280	2	US-10-003-690-8	Sequence 8, Appli
279	590.5	10.4	280	2	US-09-515-806-15	Sequence 15, Appl
280	590	10.4	869	1	US-08-374-834-16	Sequence 16, Appl
281	590	10.4	869	1	US-08-644-271-29	Sequence 29, Appl
282	590	10.4	869	2	US-09-077-955-33	Sequence 33, Appl
283	590	10.4	869	2	US-10-016-283-33	Sequence 33, Appl
284	588	10.4	869	2	US-09-715-249-8	Sequence 8, Appli
285	584.5	10.3	481	2	US-07-912-122-4	Sequence 4, Appli
286	584.5	10.3	481	4	PCT-US93-06404-4	Sequence 4, Appli
287	582	10.3	1122	1	US-08-278-089A-6	Sequence 6, Appli
288	582	10.3	1122	1	US-08-838-957A-6	Sequence 6, Appli
289	580.5	10.3	1135	1	US-08-469-537A-97	Sequence 97, Appl
290	580	10.3	1101	1	US-08-469-537A-96	Sequence 96, Appl
291	578	10.2	1124	1	US-08-323-474-2	Sequence 2, Appli
292	578	10.2	1124	2	US-09-949-016-5946	Sequence 5946, Ap
293	578	10.2	1124	4	PCT-US93-06093-2	Sequence 2, Appli
294	575	10.2	1118	1	US-07-934-393B-2	Sequence 2, Appli
295	575	10.2	1118	1	US-08-278-089A-2	Sequence 2, Appli
296	575	10.2	1118	1	US-08-838-957A-2	Sequence 2, Appli
297	575	10.2	1157	2	US-09-949-016-9568	Sequence 9568, Ap
298	570	10.1	348	1	US-08-222-616-18	Sequence 18, Appl
299	570	10.1	348	2	US-08-446-648-18	Sequence 18, Appl
300	570	10.1	348	2	US-09-982-610-18	Sequence 18, Appl
301	570	10.1	348	4	PCT-US95-04228-18	Sequence 18, Appl
302	556.5	9.8	1138	1	US-08-220-240A-5	Sequence 5, Appli
303	556.5	9.8	1150	2	US-09-949-016-7769	Sequence 7769, Ap
304	545.5	9.7	923	2	US-09-345-473E-23	Sequence 23, Appl
305	545.5	9.7	923	2	US-09-862-027-23	Sequence 23, Appl
306	543.5	9.6	430	2	US-09-345-473E-22	Sequence 22, Appl
307	543.5	9.6	430	2	US-09-862-027-22	Sequence 22, Appl
308	542	9.6	821	1	US-08-339-578-2	Sequence 2, Appli
309	540.5	9.6	1138	1	US-08-323-474-8	Sequence 8, Appli
310	540.5	9.6	1138	1	US-08-469-537A-98	Sequence 98, Appl
311	540	9.6	822	1	US-08-359-705B-2	Sequence 2, Appli
312	540	9.6	822	1	US-08-286-846A-2	Sequence 2, Appli
313	540	9.6	822	1	US-08-457-880A-2	Sequence 2, Appli
314	540	9.6	822	2	US-08-444-622A-2	Sequence 2, Appli
315	540	9.6	822	2	US-08-942-562-2	Sequence 2, Appli
316	540	9.6	822	2	US-09-156-923-2	Sequence 2, Appli
317	540	9.6	822	2	US-09-949-016-6698	Sequence 6698, Ap
318	540	9.6	847	1	US-08-286-305A-5	Sequence 5, Appli
319	540	9.6	847	1	US-08-441-104A-5	Sequence 5, Appli
320	540	9.6	847	1	US-08-440-816A-5	Sequence 5, Appli
321	540	9.6	847	2	US-09-417-381A-5	Sequence 5, Appli
322	534	9.4	850	1	US-08-286-305A-7	Sequence 7, Appli
323	534	9.4	850	1	US-08-441-104A-7	Sequence 7, Appli
324	534	9.4	850	1	US-08-440-816A-7	Sequence 7, Appli
325	534	9.4	850	2	US-09-417-381A-7	Sequence 7, Appli
326	531.5	9.4	1367	1	US-08-249-687C-2	Sequence 2, Appli
327	531.5	9.4	1367	1	US-08-625-819-2	Sequence 2, Appli
328	531.5	9.4	1367	2	US-08-746-559A-2	Sequence 2, Appli
329	531.5	9.4	1367	2	US-08-864-641B-18	Sequence 18, Appl
330	531.5	9.4	1367	2	US-09-343-551-2	Sequence 2, Appli
331	531.5	9.4	1367	2	US-09-949-001-18	Sequence 18, Appl
332	531.5	9.4	1377	2	US-09-949-001-21	Sequence 21, Appl
333	530.5	9.4	301	1	US-07-934-393B-4	Sequence 4, Appli
334	530.5	9.4	301	1	US-08-278-089A-4	Sequence 4, Appli
335	530.5	9.4	301	1	US-08-278-089A-14	Sequence 14, Appl
336	530.5	9.4	301	1	US-08-469-537A-99	Sequence 99, Appl
337	530.5	9.4	301	1	US-08-838-957A-4	Sequence 4, Appli
338	524.5	9.3	530	4	PCT-US95-08493-2	Sequence 2, Appli
339	524	9.3	946	4	PCT-US95-08493-13	Sequence 13, Appl
340	522	9.2	291	1	US-08-701-191A-22	Sequence 22, Appl
341	522	9.2	291	2	US-09-664-526-22	Sequence 22, Appl
342	518	9.2	839	1	US-08-359-705B-6	Sequence 6, Appli
343	518	9.2	839	1	US-08-286-846A-6	Sequence 6, Appli
344	518	9.2	839	1	US-08-457-880A-6	Sequence 6, Appli
345	518	9.2	839	2	US-08-444-622A-6	Sequence 6, Appli
346	518	9.2	839	2	US-08-942-562-6	Sequence 6, Appli
347	518	9.2	839	2	US-09-156-923-6	Sequence 6, Appli
348	516	9.1	370	2	US-08-857-076-107	Sequence 107, App
349	516	9.1	370	2	US-09-205-658-107	Sequence 107, App
350	513.5	9.1	885	1	US-08-372-892-4	Sequence 4, Appli
351	513.5	9.1	885	2	US-09-919-497-52	Sequence 52, Appl
352	513	9.1	822	2	US-09-886-319A-64	Sequence 64, Appl
353	513	9.1	822	2	US-09-538-092-941	Sequence 941, App
354	513	9.1	894	1	US-08-372-892-2	Sequence 2, Appli
355	513	9.1	894	1	US-08-445-640-34	Sequence 34, Appl
356	513	9.1	894	2	US-08-170-558-34	Sequence 34, Appl
357	513	9.1	894	2	US-08-447-314-34	Sequence 34, Appl
358	513	9.1	894	2	US-08-445-461-34	Sequence 34, Appl
359	513	9.1	894	2	US-09-223-490-34	Sequence 34, Appl
360	513	9.1	975	2	US-09-949-016-7595	Sequence 7595, Ap
361	511	9.0	304	1	US-08-701-191A-30	Sequence 30, Appl
362	511	9.0	304	2	US-09-664-526-30	Sequence 30, Appl
363	511	9.0	880	1	US-08-445-640-10	Sequence 10, Appl
364	511	9.0	880	2	US-08-170-558-10	Sequence 10, Appl
365	511	9.0	880	2	US-08-447-314-10	Sequence 10, Appl
366	511	9.0	880	2	US-08-445-461-10	Sequence 10, Appl
367	511	9.0	880	2	US-09-223-490-10	Sequence 10, Appl
368	509.5	9.0	293	1	US-08-701-191A-26	Sequence 26, Appl
369	509.5	9.0	293	2	US-09-664-526-26	Sequence 26, Appl
370	508	9.0	825	1	US-07-912-952-2	Sequence 2, Appli
371	508	9.0	874	1	US-08-456-647B-6	Sequence 6, Appli
372	508	9.0	874	1	US-08-237-401A-6	Sequence 6, Appli
373	506.5	9.0	890	1	US-08-445-640-2	Sequence 2, Appli
374	506.5	9.0	890	2	US-08-170-558-2	Sequence 2, Appli
375	506.5	9.0	890	2	US-08-447-314-2	Sequence 2, Appli
376	506.5	9.0	890	2	US-08-445-461-2	Sequence 2, Appli
377	506.5	9.0	890	2	US-09-223-490-2	Sequence 2, Appli
378	506.5	9.0	911	1	US-08-286-305A-1	Sequence 1, Appli
379	506.5	9.0	911	1	US-08-441-104A-1	Sequence 1, Appli
380	506.5	9.0	911	1	US-08-440-816A-1	Sequence 1, Appli
381	506.5	9.0	911	2	US-09-417-381A-1	Sequence 1, Appli
382	505	8.9	823	2	US-09-886-319A-63	Sequence 63, Appl
383	503.5	8.9	991	1	US-08-449-645A-13	Sequence 13, Appl
384	503.5	8.9	991	1	US-08-702-367A-13	Sequence 13, Appl
385	503.5	8.9	991	4	PCT-US95-04681-13	Sequence 13, Appl
386	502	8.9	728	1	US-07-912-952-4	Sequence 4, Appli
387	500	8.8	1070	2	US-09-961-403-3	Sequence 3, Appli
388	498.5	8.8	967	1	US-08-449-645A-30	Sequence 30, Appl
389	498.5	8.8	967	1	US-08-702-367A-30	Sequence 30, Appl
390	498	8.8	888	1	US-08-445-640-35	Sequence 35, Appl
391	498	8.8	888	2	US-08-170-558-35	Sequence 35, Appl
392	498	8.8	888	2	US-08-447-314-35	Sequence 35, Appl

393	498	8.8	888	2	US-08-445-461-35	Sequence 35, Appl
394	498	8.8	888	2	US-09-223-490-35	Sequence 35, Appl
395	497	8.8	975	2	US-09-751-389-8	Sequence 8, Appli
396	496.5	8.8	1005	1	US-08-469-537A-103	Sequence 103, App
397	496	8.8	1382	1	US-08-737-715-2	Sequence 2, Appli
398	496	8.8	1382	2	US-09-457-040B-7	Sequence 7, Appli
399	495	8.8	332	1	US-08-469-537A-75	Sequence 75, Appl
400	494	8.7	790	1	US-08-359-705B-9	Sequence 9, Appli
401	494	8.7	790	1	US-08-286-846A-9	Sequence 9, Appli
402	494	8.7	790	1	US-08-457-880A-9	Sequence 9, Appli
403	494	8.7	790	2	US-08-444-622A-9	Sequence 9, Appli
404	494	8.7	790	2	US-08-942-562-9	Sequence 9, Appli
405	494	8.7	790	2	US-09-156-923-9	Sequence 9, Appli
406	494	8.7	814	1	US-08-286-305A-3	Sequence 3, Appli
407	494	8.7	814	1	US-08-441-104A-3	Sequence 3, Appli
408	494	8.7	814	1	US-08-440-816A-3	Sequence 3, Appli
409	494	8.7	814	2	US-09-417-381A-3	Sequence 3, Appli
410	493.5	8.7	274	1	US-08-469-537A-55	Sequence 55, Appl
411	492	8.7	928	1	US-08-442-248-2	Sequence 2, Appli
412	492	8.7	928	1	US-08-440-815-2	Sequence 2, Appli
413	492	8.7	928	2	US-08-486-449-2	Sequence 2, Appli
414	492	8.7	928	2	US-08-578-684-2	Sequence 2, Appli
415	491	8.7	953	2	US-09-751-389-7	Sequence 7, Appli
416	490.5	8.7	572	1	US-08-160-861-3	Sequence 3, Appli
417	490.5	8.7	643	1	US-08-471-570-6	Sequence 6, Appli
418	490.5	8.7	1620	1	US-08-542-363-2	Sequence 2, Appli
419	490.5	8.7	1620	2	US-09-100-089-2	Sequence 2, Appli
420	490.5	8.7	1620	2	US-09-670-827-2	Sequence 2, Appli
421	490.5	8.7	1620	2	US-09-827-949-2	Sequence 2, Appli
422	489	8.7	1130	2	US-09-538-092-834	Sequence 834, App
423	489	8.7	1148	2	US-09-949-016-6798	Sequence 6798, Ap
424	489	8.7	1169	2	US-09-949-016-9630	Sequence 9630, Ap
425	485	8.6	275	1	US-07-857-224B-71	Sequence 71, Appl
426	483.5	8.6	275	1	US-08-701-191A-36	Sequence 36, Appl
427	483.5	8.6	275	2	US-09-664-526-36	Sequence 36, Appl
428	481.5	8.5	403	2	US-08-485-393-4	Sequence 4, Appli
429	480	8.5	374	2	US-08-857-076-108	Sequence 108, App
430	480	8.5	374	2	US-09-205-658-108	Sequence 108, App
431	474	8.4	983	1	US-08-167-919A-10	Sequence 10, Appl
432	474	8.4	983	2	US-08-715-106-10	Sequence 10, Appl
433	474	8.4	983	2	US-09-442-649-10	Sequence 10, Appl
434	473	8.4	822	2	US-09-538-092-866	Sequence 866, App
435	472.5	8.4	276	1	US-07-857-224B-72	Sequence 72, Appl
436	472.5	8.4	588	1	US-08-391-615-5	Sequence 5, Appli
437	472	8.4	525	1	US-08-160-861-4	Sequence 4, Appli
438	472	8.4	680	1	US-08-542-363-4	Sequence 4, Appli
439	472	8.4	680	2	US-09-100-089-4	Sequence 4, Appli
440	472	8.4	680	2	US-09-670-827-4	Sequence 4, Appli
441	472	8.4	680	2	US-09-827-949-4	Sequence 4, Appli
442	471.5	8.3	512	2	US-08-426-509A-16	Sequence 16, Appl
443	471.5	8.3	512	2	US-08-232-545-16	Sequence 16, Appl
444	471.5	8.3	512	2	US-09-977-261-16	Sequence 16, Appl
445	471.5	8.3	512	4	PCT-US95-05008-16	Sequence 16, Appl
446	471	8.3	641	2	US-09-167-206-4	Sequence 4, Appli
447	471	8.3	983	1	US-08-449-645A-21	Sequence 21, Appl
448	471	8.3	983	1	US-08-702-367A-21	Sequence 21, Appl
449	471	8.3	983	4	PCT-US95-04681-21	Sequence 21, Appl
450	470	8.3	505	2	US-08-426-509A-17	Sequence 17, Appl
451	470	8.3	505	2	US-08-232-545-17	Sequence 17, Appl
452	470	8.3	505	2	US-09-977-261-17	Sequence 17, Appl
453	470	8.3	505	4	PCT-US95-05008-17	Sequence 17, Appl
454	470	8.3	511	2	US-08-232-545-6	Sequence 6, Appli
455	470	8.3	511	4	PCT-US95-05008-6	Sequence 6, Appli
456	470	8.3	573	2	US-09-949-016-10415	Sequence 10415, A
457	470	8.3	983	2	US-09-771-161A-227	Sequence 227, App
458	469	8.3	306	1	US-08-701-191A-12	Sequence 12, Appl
459	469	8.3	306	2	US-09-664-526-12	Sequence 12, Appl
460	468.5	8.3	508	2	US-09-862-154-1	Sequence 1, Appli
461	468.5	8.3	509	2	US-09-039-555B-17	Sequence 17, Appl
462	468.5	8.3	509	2	US-08-426-509A-18	Sequence 18, Appl
463	468.5	8.3	509	2	US-09-457-040B-8	Sequence 8, Appli
464	468.5	8.3	509	2	US-08-232-545-18	Sequence 18, Appl
465	468.5	8.3	509	2	US-09-977-261-18	Sequence 18, Appl
466	468.5	8.3	509	4	PCT-US95-05008-18	Sequence 18, Appl
467	468	8.3	297	2	US-09-390-326-8	Sequence 8, Appli
468	468	8.3	297	2	US-09-939-833-8	Sequence 8, Appli
469	468	8.3	297	2	US-09-506-906-8	Sequence 8, Appli
470	468	8.3	297	2	US-09-939-832-8	Sequence 8, Appli
471	468	8.3	297	2	US-09-939-754-8	Sequence 8, Appli
472	468	8.3	306	2	US-09-457-040B-40	Sequence 40, Appl
473	467	8.3	822	2	US-09-817-180-4	Sequence 4, Appli
474	467	8.3	822	2	US-10-003-295-4	Sequence 4, Appli
475	466.5	8.3	340	1	US-08-469-537A-76	Sequence 76, Appl
476	466.5	8.3	999	1	US-08-252-626A-2	Sequence 2, Appli
477	466.5	8.3	999	2	US-09-949-016-6718	Sequence 6718, Ap
478	466	8.2	261	1	US-07-857-224B-60	Sequence 60, Appl
479	466	8.2	496	1	US-09-006-675-2	Sequence 2, Appli
480	466	8.2	496	2	US-09-228-603A-2	Sequence 2, Appli
481	465.5	8.2	260	1	US-09-006-675-8	Sequence 8, Appli
482	465.5	8.2	260	2	US-09-228-603A-8	Sequence 8, Appli
483	464.5	8.2	505	2	US-08-492-723-2	Sequence 2, Appli
484	464	8.2	506	2	US-08-426-509A-6	Sequence 6, Appli
485	464	8.2	513	2	US-09-949-016-11517	Sequence 11517, A
486	463.5	8.2	675	2	US-08-426-509A-4	Sequence 4, Appli
487	463.5	8.2	675	2	US-08-232-545-4	Sequence 4, Appli
488	463.5	8.2	675	2	US-09-977-261-4	Sequence 4, Appli
489	463.5	8.2	675	4	PCT-US95-05008-4	Sequence 4, Appli
490	463	8.2	290	1	US-08-701-191A-15	Sequence 15, Appl
491	462	8.2	504	2	US-09-538-092-1170	Sequence 1170, Ap
492	462	8.2	505	2	US-09-949-016-6117	Sequence 6117, Ap
493	461.5	8.2	505	1	US-08-222-616-20	Sequence 20, Appl
494	461.5	8.2	505	2	US-08-446-648-20	Sequence 20, Appl
495	461.5	8.2	505	2	US-09-982-610-20	Sequence 20, Appl
496	461.5	8.2	505	2	US-09-977-261-6	Sequence 6, Appli
497	461.5	8.2	505	4	PCT-US95-04228-20	Sequence 20, Appl
498	461	8.2	306	2	US-09-457-040B-39	Sequence 39, Appl
499	460.5	8.1	877	1	US-08-673-789-2	Sequence 2, Appli
500	460	8.1	261	1	US-07-857-224B-59	Sequence 59, Appl

ALIGNMENTS

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RESULT 1
US-08-168-917-4
; Sequence 4, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-168-917-4

  Query Match           100.0%;  Score 5652;  DB 1;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 2
US-08-460-510-4
; Sequence 4, Application US/08460510
; Patent No. 5872218
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,510
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-460-510-4

  Query Match           100.0%;  Score 5652;  DB 1;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

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Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 3
US-08-460-490-4
; Sequence 4, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Steuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,490
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-490-4

Query Match 100.0%; Score 5652; DB 1; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 4
US-08-462-728-2
; Sequence 2, Application US/08462728
; Patent No. 6043211
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,728
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-728-2

  Query Match             100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 5
US-08-461-917-2
; Sequence 2, Application US/08461917
; Patent No. 6372438
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,917
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-917-2

  Query Match            100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 6
US-08-464-436-2
; Sequence 2, Application US/08464436
; Patent No. 6514723
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,436
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-436-2

  Query Match           100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 7
US-08-464-436-2
; Sequence 2, Application US/08464436
; Patent No. 6642022
;   GENERAL INFORMATION:
;        APPLICANT: WILLIAMS, Lewis T.
;                   ESCOBEDO, Jaime A.
;        TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew
;             STREET: One Market, Steuart Street Tower, 20th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,436
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/309,322
;             FILING DATE: 10-FEB-1989
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dow, Karen B.
;             REGISTRATION NUMBER: 29,684
;             REFERENCE/DOCKET NUMBER: 2307K-267-2-3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1090 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-464-436-2

  Query Match             100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 8
US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. 6660488
; GENERAL INFORMATION:
;  APPLICANT: Matsui, Toshimitsu
;  APPLICANT:  Aaronson, Stuart A.
;  APPLICANT:  Pierce, Jacalyn H.
;  TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
;  FILE REFERENCE: 14014.0266U2
;  CURRENT APPLICATION NUMBER: US/09/769,987
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 08/460,656
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: US 08/439,095
;  PRIOR FILING DATE: 1995-05-11
;  PRIOR APPLICATION NUMBER: US 07/915,884
;  PRIOR FILING DATE: 1992-07-20
;  PRIOR APPLICATION NUMBER: US 07/308,282
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;  PRIOR FILING DATE: 1989-02-09
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. 6660488e =
;   OTHER INFORMATION: synthetic construct
US-09-769-987-2

  Query Match           100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 9
US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-2

  Query Match           100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 10
US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-919-497-90

  Query Match   100.0%; Score 5652; DB 2; Length 1089;
  Best Local Similarity 100.0%; Pred. No. 0;

  Matches 1089; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 11
US-09-949-016-6703
; Sequence 6703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6703
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6703

  Query Match             100.0%;  Score 5652;  DB 2;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 12
PCT-US92-00730-4
; Sequence 4, Application PC/TUS9200730
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00730
;      FILING DATE:  19920128
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-00730-4

  Query Match           100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 13
PCT-US92-00862-4
; Sequence 4, Application PC/TUS9200862
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Lewis T.
;    APPLICANT:  Escobedo, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00862
;      FILING DATE:  19920131
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,141
;      FILING DATE:  02-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  2307U-267-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-00862-4

  Query Match           100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
```

```
                                                                                                                    
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
                                                                                                                    
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
                                                                                                                    
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
                                                                                                                    
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
                                                                                                                    
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
                                                                                                                    
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
                                                                                                                    
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
                                                                                                                    
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
                                                                                                                    
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
                                                                                                                    
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
                                                                                                                    
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
                                                                                                                    
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
                                                                                                                    
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
                                                                                                                    
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
                                                                                                                    
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
                                                                                                                    
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
                                                                                                                    
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
                                                                                                                    
Db       1081 SDLVEDSFL 1089

RESULT 14
```

```
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-10

  Query Match             99.9%;  Score 5649;  DB 2;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
                                                                                                                    
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
                                                                                                                    
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
                                                                                                                    
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
                                                                                                                    
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
                                                                                                                    
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
                                                                                                                    
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
                                                                                                                    
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
                                                                                                                    
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
                                                                                                                    
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
                                                                                                                    
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
                                                                                                                    
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
                                                                                                                    
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
```

```
Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPMKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

```
RESULT 15
US-08-180-195-36
; Sequence 36, Application US/08180195
; Patent No. 5567584
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/180,195
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,510
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-180-195-36

  Query Match             99.9%;  Score 5648;  DB 1;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
```

```
Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 16
US-08-477-329-36
; Sequence 36, Application US/08477329
; Patent No. 5750375
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,329
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-329-36

  Query Match             99.9%;  Score 5648;  DB 1;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 17
US-08-475-458-36
; Sequence 36, Application US/08475458
; Patent No. 5843725
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
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;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,458
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446D5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-475-458-36

  Query Match             99.9%;  Score 5648;  DB 1;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 18
US-08-980-400-36
; Sequence 36, Application US/08980400
; Patent No. 6018026
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/980,400
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,329
;      FILING DATE:  07-JUN-1995
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```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-980-400-36

  Query Match           99.9%;  Score 5648;  DB 2;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 19
US-09-583-459A-36
; Sequence 36, Application US/09583459A
; Patent No. 6291212
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,459A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-09-583-459A-36

Query Match 99.9%; Score 5648; DB 2; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

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Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 20
US-09-583-210-36
; Sequence 36, Application US/09583210
; Patent No. 6291646
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,210
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1089 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-583-210-36

Query Match 99.9%; Score 5648; DB 2; Length 1089;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 21
US-09-583-449A-36
; Sequence 36, Application US/09583449A
; Patent No. 6300099

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;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,449A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-583-449A-36

  Query Match             99.9%;  Score 5648;  DB 2;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 22
US-09-435-059-36
; Sequence 36, Application US/09435059
; Patent No. 6323323
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne.R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/435,059
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/477,329
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1089 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-435-059-36

  Query Match           99.9%;  Score 5648;  DB 2;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089

Db       1081 SDLVEDSFL 1089


RESULT 23
US-09-866-510-4
; Sequence 4, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-4

  Query Match            99.9%;  Score 5648;  DB 2;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWKFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089

Db       1081 SDLVEDSFL 1089


RESULT 24
US-09-866-510-8
; Sequence 8, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
```

```
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-8

  Query Match           99.9%;  Score 5647;  DB 2;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRNLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 25
US-09-866-510-6
; Sequence 6, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-6

  Query Match           99.9%;  Score 5646;  DB 2;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACMKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 26
US-09-961-403-4
; Sequence 4, Application US/09961403
; Patent No. 6780594
; GENERAL INFORMATION:
;  APPLICANT: HE-STUMPP, HOLGER
;  APPLICANT:  HAENDLER, BERNARD
;  APPLICANT:  KRAETZSCHMAR, JOERN
;  APPLICANT:  KREFT, BERTHOLT
;  APPLICANT:  WINTERHAGER, ELKE
;  APPLICANT:  REGIDOR, PEDRO
;  APPLICANT:  SCOTTI, SIMONE
;  TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
;  FILE REFERENCE: SCH-1789
;  CURRENT APPLICATION NUMBER: US/09/961,403
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4
;   LENGTH: 1088
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-961-403-4

  Query Match           99.7%;  Score 5636.5;  DB 2;  Length 1088;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARM-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1019

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1079

Qy       1081 SDLVEDSFL 1089
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Db       1080 SDLVEDSFL 1088
```

RESULT 27
US-09-949-016-7568
; Sequence 7568, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7568
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7568

Query Match 63.0%; Score 3560.5; DB 2; Length 762;
Best Local Similarity 80.2%; Pred. No. 1.8e-239;
Matches 715; Conservative 6; Mismatches 10; Indels 161; Gaps 4;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||                : :|||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTALF----------------LSRCNNETSWTILANNVSNIITEIHSRD 463

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 523

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 583

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              |||||||||||||||||||||||||||||||
Db        584 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLK---------------------------- 613

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 ------------------------------------------------------------ 613

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
                                      :|||||||||||||||||||||||||||   |
Db        614 -------------------------QRKEVSKYSDIQRSLYDRPASYKKKSMLGKSV-- 645

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
                                  :|:         :   |||||||||||||||||||||||||
Db        646 -----------------YTH---------SGCWCVHRDLAARNVLLAQGKIVKICDFGLA 679

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLG 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLG 731
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RESULT 28
US-09-866-510-12
; Sequence 12, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-12

Query Match 53.9%; Score 3046; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 8.6e-204;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
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RESULT 29
US-08-180-195-2
; Sequence 2, Application US/08180195
; Patent No. 5567584
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/180,195
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,510
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-180-195-2

  Query Match             41.7%;  Score 2354.5;  DB 1;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | ||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944
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```
Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              |  ||| |  |  ::| ||   ||| |::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 30
US-08-477-329-2
; Sequence 2, Application US/08477329
; Patent No. 5750375
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,329
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-329-2

  Query Match             41.7%;  Score 2354.5;  DB 1;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |    | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :       |:   ||  :   |  |||||  : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: ||||:|:::|::|||||||:||||:| ||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       | :  :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 31
US-08-475-458-2
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; Sequence 2, Application US/08475458
; Patent No. 5843725
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,458
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446D5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-475-458-2

  Query Match             41.7%;  Score 2354.5;  DB 1;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |    ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
                : :: | : |:| | |:: :      |:   ||  :   |  |||||  : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| : | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
                :|:| : |  | | |||||   | | |:| |  |:|:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                  |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  ||||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :             :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 32
US-08-980-400-2
; Sequence 2, Application US/08980400
; Patent No. 6018026
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

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;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/980,400
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,329
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-980-400-2

  Query Match             41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | ||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: ||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| ||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :|: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :          ||                  |: |||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              | | :   ::|||       :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 33
US-09-583-459A-2
; Sequence 2, Application US/09583459A
; Patent No. 6291212
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,459A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
```

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;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-583-459A-2

  Query Match             41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||||  : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | ||| |:| |:| |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  ||||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                    |: |||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 34
US-09-583-210-2
; Sequence 2, Application US/09583210
; Patent No. 6291646
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,210
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
```

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-583-210-2

  Query Match             41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |    ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :       |:   ||  :   |  |||||  : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:|  ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
```

```
              | || |  |  ::| ||   ||| |::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                   |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 35
US-09-583-449A-2
; Sequence 2, Application US/09583449A
; Patent No. 6300099
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,449A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-583-449A-2

  Query Match             41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
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```
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|     :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||       : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:|||||||  : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :         ||                |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106
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RESULT 36
US-09-435-059-2
; Sequence 2, Application US/09435059
; Patent No. 6323323
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,329
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-435-059-2

Query Match 41.7%; Score 2354.5; DB 2; Length 1106;
Best Local Similarity 44.1%; Pred. No. 3e-155;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;

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Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|     :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
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Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984

Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 37
US-09-866-510-22
; Sequence 22, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-22

  Query Match           41.7%;  Score 2354.5;  DB 2;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 3e-155;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824
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Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPMKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
               :       ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 38
US-08-168-917-2
; Sequence 2, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-168-917-2
```

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  Query Match           41.6%;  Score 2351.5;  DB 1;  Length 1106;
  Best Local Similarity  44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :       |:   || :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||       : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                  |:  ::|||  :| :| | : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| |||||:||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:||||||||| ||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |        |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              ||||||||: :||:|||||||||||||| ||||:||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004
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Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106


RESULT 39
US-08-460-510-2
; Sequence 2, Application US/08460510
; Patent No. 5872218
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,510
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-460-510-2

  Query Match             41.6%;  Score 2351.5;  DB 1;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106


RESULT 40
US-08-460-490-2
; Sequence 2, Application US/08460490
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; Patent No. 5891652
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,490
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-460-490-2

  Query Match             41.6%;  Score 2351.5;  DB 1;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                 | : | :|  ||:                  |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|:|||||||:||||:| ||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:||||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||| ||||:||||||||:||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||||  : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :             :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :         ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 41
US-08-462-728-4
; Sequence 4, Application US/08462728
; Patent No. 6043211
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/462,728
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/309,322
;       FILING DATE:  10-FEB-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/151,414
;       FILING DATE:  02-FEB-1988
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Dow, Karen B.
;       REGISTRATION NUMBER:  29,684
;       REFERENCE/DOCKET NUMBER:  2307K-267-2-2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/326-2400
;       TELEFAX:  415/326-2422
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH: 1106 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-462-728-4

  Query Match             41.6%;  Score 2351.5;  DB 2;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|  :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |     |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |    ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   || :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | ||||   | | |:| |  |:|:|:|  |    |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::||| :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      | :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :          ||                    |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||       :: :||          :|   ::: : | |  :      ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 42
US-08-461-917-4
; Sequence 4, Application US/08461917
; Patent No. 6372438
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,917
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
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;      REFERENCE/DOCKET NUMBER:  2307K-267-2-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-917-4

  Query Match           41.6%;  Score 2351.5;  DB 2;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :    |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::  ||       : | || |:| |:| |  ::|||| : |:|||    :|:|  ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :|: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||| ||||:||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :            :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :       ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 43
US-08-464-436-4
; Sequence 4, Application US/08464436
; Patent No. 6514723
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,436
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 1106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-436-4

  Query Match           41.6%;  Score 2351.5;  DB 2;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;
```

```
Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYVALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |  |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| | :|||    :|:|  ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||   | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :       ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
                |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
                |||
Db       1104 SFL 1106


RESULT 44
US-08-464-436-4
; Sequence 4, Application US/08464436
; Patent No. 6642022
;   GENERAL INFORMATION:
;        APPLICANT: WILLIAMS, Lewis T.
;                   ESCOBEDO, Jaime A.
;        TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew
;             STREET: One Market, Steuart Street Tower, 20th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,436
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/309,322
;             FILING DATE: 10-FEB-1989
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dow, Karen B.
;             REGISTRATION NUMBER: 29,684
;             REFERENCE/DOCKET NUMBER: 2307K-267-2-3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1107 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-464-436-4

  Query Match             41.6%;  Score 2351.5;  DB 2;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYVALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
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Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984

Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 45
PCT-US92-00730-2
; Sequence 2, Application PC/TUS9200730
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00730
;      FILING DATE:  19920128
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-00730-2

  Query Match           41.6%;  Score 2351.5;  DB 4;  Length 1106;
  Best Local Similarity  44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
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Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                  | : | :|  ||:                  |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :             :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 46
PCT-US92-00862-2
; Sequence 2, Application PC/TUS9200862
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Lewis T.
;    APPLICANT:  Escobedo, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00862
;      FILING DATE:  19920131
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,141
;      FILING DATE:  02-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  2307U-267-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-00862-2

  Query Match             41.6%;  Score 2351.5;  DB 4;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 4.9e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENLELEGRHIYIYV 121
               |:|   ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|     :  : : :     |||| |||:  |||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |     |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :   :  |     | :| | ::||| | |    ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::  ||      : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                  | : | :|  ||:                  |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
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Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |    |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| |||:|||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||||  : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  | ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: |||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 47
US-09-866-510-16
; Sequence 16, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-16

  Query Match             41.6%;  Score 2350.5;  DB 2;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 5.7e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   |||||  : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||  | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| |: ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWKLPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| |||:|||||||||:|||||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||||  : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  | ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 48
US-09-866-510-20
; Sequence 20, Application US/09866510
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; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-20

  Query Match           41.6%;  Score 2349.5;  DB 2;  Length 1106;
  Best Local Similarity  44.0%;  Pred. No. 6.7e-155;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |     |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :       |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |   | | |||||    | | |:| |   |:|:|:|   |    |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| |||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| ||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
                |   | ||   | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |:|||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RNLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:|||||||  : ::  ||| || |||||:|  ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :          ||                |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              | | :  ::|||       :: :||           :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 49
US-09-866-510-18
; Sequence 18, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-18

  Query Match           41.6%;  Score 2348.5;  DB 2;  Length 1106;
  Best Local Similarity  44.0%;  Pred. No. 7.9e-155;
  Matches  503;  Conservative  195;  Mismatches  342;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|     |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|    ::      :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |     |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
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Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACMKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984

Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 50
US-09-866-510-14
; Sequence 14, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 1090
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-14

  Query Match             41.5%;  Score 2347;  DB 2;  Length 1090;
  Best Local Similarity   44.8%;  Pred. No. 9.9e-155;
  Matches  496;  Conservative  189;  Mismatches  331;  Indels   90;  Gaps   22;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

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Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
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Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR----------VDS 984
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Qy       1045 SEESAIETGSSSSTF-----IKREDE 1065
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Search completed: May 15, 2006, 08:54:05
Job time : 50 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 15, 2006, 08:59:38 ; Search time 103 Seconds
(without alignments)
4417.632 Million cell updates/sec

Title: US-08-439-095-1
Perfect score: 5652
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5652	100.0	1089	3	US-09-919-497-90	Sequence 90, Appl
3	5652	100.0	1089	3	US-09-866-510-2	Sequence 2, Appli
4	5652	100.0	1089	4	US-10-027-400-2	Sequence 2, Appli
5	5652	100.0	1089	4	US-10-394-322A-50	Sequence 50, Appl
6	5652	100.0	1089	4	US-10-367-639-35	Sequence 35, Appl
7	5652	100.0	1089	4	US-10-322-696-168	Sequence 168, App
8	5652	100.0	1089	4	US-10-741-601-439	Sequence 439, App
9	5652	100.0	1089	5	US-10-723-860-650	Sequence 650, App
10	5652	100.0	1089	5	US-10-741-600-1304	Sequence 1304, Ap
11	5652	100.0	1089	5	US-10-926-806-14	Sequence 14, Appl
12	5652	100.0	1089	5	US-10-700-249-2	Sequence 2, Appli
13	5652	100.0	1089	5	US-10-756-149-4888	Sequence 4888, Ap
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16	5648	99.9	1089	3	US-09-955-363-36	Sequence 36, Appl
17	5647	99.9	1089	3	US-09-866-510-8	Sequence 8, Appli
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20	5232	92.6	1096	4	US-10-322-696-165	Sequence 165, App
21	3046	53.9	589	3	US-09-866-510-12	Sequence 12, Appl
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24	2676.5	47.4	811	4	US-10-637-356-4	Sequence 4, Appli
25	2676.5	47.4	826	4	US-10-637-356-3	Sequence 3, Appli
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83	1287	22.8	1338	4	US-10-211-462-215	Sequence 215, App
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86	1287	22.8	1338	5	US-10-926-806-8	Sequence 8, Appli
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113	1206.5	21.3	1354	4	US-10-669-176-30	Sequence 30, Appl
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124	1166	20.6	993	5	US-10-741-600-1656	Sequence 1656, Ap
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158	1160.5	20.5	1298	5	US-10-473-127-970	Sequence 970, App
159	1160.5	20.5	1298	5	US-10-781-581-222	Sequence 222, App
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163	1152.5	20.4	992	3	US-09-872-136-2	Sequence 2, Appli
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177	1147	20.3	986	3	US-09-942-711-18	Sequence 18, Appl
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187	1105	19.6	218	5	US-10-741-600-1305	Sequence 1305, Ap
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207	859.5	15.2	822	5	US-10-723-860-475	Sequence 475, App
208	859.5	15.2	822	5	US-10-285-405-3	Sequence 3, Appli
209	859.5	15.2	822	5	US-10-287-436A-508	Sequence 508, App
210	859.5	15.2	822	5	US-10-287-436A-511	Sequence 511, App
211	859.5	15.2	822	5	US-10-287-436A-1201	Sequence 1201, Ap
212	859.5	15.2	822	5	US-10-287-436A-1202	Sequence 1202, Ap
213	857.5	15.2	759	5	US-10-941-486-9	Sequence 9, Appli
214	857.5	15.2	820	6	US-11-037-713-16	Sequence 16, Appl
215	853.5	15.1	561	3	US-09-866-510-24	Sequence 24, Appl
216	853	15.1	316	5	US-10-824-982-3	Sequence 3, Appli
217	852.5	15.1	820	4	US-10-302-812-42	Sequence 42, Appl
218	852.5	15.1	820	5	US-10-482-029-164	Sequence 164, App
219	852.5	15.1	822	3	US-09-757-415A-2	Sequence 2, Appli
220	849.5	15.0	317	3	US-09-939-754-5	Sequence 5, Appli
221	849.5	15.0	317	3	US-09-939-832-5	Sequence 5, Appli
222	849.5	15.0	317	3	US-09-939-833-5	Sequence 5, Appli
223	847.5	15.0	294	4	US-10-763-418-17	Sequence 17, Appl
224	845	15.0	316	5	US-10-941-635-26	Sequence 26, Appl
225	845	15.0	316	5	US-10-965-313-10	Sequence 10, Appl
226	845	15.0	316	6	US-11-092-809-10	Sequence 10, Appl
227	845	15.0	316	6	US-11-092-863-10	Sequence 10, Appl
228	844	14.9	299	4	US-10-334-143-202	Sequence 202, App
229	844	14.9	764	3	US-09-925-302-714	Sequence 714, App
230	844	14.9	764	3	US-09-925-302-714	Sequence 714, App
231	842	14.9	824	4	US-10-307-817-4	Sequence 4, Appli
232	833.5	14.7	735	4	US-10-307-817-6	Sequence 6, Appli
233	833.5	14.7	821	4	US-10-394-322A-27	Sequence 27, Appl
234	833.5	14.7	821	4	US-10-302-812-44	Sequence 44, Appl
235	833.5	14.7	821	5	US-10-941-486-8	Sequence 8, Appli
236	833.5	14.7	821	6	US-11-019-829-99	Sequence 99, Appl
237	833	14.7	822	6	US-11-019-829-103	Sequence 103, App
238	831.5	14.7	768	6	US-11-019-829-104	Sequence 104, App
239	831	14.7	788	6	US-11-019-829-108	Sequence 108, App
240	828	14.6	822	4	US-10-648-593-254	Sequence 254, App
241	828	14.6	822	6	US-11-019-829-100	Sequence 100, App
242	826	14.6	769	6	US-11-019-829-105	Sequence 105, App
243	821.5	14.5	291	4	US-10-377-268-28	Sequence 28, Appl
244	821.5	14.5	291	5	US-10-789-818-16	Sequence 16, Appl
245	807	14.3	806	4	US-10-394-322A-28	Sequence 28, Appl
246	807	14.3	806	4	US-10-403-161-58	Sequence 58, Appl

247	807	14.3	806	5	US-10-696-639-42	Sequence 42, Appl
248	807	14.3	806	5	US-10-941-486-7	Sequence 7, Appli
249	807	14.3	806	5	US-10-734-661A-1	Sequence 1, Appli
250	804	14.2	732	6	US-11-019-829-109	Sequence 109, App
251	799.5	14.1	731	6	US-11-019-829-106	Sequence 106, App
252	798	14.1	808	4	US-10-403-161-60	Sequence 60, Appl
253	797.5	14.1	682	5	US-10-868-577A-21	Sequence 21, Appl
254	791.5	14.0	705	6	US-11-019-829-101	Sequence 101, App
255	786	13.9	705	6	US-11-019-829-111	Sequence 111, App
256	785	13.9	707	6	US-11-019-829-110	Sequence 110, App
257	766.5	13.6	1052	6	US-11-097-143-41298	Sequence 41298, A
258	765.5	13.5	891	3	US-09-862-027-25	Sequence 25, Appl
259	765.5	13.5	891	5	US-10-989-228-25	Sequence 25, Appl
260	763	13.5	694	4	US-10-302-812-46	Sequence 46, Appl
261	761.5	13.5	310	4	US-10-664-421-27	Sequence 27, Appl
262	761.5	13.5	310	5	US-10-941-635-27	Sequence 27, Appl
263	761.5	13.5	310	5	US-10-965-313-9	Sequence 9, Appli
264	761.5	13.5	310	6	US-11-092-809-9	Sequence 9, Appli
265	761.5	13.5	310	6	US-11-092-863-9	Sequence 9, Appli
266	761.5	13.5	315	4	US-10-763-418-2	Sequence 2, Appli
267	761.5	13.5	351	4	US-10-763-418-3	Sequence 3, Appli
268	760	13.4	1072	5	US-10-473-127-659	Sequence 659, App
269	760	13.4	1089	5	US-10-473-127-664	Sequence 664, App
270	760	13.4	1106	5	US-10-473-127-658	Sequence 658, App
271	760	13.4	1114	4	US-10-241-220-74	Sequence 74, Appl
272	760	13.4	1114	4	US-10-415-011-19	Sequence 19, Appl
273	760	13.4	1114	5	US-10-872-972-74	Sequence 74, Appl
274	760	13.4	1114	5	US-10-473-127-660	Sequence 660, App
275	760	13.4	1114	5	US-10-473-127-661	Sequence 661, App
276	760	13.4	1114	5	US-10-473-127-662	Sequence 662, App
277	760	13.4	1114	5	US-10-872-991-74	Sequence 74, Appl
278	760	13.4	1114	5	US-10-756-149-4690	Sequence 4690, Ap
279	759.5	13.4	299	4	US-10-334-143-203	Sequence 203, App
280	758.5	13.4	650	4	US-10-193-477-119	Sequence 119, App
281	758.5	13.4	650	4	US-10-403-847-116	Sequence 116, App
282	757.5	13.4	310	3	US-09-939-754-7	Sequence 7, Appli
283	757.5	13.4	310	3	US-09-939-832-7	Sequence 7, Appli
284	757.5	13.4	310	3	US-09-939-833-7	Sequence 7, Appli
285	757.5	13.4	310	4	US-10-763-418-1	Sequence 1, Appli
286	757.5	13.4	310	4	US-10-763-418-6	Sequence 6, Appli
287	757.5	13.4	379	4	US-10-664-421-45	Sequence 45, Appl
288	757.5	13.4	379	5	US-10-941-635-45	Sequence 45, Appl
289	756	13.4	1072	5	US-10-473-127-654	Sequence 654, App
290	756	13.4	1072	5	US-10-473-127-663	Sequence 663, App
291	755.5	13.4	301	4	US-10-470-957-21	Sequence 21, Appl
292	753.5	13.3	299	4	US-10-763-418-13	Sequence 13, Appl
293	753.5	13.3	300	4	US-10-763-418-31	Sequence 31, Appl
294	751.5	13.3	1091	5	US-10-473-127-656	Sequence 656, App
295	751.5	13.3	1091	5	US-10-473-127-665	Sequence 665, App
296	751	13.3	860	5	US-10-473-127-655	Sequence 655, App
297	748	13.2	802	4	US-10-302-812-48	Sequence 48, Appl
298	744	13.2	802	3	US-09-758-386-3	Sequence 3, Appli
299	744	13.2	802	4	US-10-011-548-33	Sequence 33, Appl
300	744	13.2	802	4	US-10-354-358-44	Sequence 44, Appl
301	744	13.2	802	4	US-10-116-275-245	Sequence 245, App
302	744	13.2	802	4	US-10-394-322A-29	Sequence 29, Appl
303	744	13.2	802	5	US-10-941-486-6	Sequence 6, Appli
304	738.5	13.1	394	4	US-10-087-192-1131	Sequence 1131, Ap
305	731.5	12.9	310	4	US-10-763-418-7	Sequence 7, Appli
306	727.5	12.9	290	4	US-10-377-268-29	Sequence 29, Appl
307	727.5	12.9	290	5	US-10-789-818-17	Sequence 17, Appl
308	707	12.5	806	5	US-10-450-763-51719	Sequence 51719, A
309	705.5	12.5	309	4	US-10-763-418-9	Sequence 9, Appli
310	705.5	12.5	789	5	US-10-659-004-2	Sequence 2, Appli
311	705.5	12.5	789	5	US-10-659-004-12	Sequence 12, Appl
312	705.5	12.5	789	5	US-10-659-004-14	Sequence 14, Appl
313	705.5	12.5	789	5	US-10-659-004-20	Sequence 20, Appl
314	705.5	12.5	789	5	US-10-659-004-24	Sequence 24, Appl
315	705.5	12.5	789	5	US-10-659-004-28	Sequence 28, Appl
316	705.5	12.5	789	5	US-10-659-004-32	Sequence 32, Appl
317	705.5	12.5	789	5	US-10-659-004-38	Sequence 38, Appl
318	705	12.5	384	4	US-10-664-421-67	Sequence 67, Appl
319	705	12.5	384	5	US-10-941-635-67	Sequence 67, Appl
320	705	12.5	789	5	US-10-659-004-30	Sequence 30, Appl
321	704.5	12.5	789	5	US-10-659-004-4	Sequence 4, Appli
322	704.5	12.5	789	5	US-10-659-004-6	Sequence 6, Appli
323	704.5	12.5	789	5	US-10-659-004-22	Sequence 22, Appl
324	704.5	12.5	789	5	US-10-659-004-34	Sequence 34, Appl
325	703.5	12.4	789	5	US-10-659-004-36	Sequence 36, Appl
326	702.5	12.4	310	4	US-10-763-418-8	Sequence 8, Appli
327	702.5	12.4	789	5	US-10-659-004-10	Sequence 10, Appl
328	702.5	12.4	789	5	US-10-659-004-26	Sequence 26, Appl
329	701.5	12.4	789	5	US-10-659-004-16	Sequence 16, Appl
330	701.5	12.4	789	5	US-10-659-004-18	Sequence 18, Appl
331	699.5	12.4	789	5	US-10-659-004-8	Sequence 8, Appli
332	698	12.3	729	6	US-11-097-143-16098	Sequence 16098, A
333	698	12.3	729	6	US-11-097-143-26028	Sequence 26028, A
334	697	12.3	304	4	US-10-763-418-27	Sequence 27, Appl
335	689	12.2	729	4	US-10-108-605-251	Sequence 251, App
336	685	12.1	979	4	US-10-723-606-7	Sequence 7, Appli
337	685	12.1	1103	4	US-10-369-493-6904	Sequence 6904, Ap
338	684	12.1	274	4	US-10-470-957-23	Sequence 23, Appl
339	679.5	12.0	702	3	US-09-805-020-47	Sequence 47, Appl
340	669.5	11.8	318	4	US-10-763-418-10	Sequence 10, Appl
341	652	11.5	962	6	US-11-097-143-111	Sequence 111, App
342	644	11.4	788	5	US-10-659-004-40	Sequence 40, Appl
343	641.5	11.3	1227	4	US-10-369-493-6903	Sequence 6903, Ap
344	626	11.1	257	3	US-09-823-187-46	Sequence 46, Appl
345	622.5	11.0	258	3	US-09-964-956-75	Sequence 75, Appl
346	622.5	11.0	258	4	US-10-042-865-100	Sequence 100, App
347	622.5	11.0	258	4	US-10-072-012-801	Sequence 801, App
348	622.5	11.0	258	4	US-10-072-012-858	Sequence 858, App
349	618.5	10.9	256	3	US-09-976-782-40	Sequence 40, Appl
350	618.5	10.9	257	3	US-09-976-782-29	Sequence 29, Appl
351	618.5	10.9	257	4	US-10-087-684-100	Sequence 100, App
352	618.5	10.9	257	4	US-10-218-779-100	Sequence 100, App
353	618	10.9	257	3	US-09-863-776-42	Sequence 42, Appl
354	614.5	10.9	322	4	US-10-763-418-11	Sequence 11, Appl
355	612	10.8	254	4	US-10-052-648A-43	Sequence 43, Appl
356	601.5	10.6	868	4	US-10-016-283-1	Sequence 1, Appli
357	598	10.6	250	4	US-10-074-978A-153	Sequence 153, App
358	590.5	10.4	280	3	US-09-515-806-15	Sequence 15, Appl
359	590.5	10.4	280	4	US-10-423-543-17	Sequence 17, Appl
360	590.5	10.4	280	5	US-10-892-276-16	Sequence 16, Appl
361	590	10.4	869	4	US-10-016-283-33	Sequence 33, Appl
362	590	10.4	869	5	US-10-745-237-274	Sequence 274, App
363	588	10.4	869	3	US-09-817-487A-2	Sequence 2, Appli
364	582	10.3	244	4	US-10-042-865-85	Sequence 85, Appl
365	581	10.3	1122	5	US-10-732-923-13434	Sequence 13434, A
366	580	10.3	1083	5	US-10-732-923-13449	Sequence 13449, A
367	578	10.2	1124	4	US-10-223-085-82	Sequence 82, Appl
368	578	10.2	1124	4	US-10-223-084-82	Sequence 82, Appl
369	578	10.2	1124	4	US-10-223-088-82	Sequence 82, Appl
370	578	10.2	1124	4	US-10-223-090-82	Sequence 82, Appl
371	578	10.2	1124	4	US-10-223-087-82	Sequence 82, Appl
372	578	10.2	1124	4	US-10-223-083-82	Sequence 82, Appl
373	578	10.2	1124	4	US-10-223-089-82	Sequence 82, Appl
374	578	10.2	1124	4	US-10-021-660-112	Sequence 112, App
375	578	10.2	1124	4	US-10-223-081-82	Sequence 82, Appl
376	578	10.2	1124	4	US-10-223-082-82	Sequence 82, Appl
377	578	10.2	1124	4	US-10-305-654-82	Sequence 82, Appl
378	578	10.2	1124	4	US-10-394-322A-64	Sequence 64, Appl
379	578	10.2	1124	4	US-10-211-462-147	Sequence 147, App
380	578	10.2	1124	4	US-10-081-056-82	Sequence 82, Appl
381	578	10.2	1124	6	US-11-019-855-47	Sequence 47, Appl
382	578	10.2	1127	3	US-09-815-341A-1	Sequence 1, Appli
383	576	10.2	1225	5	US-10-450-763-34308	Sequence 34308, A
384	574.5	10.2	278	4	US-10-172-088-9	Sequence 9, Appli
385	573.5	10.1	1125	5	US-10-732-923-13691	Sequence 13691, A
386	570	10.1	348	3	US-09-982-610-18	Sequence 18, Appl
387	560	9.9	887	5	US-10-732-923-13568	Sequence 13568, A
388	556.5	9.8	245	4	US-10-334-143-182	Sequence 182, App
389	556.5	9.8	1138	4	US-10-021-660-101	Sequence 101, App
390	556.5	9.8	1138	4	US-10-394-322A-63	Sequence 63, Appl
391	556.5	9.8	1138	4	US-10-211-462-113	Sequence 113, App
392	556.5	9.8	1138	5	US-10-916-840-2	Sequence 2, Appli

393	556.5	9.8	1138	5	US-10-846-113A-28	Sequence 28, Appl
394	556	9.8	1134	4	US-10-116-275-137	Sequence 137, App
395	555	9.8	236	4	US-10-231-913-270	Sequence 270, App
396	546	9.7	757	6	US-11-097-143-6117	Sequence 6117, Ap
397	545.5	9.7	821	4	US-10-205-219-11	Sequence 11, Appl
398	545.5	9.7	923	3	US-09-862-027-23	Sequence 23, Appl
399	545.5	9.7	923	5	US-10-989-228-23	Sequence 23, Appl
400	545	9.6	495	4	US-10-369-493-5519	Sequence 5519, Ap
401	543.5	9.6	430	3	US-09-862-027-22	Sequence 22, Appl
402	543.5	9.6	430	5	US-10-989-228-22	Sequence 22, Appl
403	543.5	9.6	923	6	US-11-097-143-993	Sequence 993, App
404	543.5	9.6	2347	5	US-10-756-149-4720	Sequence 4720, Ap
405	542	9.6	821	4	US-10-645-546-10	Sequence 10, Appl
406	540	9.6	822	3	US-09-966-147-2	Sequence 2, Appli
407	540	9.6	822	4	US-10-374-469-2	Sequence 2, Appli
408	540	9.6	822	4	US-10-366-288-24	Sequence 24, Appl
409	540	9.6	822	4	US-10-295-027-394	Sequence 394, App
410	540	9.6	822	4	US-10-295-027-1272	Sequence 1272, Ap
411	540	9.6	822	4	US-10-698-597-2	Sequence 2, Appli
412	540	9.6	822	4	US-10-645-546-2	Sequence 2, Appli
413	540	9.6	822	5	US-10-938-409-24	Sequence 24, Appl
414	540	9.6	838	4	US-10-295-027-396	Sequence 396, App
415	540	9.6	847	3	US-09-924-859A-5	Sequence 5, Appli
416	534.5	9.5	666	5	US-10-732-923-13569	Sequence 13569, A
417	534	9.4	850	3	US-09-924-859A-7	Sequence 7, Appli
418	532	9.4	821	4	US-10-388-838-74	Sequence 74, Appl
419	532	9.4	821	4	US-10-388-838-80	Sequence 80, Appl
420	531.5	9.4	1359	4	US-10-388-838-54	Sequence 54, Appl
421	531.5	9.4	1360	4	US-10-388-838-50	Sequence 50, Appl
422	531.5	9.4	1363	5	US-10-732-923-13625	Sequence 13625, A
423	531.5	9.4	1367	3	US-09-870-759-120	Sequence 120, App
424	531.5	9.4	1367	3	US-09-751-708A-120	Sequence 120, App
425	531.5	9.4	1367	4	US-10-177-293-226	Sequence 226, App
426	531.5	9.4	1367	4	US-10-443-466A-19	Sequence 19, Appl
427	531.5	9.4	1367	4	US-10-632-139-1	Sequence 1, Appli
428	531.5	9.4	1367	4	US-10-365-352-98	Sequence 98, Appl
429	531.5	9.4	1367	4	US-10-428-817A-116	Sequence 116, App
430	531.5	9.4	1367	5	US-10-741-600-860	Sequence 860, App
431	531.5	9.4	1367	5	US-10-482-029-291	Sequence 291, App
432	531.5	9.4	1367	5	US-10-937-758A-97	Sequence 97, Appl
433	531.5	9.4	1367	5	US-10-993-395-11	Sequence 11, Appl
434	531.5	9.4	1367	5	US-10-893-315-67	Sequence 67, Appl
435	531.5	9.4	1367	5	US-10-756-149-5445	Sequence 5445, Ap
436	531.5	9.4	1368	5	US-10-741-600-861	Sequence 861, App
437	531.5	9.4	1376	4	US-10-276-774-2170	Sequence 2170, Ap
438	531.5	9.4	1377	5	US-10-893-315-96	Sequence 96, Appl
439	529.5	9.4	295	4	US-10-377-268-27	Sequence 27, Appl
440	529.5	9.4	295	5	US-10-789-818-15	Sequence 15, Appl
441	529.5	9.4	327	4	US-10-664-421-28	Sequence 28, Appl
442	529.5	9.4	327	5	US-10-941-635-28	Sequence 28, Appl
443	529.5	9.4	351	4	US-10-664-421-58	Sequence 58, Appl
444	529.5	9.4	351	5	US-10-941-635-58	Sequence 58, Appl
445	524.5	9.3	326	3	US-09-815-341A-2	Sequence 2, Appli
446	522	9.2	291	4	US-10-763-418-22	Sequence 22, Appl
447	521	9.2	1070	4	US-10-295-027-534	Sequence 534, App
448	521	9.2	1070	4	US-10-295-027-1334	Sequence 1334, Ap
449	521	9.2	1070	4	US-10-173-999-60	Sequence 60, Appl
450	521	9.2	1070	4	US-10-618-941-114	Sequence 114, App
451	519.5	9.2	624	4	US-10-378-393-7	Sequence 7, Appli
452	519.5	9.2	1367	5	US-10-732-923-13690	Sequence 13690, A
453	519	9.2	658	5	US-10-732-923-13643	Sequence 13643, A
454	518	9.2	808	4	US-10-312-316-56	Sequence 56, Appl
455	518	9.2	839	3	US-09-966-147-6	Sequence 6, Appli
456	518	9.2	839	4	US-10-374-469-6	Sequence 6, Appli
457	518	9.2	839	4	US-10-698-597-6	Sequence 6, Appli
458	518	9.2	839	4	US-10-645-546-14	Sequence 14, Appl
459	517.5	9.2	373	4	US-10-664-421-68	Sequence 68, Appl
460	516.5	9.1	373	5	US-10-941-635-68	Sequence 68, Appl
461	516.5	9.1	403	4	US-10-378-393-5	Sequence 5, Appli
462	516	9.1	370	3	US-09-205-658-107	Sequence 107, App
463	516	9.1	370	3	US-09-844-353A-107	Sequence 107, App
464	516	9.1	370	3	US-09-963-693-107	Sequence 107, App
465	516	9.1	835	4	US-10-388-838-78	Sequence 78, Appl
466	516	9.1	2029	4	US-10-746-545-33	Sequence 33, Appl
467	514	9.1	1701	6	US-11-097-143-18063	Sequence 18063, A
468	513.5	9.1	823	5	US-10-732-923-13685	Sequence 13685, A
469	513.5	9.1	885	3	US-09-919-497-52	Sequence 52, Appl
470	513.5	9.1	885	4	US-10-365-135-4	Sequence 4, Appli
471	513.5	9.1	885	5	US-10-696-909A-6	Sequence 6, Appli
472	513.5	9.1	885	5	US-10-631-467-608	Sequence 608, App
473	513	9.1	822	3	US-09-886-319A-64	Sequence 64, Appl
474	513	9.1	822	4	US-10-376-564-64	Sequence 64, Appl
475	513	9.1	894	3	US-09-223-490-34	Sequence 34, Appl
476	513	9.1	894	3	US-09-236-939-34	Sequence 34, Appl
477	513	9.1	894	5	US-10-646-760-34	Sequence 34, Appl
478	513	9.1	894	5	US-10-696-909A-4	Sequence 4, Appli
479	513	9.1	894	5	US-10-631-467-609	Sequence 609, App
480	512	9.1	839	5	US-10-938-409-25	Sequence 25, Appl
481	511.5	9.0	216	4	US-10-074-978A-164	Sequence 164, App
482	511.5	9.0	876	3	US-09-985-675-3	Sequence 3, Appli
483	511.5	9.0	882	4	US-10-399-225-14	Sequence 14, Appl
484	511	9.0	304	4	US-10-763-418-30	Sequence 30, Appl
485	511	9.0	874	3	US-09-985-675-1	Sequence 1, Appli
486	511	9.0	880	3	US-09-223-490-10	Sequence 10, Appl
487	511	9.0	880	3	US-09-236-939-10	Sequence 10, Appl
488	511	9.0	880	5	US-10-646-760-10	Sequence 10, Appl
489	510	9.0	1418	5	US-10-732-923-13624	Sequence 13624, A
490	509.5	9.0	293	4	US-10-763-418-26	Sequence 26, Appl
491	509.5	9.0	1037	4	US-10-316-124-3	Sequence 3, Appli
492	509.5	9.0	1037	4	US-10-353-690-40	Sequence 40, Appl
493	509.5	9.0	1037	6	US-11-064-551-3	Sequence 3, Appli
494	509	9.0	894	4	US-10-365-135-2	Sequence 2, Appli
495	509	9.0	894	4	US-10-210-130-164	Sequence 164, App
496	509	9.0	947	5	US-10-450-763-52541	Sequence 52541, A
497	508.5	9.0	1314	5	US-10-732-923-13505	Sequence 13505, A
498	508	9.0	249	6	US-11-097-143-21660	Sequence 21660, A
499	508	9.0	874	3	US-09-158-722-6	Sequence 6, Appli
500	507.5	9.0	850	3	US-09-985-675-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-769-987-2
; Sequence 2, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
; APPLICANT: Matsui, Toshimitsu
; APPLICANT: Aaronson, Stuart A.
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
; FILE REFERENCE: 14014.0266U2
; CURRENT APPLICATION NUMBER: US/09/769,987
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 08/460,656
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/439,095
; PRIOR FILING DATE: 1995-05-11
; PRIOR APPLICATION NUMBER: US 07/915,884
; PRIOR FILING DATE: 1992-07-20
; PRIOR APPLICATION NUMBER: US 07/308,282
; PRIOR FILING DATE: 1989-02-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020055129A1e =
; OTHER INFORMATION: synthetic construct
US-09-769-987-2

Query Match 100.0%; Score 5652; DB 3; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.6e-311;

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  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 2
US-09-919-497-90
; Sequence 90, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George L.
;  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
;  FILE REFERENCE: B0801/7225
;  CURRENT APPLICATION NUMBER: US/09/919,497
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221,735
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-919-497-90

  Query Match           100.0%;  Score 5652;  DB 3;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Qy       1081 SDLVEDSFL 1089
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RESULT 3
US-09-866-510-2
; Sequence 2, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-2

Query Match 100.0%; Score 5652; DB 3; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.6e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 4
US-10-027-400-2
; Sequence 2, Application US/10027400
; Publication No. US20030017535A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS

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;       NUMBER OF SEQUENCES: 14
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew
;            STREET: One Market, Steuart Street Tower, 20th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94105
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/027,400
;            FILING DATE: 19-Dec-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/461,917
;            FILING DATE: 05-JUN-1995
;            APPLICATION NUMBER: US 07/151,414
;            FILING DATE: 02-FEB-1988
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dow, Karen B.
;            REGISTRATION NUMBER: 29,684
;            REFERENCE/DOCKET NUMBER: 2307K-267-2-4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/326-2400
;            TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1089 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-027-400-2

  Query Match            100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089


RESULT 5
US-10-394-322A-50
; Sequence 50, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
;  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;  APPLICANT:  Prescott, John C.
;  TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;  FILE REFERENCE: 39750-0006 US
;  CURRENT APPLICATION NUMBER: US/10/394,322A
;  CURRENT FILING DATE:  2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/366,892
;  PRIOR FILING DATE: 2002-03-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-322A-50

  Query Match            100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 6
US-10-367-639-35
; Sequence 35, Application US/10367639
; Publication No. US20040001807A1
; GENERAL INFORMATION:
;  APPLICANT: Cornell Research Foundation, Inc.
;  APPLICANT:  Edelberg, Jay M.
;  APPLICANT:  Rafii, Shahin
;  APPLICANT:  Hong, Mun K.
;  APPLICANT:  Lanza, Robert P.
;  APPLICANT:  West, Michael D.
;  TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular F
;  FILE REFERENCE: 1676.004US1
;  CURRENT APPLICATION NUMBER: US/10/367,639
;  CURRENT FILING DATE:  2003-02-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-367-639-35

  Query Match           100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 7
US-10-322-696-168
; Sequence 168, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-696-168

Query Match 100.0%; Score 5652; DB 4; Length 1089;
Best Local Similarity 100.0%; Pred. No. 1.6e-311;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 8
US-10-741-601-439
; Sequence 439, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 439
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-439

  Query Match           100.0%;  Score 5652;  DB 4;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 9
US-10-723-860-650
; Sequence 650, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 650
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-723-860-650

  Query Match           100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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```
RESULT 10
US-10-741-600-1304
; Sequence 1304, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1304
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1304

  Query Match            100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089

RESULT 11
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US-10-926-806-14
; Sequence 14, Application US/10926806
; Publication No. US20050096257A1
; GENERAL INFORMATION:
;  APPLICANT: SHIMA, DAVID
;  APPLICANT:  CALIAS, PERRY
;  APPLICANT:  ADAMIS, ANTHONY P.
;  TITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
;  TITLE OF INVENTION:  NEOVASCULAR DISORDERS
;  FILE REFERENCE: 112089.184 EYE-013
;  CURRENT APPLICATION NUMBER: US/10/926,806
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/556,837
;  PRIOR FILING DATE: 2004-03-26
;  PRIOR APPLICATION NUMBER: 60/498,407
;  PRIOR FILING DATE: 2003-08-27
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-926-806-14

  Query Match           100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 12
US-10-700-249-2
; Sequence 2, Application US/10700249
; Publication No. US20050112582A1
; GENERAL INFORMATION:
;  APPLICANT: Matsui, Toshimitsu
;  APPLICANT:  Aaronson, Stuart A.
;  APPLICANT:  Pierce, Jacalyn H.
;  TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
;  FILE REFERENCE: 14014.0266U2
;  CURRENT APPLICATION NUMBER: US/10/700,249
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: US/09/769,987
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 08/460,656
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: US 08/439,095
;  PRIOR FILING DATE: 1995-05-11
;  PRIOR APPLICATION NUMBER: US 07/915,884
;  PRIOR FILING DATE: 1992-07-20
;  PRIOR APPLICATION NUMBER: US 07/308,282
;  PRIOR FILING DATE: 1989-02-09
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; Note =
;   OTHER INFORMATION: synthetic construct
US-10-700-249-2

  Query Match           100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 13
US-10-756-149-4888
; Sequence 4888, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
;  TITLE OF INVENTION:  METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/756,149
;  CURRENT FILING DATE:  2004-01-12
;  NUMBER OF SEQ ID NOS: 5818
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4888
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-756-149-4888

  Query Match             100.0%;  Score 5652;  DB 5;  Length 1089;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-311;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
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Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 14
US-09-866-510-10
; Sequence 10, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-10

Query Match 99.9%; Score 5649; DB 3; Length 1089;
Best Local Similarity 99.9%; Pred. No. 2.4e-311;
Matches 1088; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy          61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy         121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy         181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy         241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy         301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy         361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy         421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy         481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy         541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy         601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy         661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy         721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy         781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy         841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
               ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db         841 RDIMHDSNYVSKGSTFLPMKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy         901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy         961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy        1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy        1081 SDLVEDSFL 1089
               |||||||||
Db        1081 SDLVEDSFL 1089
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RESULT 15
US-09-866-510-4
; Sequence 4, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103

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;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-4

  Query Match            99.9%;  Score 5648;  DB 3;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-311;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWKFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 16
US-09-955-363-36
; Sequence 36, Application US/09955363
; Patent No. US20020173621A1
;   GENERAL INFORMATION:
;        APPLICANT: Sledziewski Ph.D., Andrzej Z
;                   Bell, Lillian A.
;                   Kindsvogel Ph.D., Wayne R.
;        TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;                            AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;                            FUSIONS
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed and Berry
;             STREET: 6300 Columbia Center
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.24
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/955,363
;             FILING DATE: 18-Sep-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/634,510
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 07/347,291
;             FILING DATE: 02-MAY-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki J.D., David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 990008.446C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-622-4900
;             TELEFAX: 206-682-6031
;             TELEX: 3723836
;   INFORMATION FOR SEQ ID NO: 36:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1089 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-955-363-36

  Query Match            99.9%;  Score 5648;  DB 3;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-311;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITILEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 17
US-09-866-510-8
; Sequence 8, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-8

  Query Match             99.9%;  Score 5647;  DB 3;  Length 1089;
  Best Local Similarity   99.9%;  Pred. No. 3.1e-311;
  Matches 1088;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRNLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 18
US-09-866-510-6
; Sequence 6, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-6

Query Match 99.9%; Score 5646; DB 3; Length 1089;
Best Local Similarity 99.9%; Pred. No. 3.6e-311;
Matches 1088; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACMKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 19
US-09-961-403-4
; Sequence 4, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMPP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLT

```
;  APPLICANT:  WINTERHAGER, ELKE
;  APPLICANT:  REGIDOR, PEDRO
;  APPLICANT:  SCOTTI, SIMONE
;  TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
;  FILE REFERENCE: SCH-1789
;  CURRENT APPLICATION NUMBER: US/09/961,403
;  CURRENT FILING DATE:  2001-09-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1088
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-961-403-4

  Query Match             99.7%;  Score 5636.5;  DB 3;  Length 1088;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-310;
  Matches 1088;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARM-VDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1019

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1020 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1079

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1080 SDLVEDSFL 1088


RESULT 20
US-10-322-696-165
; Sequence 165, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 529452001200
;  CURRENT APPLICATION NUMBER: US/10/322,696
;  CURRENT FILING DATE:  2003-10-17
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
;   LENGTH: 1096
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-322-696-165

  Query Match             92.6%;  Score 5232;  DB 4;  Length 1096;
  Best Local Similarity   91.8%;  Pred. No. 1e-287;
  Matches 1000;  Conservative   48;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||  |||| |||||  || ||| ||||||||||:|||||||||| ||||||||:|
Db          8 MGTSHQVFLVLSCLLTGPGLISCQLLLPSILPNENEKIVQLNSSFSLRCVGESEVSWQHP 67

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||:  :||||:|||||||||||||| :|||||| ||||||||||:|:|:|||||||
Db         68 MSEEDDPNVEIRSEENNSGLFVTVLEVVNASAAHTGWYTCYYNHTQTDESEIEGRHIYIY 127

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||:|||||||| |||||:|||||||||||||||| |||||:  :|||||||||||||
Db        128 VPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVTLHNNGRLVPASYDSRQGFNG 187

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||:|||||||||||: |:|  |||||||||||:|||:| :||||:|||||||||||||||
Db        188 TFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEMDARQTVYKAGETIVVTCAVFNN 247

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||: |||||||||:|||||||||||||:|||||||:|||||||||||||
Db        248 EVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLTVPKATVKDSGEYECAARQATKEVK 307

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||:|||||||||:||:|||  |||||||||: |||||:||| |||||||:|||||||||
Db        308 EMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVREFVVEVQAYPTPRISWLKDNLTLIENL 367

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||:| || ||:|||||||||||||||||: |||| |||||||| | ||:|||||
Db        368 TEITTDVQKSQETRYQSKLKLIRAKEEDSGHYTIIVQNEDDVKSYTFELSTLVPASILDL 427
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Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||| |||||||||||||||:|:||||| ||||||:||||:||:||||||||:  |
Db        428 VDDHHGSGGGQTVRCTAEGTPLPEIDWMICKHIKKCNNDTSWTVLASNVSNIITELPRRG 487

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||:|||||||||||||||| |    ||||||||||||||||||||||||||:
Db        488 RSTVEGRVSFAKVEETIAVRCLAKNNLSVVARELKLVAPTLRSELTVAAAVLVLLVIVIV 547

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        548 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRILG 607

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 667

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||:| |||||||:||||||||||||||||||||
Db        668 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFMSQHPEKPKKDLDIFGLNPADESTRSY 727

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 787

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 LLSDDDSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 847

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 907

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        908 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVQCWNSEPEKRPSFYHLSEIVENLLPGQYKK 967

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1027

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1087

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1088 SDLVEDSFL 1096
```

RESULT 21
US-09-866-510-12
; Sequence 12, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-12

```
  Query Match           53.9%;  Score 3046;  DB 3;  Length 589;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-164;
  Matches  589;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFP 589
```

RESULT 22
US-10-637-356-2
; Sequence 2, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
; APPLICANT: Briesewitz, Roger
; APPLICANT: Griffin, John
; TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
; TITLE OF INVENTION: ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P-153-US1
; CURRENT APPLICATION NUMBER: US/10/637,356
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,330
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/440,491
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 834
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-637-356-2

```
  Query Match           47.7%;  Score 2693.5;  DB 4;  Length 834;
  Best Local Similarity  74.6%;  Pred. No. 4.6e-144;
  Matches  551;  Conservative   28;  Mismatches   61;  Indels   99;  Gaps   12;
```

```
Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        194 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRTGN----SEKETALPSTKAE-FT 243

Qy        412 QVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVS 470
Db        244 SPPSLFKTGLPPSRNSTSSQSQTSTAS--------------RKANSSVGKW-------- 280

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
Db        281 --------QDR--------YGRAE----------------------SPDLR---RLPGA 298

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
Db        299 IDVIGQTITIS------------RVEGRRRANENSN-----------IQLPYDSRWEFPR 335

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
Db        336 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 395

Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
Db        396 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 455

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
Db        456 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 515

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
Db        516 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 575

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
Db        576 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 635

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
Db        636 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 695

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
Db        696 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 755

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
Db        756 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 815

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
Db        816 DMMDDIGIDSSDLVEDSFL 834
```

RESULT 23
US-10-637-356-1
; Sequence 1, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
; APPLICANT: Briesewitz, Roger
; APPLICANT: Griffin, John
; TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
; TITLE OF INVENTION: ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P-153-US1
; CURRENT APPLICATION NUMBER: US/10/637,356
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,330
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/440,491
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 849
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-637-356-1

Query Match 47.6%; Score 2692; DB 4; Length 849;
Best Local Similarity 74.6%; Pred. No. 5.7e-144;
Matches 551; Conservative 28; Mismatches 61; Indels 99; Gaps 12;

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Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        209 NKITAEDCTMEVTPGAE-IQDGRF----NLFKVQQGRTGN----SEKETALPSTKAE-FT 258

Qy        412 QVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNET-SWTILANNVS 470
Db        259 SPPSLFKTGLPPSRNSTSSQSQTSTAS--------------RKANSSVGKW-------- 295

Qy        471 NIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAA 530
Db        296 --------QDR--------YGRAE----------------------SPDLR---RLPGA 313

Qy        531 VLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPR 590
Db        314 IDVIGQTITIS------------RVEGRRRANENSN-----------IQLPYDSRWEFPR 350

Qy        591 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 650
Db        351 DGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTH 410

Qy        651 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 710
Db        411 LGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGL 470

Qy        711 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 770
Db        471 NPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKK 530

Qy        771 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 830
Db        531 KSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGK 590

Qy        831 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 890
Db        591 IVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFS 650

Qy        891 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 950
Db        651 LGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIV 710

Qy        951 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 1010
Db        711 ENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQ 770

Qy       1011 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 1070
Db        771 RLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDI 830

Qy       1071 DMMDDIGIDSSDLVEDSFL 1089
Db        831 DMMDDIGIDSSDLVEDSFL 849
```

RESULT 24
US-10-637-356-4
; Sequence 4, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
; APPLICANT: Briesewitz, Roger
; APPLICANT: Griffin, John
; TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
; TITLE OF INVENTION: ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME

```
;  FILE REFERENCE: P-153-US1
;  CURRENT APPLICATION NUMBER: US/10/637,356
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: 60/402,330
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/440,491
;  PRIOR FILING DATE: 2003-01-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 811
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-637-356-4

  Query Match             47.4%;  Score 2676.5;  DB 4;  Length 811;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-143;
  Matches  511;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        578 MQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 637
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 IQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 359

Qy        638 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 419

Qy        698 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 479

Qy        758 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 539

Qy        818 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 599

Qy        878 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 659

Qy        938 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 719

Qy        998 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 779

Qy       1058 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              |||||||||||||||||||||||||||||||
Db        780 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 811


RESULT 25
US-10-637-356-3
; Sequence 3, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
;  APPLICANT: Briesewitz, Roger
;  APPLICANT:  Griffin, John
;  TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
;  TITLE OF INVENTION:  ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
;  TITLE OF INVENTION:  NUCLEIC ACIDS ENCODING THE SAME
;  FILE REFERENCE: P-153-US1
;  CURRENT APPLICATION NUMBER: US/10/637,356
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: 60/402,330
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/440,491
;  PRIOR FILING DATE: 2003-01-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 826
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-637-356-3

  Query Match             47.4%;  Score 2676.5;  DB 4;  Length 826;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-143;
  Matches  511;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        578 MQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 637
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 IQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSE 374

Qy        638 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 KQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHH 434

Qy        698 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 PEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDI 494

Qy        758 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 QRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHR 554

Qy        818 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 DLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSD 614

Qy        878 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 VWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEP 674

Qy        938 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        675 EKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEE 734

Qy        998 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 DKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSS 794

Qy       1058 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 1089
              |||||||||||||||||||||||||||||||
Db        795 TFIKREDETIEDIDMMDDIGIDSSDLVEDSFL 826


RESULT 26
US-10-664-421-64
; Sequence 64, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
;  APPLICANT: BREMER, RYAN
;  APPLICANT:  IBRAHIM, PRABHA
;  APPLICANT:  KUMAR, ABHINAV
;  APPLICANT:  MANDIYAN, VALSAN
;  APPLICANT:  MILBURN, MICHAEL V.
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
;  FILE REFERENCE: 039363/0703
;  CURRENT APPLICATION NUMBER: US/10/664,421
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: 60/412,341
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: 60/411,398
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 169
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 64
;   LENGTH: 460
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-664-421-64

  Query Match            42.9%;  Score 2425;  DB 4;  Length 460;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-129;
  Matches  460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 60

Qy        603 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 120

Qy        663 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 180

Qy        723 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 240

Qy        783 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 300

Qy        843 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVD 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVD 360

Qy        903 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 420

Qy        963 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 1002
              ||||||||||||||||||||||||||||||||||||||||
Db        421 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 460


RESULT 27
US-10-941-635-64
; Sequence 64, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
;  APPLICANT: ARTIS, DEAN R.
;  APPLICANT:  BREMER, RYAN E.
;  APPLICANT:  GILLETTE, SAMUEL J.
;  APPLICANT:  HURT, CLARENCE R.
;  APPLICANT:  IBRAHIM, PRABHA L.
;  APPLICANT:  ZUCKERMAN, REBECCA L.
;  TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
;  FILE REFERENCE: 039363-1702
;  CURRENT APPLICATION NUMBER: US/10/941,635
;  CURRENT FILING DATE:  2004-09-15
;  PRIOR APPLICATION NUMBER: 60/503,277
;  PRIOR FILING DATE: 2003-09-15
;  NUMBER OF SEQ ID NOS: 167
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 64
;   LENGTH: 460
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Mammalian
;   OTHER INFORMATION: protein sequence
US-10-941-635-64

  Query Match            42.9%;  Score 2425;  DB 5;  Length 460;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-129;
  Matches  460;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        543 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSG 60

Qy        603 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLG 120

Qy        663 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVI 180

Qy        723 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLL 240

Qy        783 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARD 300

Qy        843 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVD 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVD 360

Qy        903 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 STFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 420

Qy        963 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 1002
              ||||||||||||||||||||||||||||||||||||||||
Db        421 EKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD 460


RESULT 28
US-09-866-510-22
; Sequence 22, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-22

  Query Match            41.7%;  Score 2354.5;  DB 3;  Length 1106;
  Best Local Similarity  44.1%;  Pred. No. 1e-124;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||   :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239
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Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPMKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE-----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106


RESULT 29
US-09-955-363-2
; Sequence 2, Application US/09955363
; Patent No. US20020173621A1
;   GENERAL INFORMATION:
;        APPLICANT: Sledziewski Ph.D., Andrzej Z
;                   Bell, Lillian A.
;                   Kindsvogel Ph.D., Wayne R.
;        TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;                            AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;                            FUSIONS
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed and Berry
;             STREET: 6300 Columbia Center
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.24
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/955,363
;             FILING DATE: 18-Sep-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/634,510
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 07/347,291
;             FILING DATE: 02-MAY-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki J.D., David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 990008.446C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-622-4900
;             TELEFAX: 206-682-6031
;             TELEX: 3723836
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-955-363-2

  Query Match             41.7%;  Score 2354.5;  DB 3;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 1e-124;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

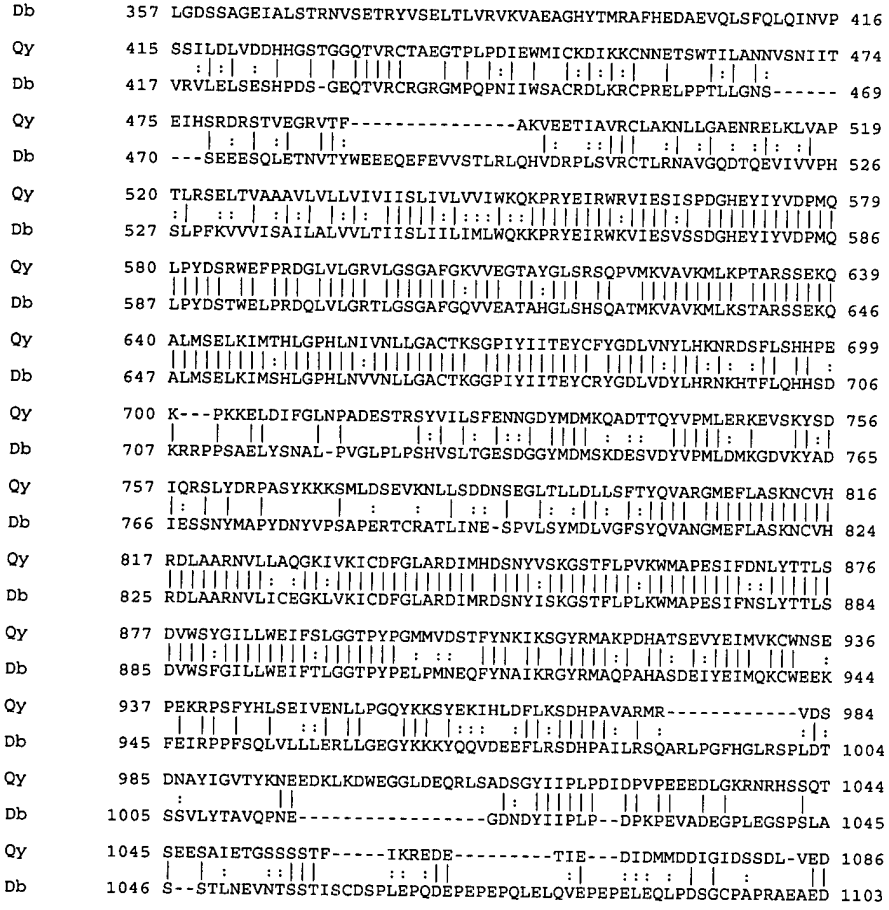
Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

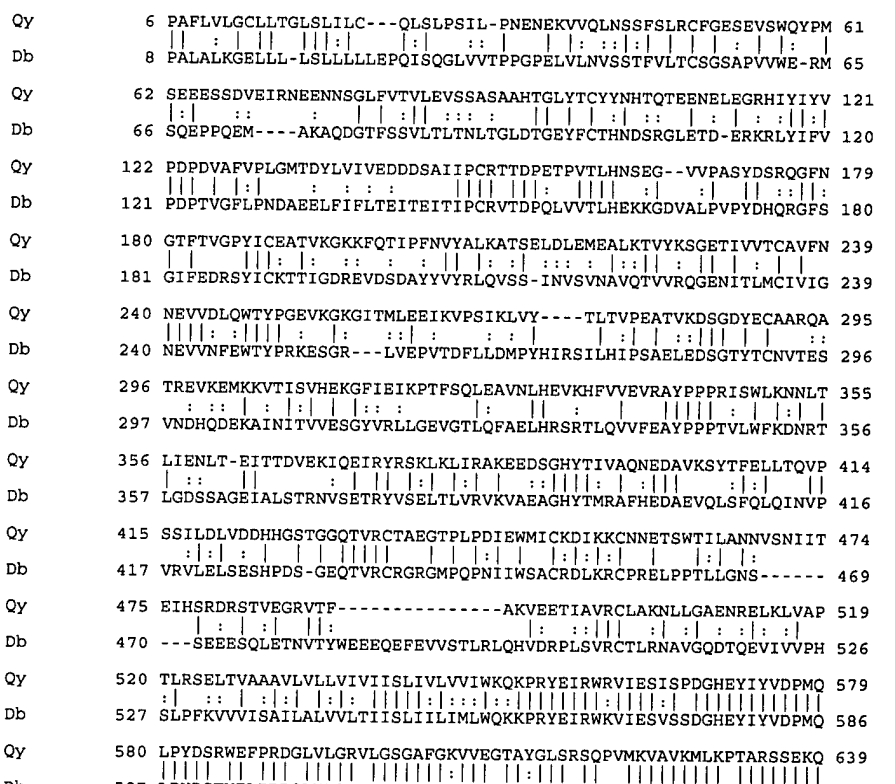
Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
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RESULT 30
US-10-394-322A-51
; Sequence 51, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 1106
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-394-322A-51

Query Match 41.7%; Score 2354.5; DB 4; Length 1106;
Best Local Similarity 44.1%; Pred. No. 1e-124;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;



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Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 31
US-10-367-639-36
; Sequence 36, Application US/10367639
; Publication No. US20040001807A1
; GENERAL INFORMATION:
;  APPLICANT: Cornell Research Foundation, Inc.
;  APPLICANT:  Edelberg, Jay M.
;  APPLICANT:  Rafii, Shahin
;  APPLICANT:  Hong, Mun K.
;  APPLICANT:  Lanza, Robert P.
;  APPLICANT:  West, Michael D.
;  TITLE OF INVENTION: Endothelial Precursor Cells for Enhancing and Restoring Vascular
;  FILE REFERENCE: 1676.004US1
;  CURRENT APPLICATION NUMBER: US/10/367,639
;  CURRENT FILING DATE:  2003-02-13
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-367-639-36

  Query Match             41.7%;  Score 2354.5;  DB 4;  Length 1106;
  Best Local Similarity   44.1%;  Pred. No. 1e-124;
  Matches  504;  Conservative  195;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61

Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179

Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239

Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295

Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355

Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414

Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474

Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469
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Qy        475 EIHSRDRSTVEGRVTF----------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519

Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579

Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639

Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816

Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876

Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936

Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984

Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044

Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086

Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089

Db       1104 SFL 1106


RESULT 32
US-10-926-806-6
; Sequence 6, Application US/10926806
; Publication No. US20050096257A1
; GENERAL INFORMATION:
;  APPLICANT: SHIMA, DAVID
;  APPLICANT:  CALIAS, PERRY
;  APPLICANT:  ADAMIS, ANTHONY P.
;  TITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
;  TITLE OF INVENTION:  NEOVASCULAR DISORDERS
;  FILE REFERENCE: 112089.184 EYE-013
;  CURRENT APPLICATION NUMBER: US/10/926,806
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/556,837
;  PRIOR FILING DATE: 2004-03-26
;  PRIOR APPLICATION NUMBER: 60/498,407
;  PRIOR FILING DATE: 2003-08-27
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-926-806-6

Query Match 41.7%; Score 2354.5; DB 5; Length 1106;
Best Local Similarity 44.1%; Pred. No. 1e-124;
Matches 504; Conservative 195; Mismatches 341; Indels 103; Gaps 25;

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Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    :|    :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :  | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :       |:   ||  :   |  ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:|  |  ::||||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| ||||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||   | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::|||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||  ||| |:::  :||:|||||: | :             :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                  |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :       ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106
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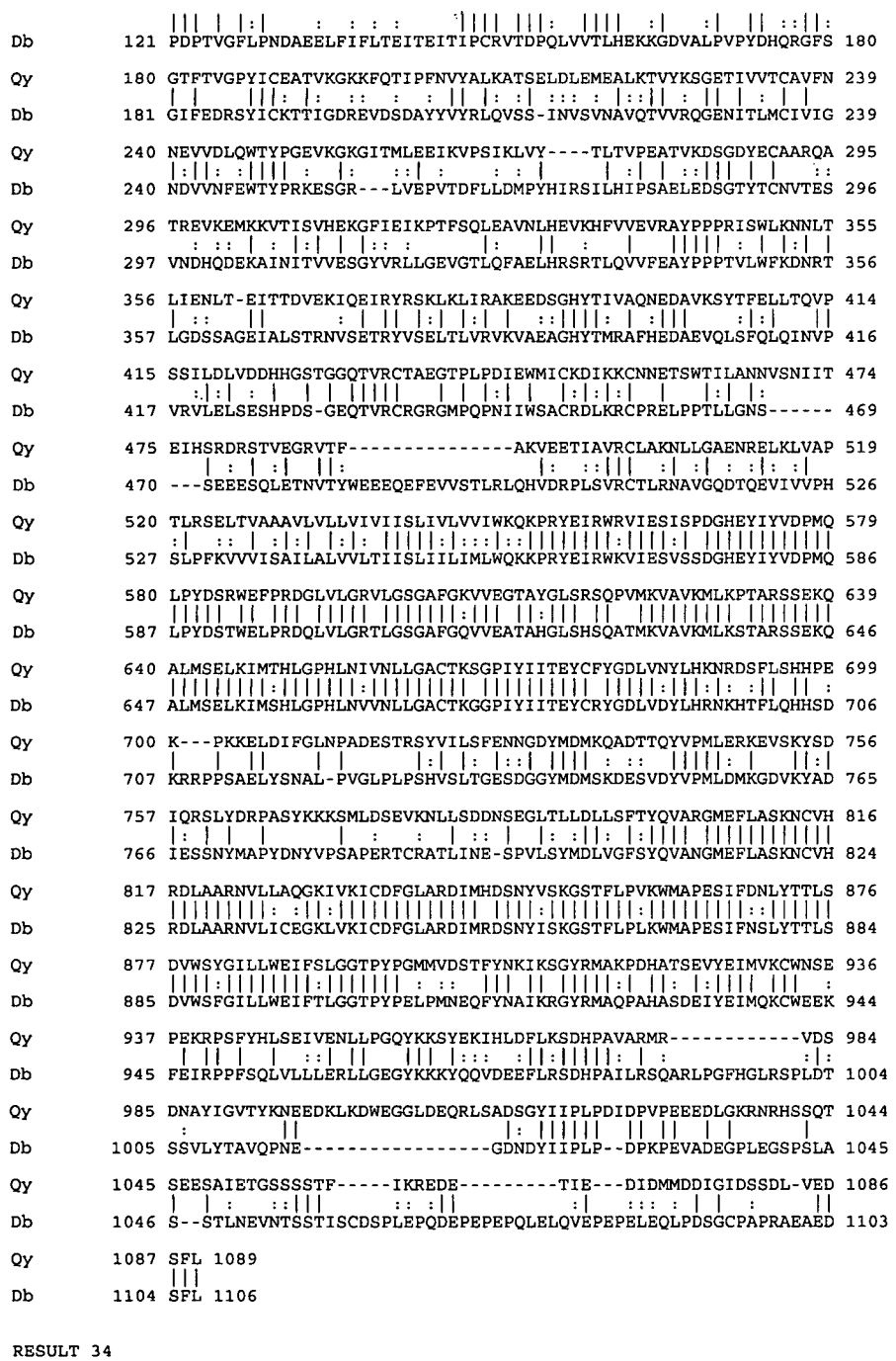
RESULT 33
US-10-027-400-4
; Sequence 4, Application US/10027400
; Publication No. US20030017535A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,400
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-027-400-4

Query Match 41.6%; Score 2351.5; DB 4; Length 1106;
Best Local Similarity 44.0%; Pred. No. 1.5e-124;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

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Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    :|    :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :  | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

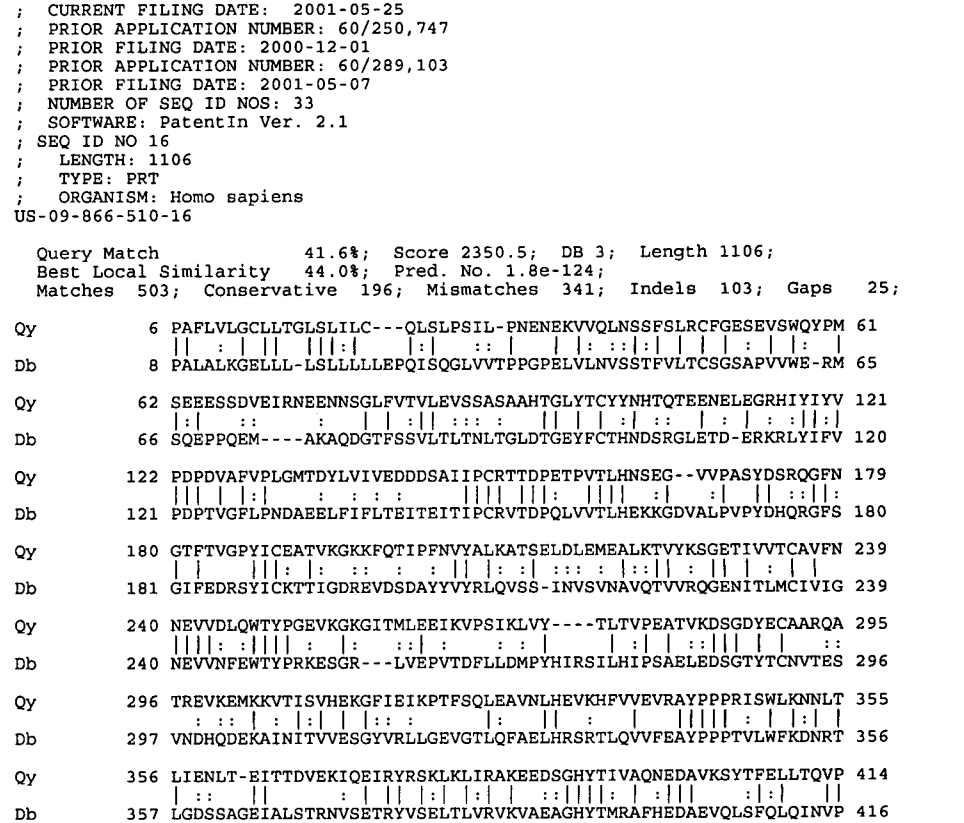
Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
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RESULT 34

US-09-866-510-16
; Sequence 16, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-16

Query Match 41.6%; Score 2350.5; DB 3; Length 1106;
Best Local Similarity 44.0%; Pred. No. 1.8e-124;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;



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Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106
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RESULT 35
US-09-866-510-20
; Sequence 20, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-510-20

Query Match 41.6%; Score 2349.5; DB 3; Length 1106;
Best Local Similarity 44.0%; Pred. No. 2e-124;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

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Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
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Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
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Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
Db        825 RNLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR------------VDS 984
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
Db       1104 SFL 1106
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RESULT 36
US-09-866-510-18
; Sequence 18, Application US/09866510
; Patent No. US20020111304A1

```
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-18

  Query Match             41.6%;  Score 2348.5;  DB 3;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 2.3e-124;
  Matches  503;  Conservative  195;  Mismatches  342;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |  |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF---------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                 |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:|  |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| ||||||||:||| ||:||| ||  |||||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||| | |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACMKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|

Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :         ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 37
US-09-866-510-14
; Sequence 14, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 1090
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-866-510-14

  Query Match             41.5%;  Score 2347;  DB 3;  Length 1090;
  Best Local Similarity   44.8%;  Pred. No. 2.7e-124;
  Matches  496;  Conservative  189;  Mismatches  331;  Indels   90;  Gaps   22;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239
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Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
                : :: | : |:| | |:: :       |:   ||  :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||       : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | ||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:|||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||   | |        |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |       |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| |||||:|||||||||:|||||||||:|||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :          ||                |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE 1065
              |  | :   ::|||      :: :||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDE 1069
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RESULT 38
US-10-450-763-51112
; Sequence 51112, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51112
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (592)..(641)
; OTHER INFORMATION: Receptor tyrosine kinase class III proteins domain identified
; OTHER INFORMATION: by eMATRIX, accession number BL00240C, p-value=1.000e-40, raw
; OTHER INFORMATION: score of 22.58
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (600)..(955)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam,
; OTHER INFORMATION: accession name pkinase, E-value=3e-74, PFam score of 260.1
US-10-450-763-51112

Query Match 40.9%; Score 2309; DB 5; Length 1089;
Best Local Similarity 44.0%; Pred. No. 3.9e-122;
Matches 499; Conservative 191; Mismatches 343; Indels 100; Gaps 26;

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Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   :: |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              ||||: :|||| :  |:   ::| :    : : |      | :| | ::||| | |   ::
Db        240 NEVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
                : :: | : |:| | |:: :       |:   ||  :   |   |||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||       : | || |:| |:| |  ::|||| | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | ||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:|||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
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                ||||||||:|||||||:||||||||| ||||||||| |||||:|||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::|||||| 
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:||||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR--VDSDNAYIGVTYK 994
              | || |  |  ::| ||   ||| |::  |       |    :|  :|: :
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQARL-------PGFHGLRSPLDTSSVLYTAVQP 997

Qy        995 NEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGS 1054
              || .                |: |||||  || ||  | |      |  |  | :   :
Db        998 NE-----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLAS--STLNEVN 1036

Qy       1055 SSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VEDSFL 1089
              :|||      :: :||          :|   ::: : | |  :     |||||
Db       1037 TSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL 1089


RESULT 39
US-09-939-754-6
; Sequence 6, Application US/09939754
; Patent No. US20020051965A1
; GENERAL INFORMATION:
;  APPLICANT: McTIGUE, MICHELE A.
;  APPLICANT:  WICKERSHAM, JOHN A.
;  APPLICANT:  PINKO, CHRIS
;  APPLICANT:  SHOWALTER, RICHARD
;  APPLICANT:  PARAST, CAMRAN V.
;  APPLICANT:  TEMPCYZK-RUSSEL, ANNA
;  APPLICANT:  GEHRING, MICHAEL R.
;  APPLICANT:  MROCZKOWSKI, BARBARA
;  APPLICANT:  KAN, CHEN-CHEN
;  APPLICANT:  VILLAFRANCA, J. ERNEST
;  APPLICANT:  APPELT, KRZYSZTOF
;  TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 0125-0016US
;  CURRENT APPLICATION NUMBER: US/09/939,754
;  CURRENT FILING DATE:  2001-08-28
;  PRIOR APPLICATION NUMBER: 09/390,326
;  PRIOR FILING DATE: 1999-09-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: E. coli
US-09-939-754-6

  Query Match             35.9%;  Score 2031;  DB 3;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-107;
  Matches  386;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 60

Qy        636 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 120

Qy        696 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 180

Qy        756 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 240

Qy        816 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 300

Qy        876 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 360

Qy        936 EPEKRPSFYHLSEIVENLLPGQYKKS 961
              |||||||||||||||||||||||||
Db        361 EPEKRPSFYHLSEIVENLLPGQYKKS 386


RESULT 40
US-09-939-832-6
; Sequence 6, Application US/09939832
; Patent No. US20020127538A1
; GENERAL INFORMATION:
;  APPLICANT: McTIGUE, MICHELE A.
;  APPLICANT:  WICKERSHAM, JOHN A.
;  APPLICANT:  PINKO, CHRIS
;  APPLICANT:  SHOWALTER, RICHARD
;  APPLICANT:  PARAST, CAMRAN V.
;  APPLICANT:  TEMPCYZK-RUSSEL, ANNA
;  APPLICANT:  GEHRING, MICHAEL R.
;  APPLICANT:  MROCZKOWSKI, BARBARA
;  APPLICANT:  KAN, CHEN-CHEN
;  APPLICANT:  VILLAFRANCA, J. ERNEST
;  APPLICANT:  APPELT, KRZYSZTOF
;  TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 0125-0016US
;  CURRENT APPLICATION NUMBER: US/09/939,832
;  CURRENT FILING DATE:  2001-08-28
;  PRIOR APPLICATION NUMBER: 09/390,326
;  PRIOR FILING DATE: 1999-09-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: E. coli
US-09-939-832-6

  Query Match             35.9%;  Score 2031;  DB 3;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-107;
  Matches  386;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 60

Qy        636 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 120

Qy        696 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 180

Qy        756 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 240
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Qy        816 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 300

Qy        876 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 360

Qy        936 EPEKRPSFYHLSEIVENLLPGQYKKS 961
              |||||||||||||||||||||||||
Db        361 EPEKRPSFYHLSEIVENLLPGQYKKS 386


RESULT 41
US-09-939-833-6
; Sequence 6, Application US/09939833
; Patent No. US20020164641A1
; GENERAL INFORMATION:
;  APPLICANT: McTIGUE, MICHELE A.
;  APPLICANT:  WICKERSHAM, JOHN A.
;  APPLICANT:  PINKO, CHRIS
;  APPLICANT:  SHOWALTER, RICHARD
;  APPLICANT:  PARAST, CAMRAN V.
;  APPLICANT:  TEMPCYZK-RUSSEL, ANNA
;  APPLICANT:  GEHRING, MICHAEL R.
;  APPLICANT:  MROCZKOWSKI, BARBARA
;  APPLICANT:  KAN, CHEN-CHEN
;  APPLICANT:  VILLAFRANCA, J. ERNEST
;  APPLICANT:  APPELT, KRZYSZTOF
;  TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
;  TITLE OF INVENTION:  METHODS OF USE
;  FILE REFERENCE: 0125-0016US
;  CURRENT APPLICATION NUMBER: US/09/939,833
;  CURRENT FILING DATE:  2001-08-28
;  PRIOR APPLICATION NUMBER: US/09/390,326
;  PRIOR FILING DATE: 1999-09-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 386
;   TYPE: PRT
;   ORGANISM: E. coli
US-09-939-833-6

  Query Match             35.9%;  Score 2031;  DB 3;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-107;
  Matches  386;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        576 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARS 60

Qy        636 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLS 120

Qy        696 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYS 180

Qy        756 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCV 240

Qy        816 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTL 300

Qy        876 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNS 360

Qy        936 EPEKRPSFYHLSEIVENLLPGQYKKS 961
              |||||||||||||||||||||||||
Db        361 EPEKRPSFYHLSEIVENLLPGQYKKS 386


RESULT 42
US-10-965-313-7
; Sequence 7, Application US/10965313
; Publication No. US20050227992A1
; GENERAL INFORMATION:
;  APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
;  APPLICANT:  Montigen Pharmaceuticals, Inc.
;  APPLICANT:  Hurley, Laurence H.
;  APPLICANT:  Mahadevan, Daruka
;  APPLICANT:  Han, Haiyong
;  APPLICANT:  Bearss, David J.
;  APPLICANT:  Vankayalapati, Hariprasad
;  APPLICANT:  Bashyam, Sridevi
;  APPLICANT:  Munoz, Ruben M.
;  APPLICANT:  Warner, Steven L.
;  APPLICANT:  Della Croce, Kimiko
;  APPLICANT:  Von Hoff, Daniel D.
;  APPLICANT:  Grand, Cory L.
;  TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
;  FILE REFERENCE: 920214.00003
;  CURRENT APPLICATION NUMBER: US/10/965,313
;  CURRENT FILING DATE:  2004-10-14
;  PRIOR APPLICATION NUMBER: US 60/608,529
;    US 60/511,486
;    US 60/511,489
;  PRIOR FILING DATE: 2004-09-09
;    2003-10-14
;    2003-10-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-965-313-7

  Query Match             35.5%;  Score 2008;  DB 5;  Length 383;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-105;
  Matches  383;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 60

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 120

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 180

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 240

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 300

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 360

Qy        959 KKSYEKIHLDFLKSDHPAVARMR 981
              |||||||||||||||||||||||
Db        361 KKSYEKIHLDFLKSDHPAVARMR 383
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RESULT 43
US-11-092-809-7
; Sequence 7, Application US/11092809
; Publication No. US20050239793A1
; GENERAL INFORMATION:
;  APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
;  APPLICANT:  Montigen Pharmaceuticals, Inc.
;  APPLICANT:  Hurley, Laurence H.
;  APPLICANT:  Mahadevan, Daruka
;  APPLICANT:  Han, Haiyong
;  APPLICANT:  Bearss, David J.
;  APPLICANT:  Vankayalapati, Hariprasad
;  APPLICANT:  Bashyam, Sridevi
;  APPLICANT:  Munoz, Ruben M.
;  APPLICANT:  Warner, Steven L.
;  APPLICANT:  Della Croce, Kimiko
;  APPLICANT:  Von Hoff, Daniel D.
;  APPLICANT:  Grand, Cory L.
;  TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
;  FILE REFERENCE: 920214.00003CONT2
;  CURRENT APPLICATION NUMBER: US/11/092,809
;  CURRENT FILING DATE:  2005-03-29
;  PRIOR APPLICATION NUMBER: US 10/965,313
;  PRIOR FILING DATE: 2004-10-14
;  PRIOR APPLICATION NUMBER: US 60/608,529
;  PRIOR FILING DATE: 2004-09-09
;  PRIOR APPLICATION NUMBER: US 60/511,486
;  PRIOR FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: US 60/511,489
;  PRIOR FILING DATE: 2003-10-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-092-809-7

  Query Match             35.5%;  Score 2008;  DB 6;  Length 383;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-105;
  Matches  383;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 60

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 120

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 180

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 240

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 300

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 360

Qy        959 KKSYEKIHLDFLKSDHPAVARMR 981
              |||||||||||||||||||||||
Db        361 KKSYEKIHLDFLKSDHPAVARMR 383


RESULT 44
US-11-092-863-7
; Sequence 7, Application US/11092863
; Publication No. US20050239794A1
; GENERAL INFORMATION:
;  APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
;  APPLICANT:  Montigen Pharmaceuticals, Inc.
;  APPLICANT:  Hurley, Laurence H.
;  APPLICANT:  Mahadevan, Daruka
;  APPLICANT:  Han, Haiyong
;  APPLICANT:  Bearss, David J.
;  APPLICANT:  Vankayalapati, Hariprasad
;  APPLICANT:  Bashyam, Sridevi
;  APPLICANT:  Munoz, Ruben M.
;  APPLICANT:  Warner, Steven L.
;  APPLICANT:  Della Croce, Kimiko
;  APPLICANT:  Von Hoff, Daniel D.
;  APPLICANT:  Grand, Cory L.
;  TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
;  FILE REFERENCE: 920214.00003CONT1
;  CURRENT APPLICATION NUMBER: US/11/092,863
;  CURRENT FILING DATE:  2005-03-29
;  PRIOR APPLICATION NUMBER: US 10/965,313
;    US 60/608,529
;    US 60/511,486
;    US 60/511,489
;  PRIOR FILING DATE: 2004-10-14
;    2004-09-09
;    2003-10-14
;    2003-10-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-092-863-7

  Query Match             35.5%;  Score 2008;  DB 6;  Length 383;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-105;
  Matches  383;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 60

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 120

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 180

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 240

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 300

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 360

Qy        959 KKSYEKIHLDFLKSDHPAVARMR 981
              |||||||||||||||||||||||
Db        361 KKSYEKIHLDFLKSDHPAVARMR 383


RESULT 45
US-10-450-763-45837
; Sequence 45837, Application US/10450763
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 45837
;   LENGTH: 2129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (1925)..(1956)
;   OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
;   OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=3.842e-18, raw
;   OTHER INFORMATION: score of 18.39
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (553)..(2069)
;   OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam,
;   OTHER INFORMATION: accession name pkinase, E-value=1.4e-126, PFam score of 433.9
US-10-450-763-45837

  Query Match             34.8%;  Score 1965.5;  DB 5;  Length 2129;
  Best Local Similarity   41.6%;  Pred. No. 2.6e-102;
  Matches  426;  Conservative  153;  Mismatches  286;  Indels  159;  Gaps   20;

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFNG 180
              || | |:|     :  : : :     |||| |||:  ||||  :|   :|  || ::||:|
Db         29 DPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFSG 88

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |  |
Db         89 IFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIGN 147

Qy        241 EVVDLQWTYP----------------GEVKG---------KGITMLEEIKVPSIKLVYT 274
              |||: :||||                | : |           :  |  : : | :||
Db        148 EVVNFEWTYPRKEVMWGQAGVGGGARNGWISGLQADFSPAPPDLGGLPNLLLQSGRLVEP 207

Qy        275 LT--------------VPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKP 319
              :|                :| | ::||| | |   ::  : :: | : |:| | |:: :
Db        208 VTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDHQDEKAINITVVESGYVRLLG 267

Qy        320 TFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLT-EITTDVEKIQEIRYRSK 378
                |:   ||  :   |   ||||| : | |:| || ::   ||      : | || |:
Db        268 EVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGDSSAGEIALSTRNVSETRYVSE 327

Qy        379 LKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAE 438
              | |:| |  ::|||| | :|||    :|:|   ||  :|:| : |  | | |||||
Db        328 LTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLELSESHPDS-GEQTVRCRGR 386

Qy        439 GTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTF-------- 490
              | | |:| |  |:|:|:|  |   |:| |:          | : | :|  ||:
Db        387 GMPQPNIIWSACRDLKRCPRELPPTLLGNS---------SEEESQLETNVTYWEEEQEFE 437

Qy        491 -------AKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLI 543
                    |:  ::|||  :| :| : :|: :|  :|  :: | :|:| |:|: |||||
Db        438 VVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLTIISLI 497

Qy        544 VLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGA 603
              :|:::|::|||||||:||||:| |||||||||||||||| || ||| |||
Db        498 ILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQLVLA------- 550

Qy        604 FGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGA 663
                                                |||||||||||||||:|||||:||||||
Db        551 ----------------------------TARSSEKQALMSELKIMSHLGPHLNVVNLLGA 582

Qy        664 CTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK---PKKELDIFGLNPADESTRSY 720
              ||| |||||||||| |||||:|||:|: :|| || :|   |  ||   | |      |:
Db        583 CTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL-PVGLPLPSH 641

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              | |: |::| |||| : ::  |||||: |   ||:||: | |  |      |  :   :
Db        642 VSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVPSAPERTCRA 701

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN-------------CVHRDLAARNVLL 826
              | :: |  |: :||: |:|||| |||||||||               ||||||||||:
Db        702 TLINE-SPVLSYMDLVGFSYQVANGMEFLASKNVRVVLVGQGSGCGECVHRDLAARNVLI 760

Qy        827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLW 886
              :||:|||||||||||| ||||:|||||||:|||||||::||||||||:|||||
Db        761 CEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLW 820

Qy        887 EIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHL 946
              |||:|||||| : ::  ||| || |||||:| ||: |:|||| ||| : | ||| |  |
Db        821 EIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQL 880

Qy        947 SEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGG 1006
              ::| ||  |||:       | |   |  :|: :        ||
Db        881 VLLLERLLGEGYKKAR-------LPGFHG--LRSPLDTSSVLYTAVQPNE---------- 921

Qy       1007 LDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTF-----IK 1061
                 |: ||||||  || ||  | |      |  |  | :   ::|||      ::
Db        922 -------GDNDYIIPLP--DPKPEVADEGPLEGSPSLAS--STLNEVNTSSTISCDSPLE 970

Qy       1062 REDE 1065
                :||
Db        971 PQDE 974


RESULT 46
US-10-450-763-51108
; Sequence 51108, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 51108
;   LENGTH: 2129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (1925)..(1956)
;   OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
;   OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=3.842e-18, raw
;   OTHER INFORMATION: score of 18.39
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (553)..(2069)
;   OTHER INFORMATION: Eukaryotic protein kinase domain identified by PFam,
;   OTHER INFORMATION: accession name pkinase, E-value=1.4e-126, PFam score of 433.9
US-10-450-763-51108

  Query Match             34.8%;  Score 1965.5;  DB 5;  Length 2129;
  Best Local Similarity   41.6%;  Pred. No. 2.6e-102;
```

```
  Matches  426;  Conservative  153;  Mismatches  286;  Indels  159;  Gaps   20;

Qy        123 DPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFNG 180
              || | |:|    :  : : :     |||| |||:  ||||  :|   :|  || ::||:|
Db         29 DPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFSG 88

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |  |
Db         89 IFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIGN 147

Qy        241 EVVDLQWTYP----------------GEVKG---------KGITMLEEIKVPSIKLVYT 274
              |||: :||||                | : |           :  |  : : | :||
Db        148 EVVNFEWTYPRKEVMWGQAGVGGGARNGWISGLQADFSPAPPDLGGLPNLLLQSGRLVEP 207

Qy        275 LT--------------VPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKP 319
              :|               :| | ::||| | |   ::  : :: | : |:| | |:: :
Db        208 VTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDHQDEKAINITVVESGYVRLLG 267

Qy        320 TFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENLT-EITTDVEKIQEIRYRSK 378
                  |:   ||  :   |   ||||| : | |:| || ::   ||       : | || |:
Db        268 EVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRTLGDSSAGEIALSTRNVSETRYVSE 327

Qy        379 LKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAE 438
              | |:| |  ::|||: | :|||    :|:|   ||  :|:| : |  | | |||||
Db        328 LTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLELSESHPDS-GEQTVRCRGR 386

Qy        439 GTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRDRSTVEGRVTF-------- 490
              | | |:| |  |:|:|:|  |   |:| |:         | : | :|  ||:
Db        387 GMPQPNIIWSACRDLKRCPRELPPTLLGNS---------SEEESQLETNVTYWEEEQEFE 437

Qy        491 -------AKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLI 543
                    |:  ::||| :| :| : :|: :|  :|  :: | :|:| |:|: |||||
Db        438 VVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLTIISLI 497

Qy        544 VLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGA 603
              :|:::|::|||||||||:||||:| |||||||||||||||| || ||| |||
Db        498 ILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQLPYDSTWELPRDQLVLA------- 550

Qy        604 FGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGA 663
                                        ||||||||||||||||:|||||||:||||||
Db        551 ----------------------------TARSSEKQALMSELKIMSHLGPHLNVVNLLGA 582

Qy        664 CTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK---PKKELDIFGLNPADESTRSY 720
              ||| |||||||||| |||||:|||:|: :|| || :|    |  ||    | |      |:
Db        583 CTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPSAELYSNAL-PVGLPLPSH 641

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              | |: |::| |||| : ::  |||||: |   ||:||: | |  |      |  :   :
Db        642 VSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVPSAPERTCRA 701

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN--------------CVHRDLAARNVLL 826
              | :: |  |: :||: |:|||| |||||||||              ||||||||||||:
Db        702 TLINE-SPVLSYMDLVGFSYQVANGMEFLASKNVRVVLVGQSGGCGECVHRDLAARNVLI 760

Qy        827 AQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLW 886
              :||:|||||||||||| ||||:|||||||:|||||||::||||||||||:|||||
Db        761 CEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLW 820

Qy        887 EIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHL 946
              |||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  : | || |  |
Db        821 EIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQL 880

Qy        947 SEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGG 1006
                ::| ||   |||:        |   |     |  :|: :        ||
Db        881 VLLLERLLGEGYKKAR-------LPGFHG--LRSPLDTSSVLYTAVQPNE---------- 921

Qy       1007 LDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTF-----IK 1061
                       |: ||||||  || ||  | |       |  |  | :   ::|||      ::
Db        922 -------GDNDYIIPLP--DPKPEVADEGPLEGSPSLAS--STLNEVNTSSTISCDSPLE 970

Qy       1062 REDE 1065
                :||
Db        971 PQDE 974
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```
RESULT 47
US-10-763-418-16
; Sequence 16, Application US/10763418
; Publication No. US20040185547A1
; GENERAL INFORMATION:
;  APPLICANT: MOHAMMADI, MOOSA
;  APPLICANT:  SCHLESSINGER, JOSEPH
;  APPLICANT:  HUBBARD, STEVAN R.
;  TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
;  TITLE OF INVENTION:  RECEPTOR TYROSINE KINASES
;  FILE REFERENCE: 038602/0847
;  CURRENT APPLICATION NUMBER: US/10/763,418
;  CURRENT FILING DATE:  2004-01-26
;  PRIOR APPLICATION NUMBER: US/09/664,526
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: 09/188,809
;  PRIOR FILING DATE: 1998-11-09
;  PRIOR APPLICATION NUMBER: 08/701,191
;  PRIOR FILING DATE: 1996-08-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-763-418-16

  Query Match             26.5%;  Score 1499.5;  DB 4;  Length 293;
  Best Local Similarity   77.1%;  Pred. No. 5.4e-77;
  Matches  293;  Conservative    0;  Mismatches    0;  Indels   87;  Gaps    1;

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 60

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 120

Qy        700 KPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759

Db        121 ------------------------------------------------------------ 120

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
                                              ||||||||||||||||||||||||||||||
Db        121 --------------------------SEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 153

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 213

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 273

Qy        940 RPSFYHLSEIVENLLPGQYK 959
              ||||||||||||||||||||
Db        274 RPSFYHLSEIVENLLPGQYK 293


RESULT 48
US-10-823-142A-2
; Sequence 2, Application US/10823142A
; Publication No. US20050181484A1
; GENERAL INFORMATION:
;  APPLICANT: AVENTIS PHARMA SA
;  APPLICANT:  GUILLAUME, Jean-Marc
;  APPLICANT:  DITTRICH, Werner
;  APPLICANT:  PEREZ, Sandrine
;  APPLICANT:  ANDREONI, Christine Michelle Pierrette
;  APPLICANT:  PAILLOT, Romain
```

```
;  TITLE OF INVENTION: METHOD FOR OBTAINING MASTOCYTE LINES FROM PIG TISSUES AND FOR PRO
;  TITLE OF INVENTION:  HEPARIN-TYPE MOLECULES
;  FILE REFERENCE: FRAV2003/0009 US NP
;  CURRENT APPLICATION NUMBER: US/10/823,142A
;  CURRENT FILING DATE:  2004-04-13
;  PRIOR APPLICATION NUMBER: 60/477,962
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: FR 0304671
;  PRIOR FILING DATE: 2003-04-14
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 972
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-10-823-142A-2

  Query Match             26.1%;  Score 1473;  DB 5;  Length 972;
  Best Local Similarity   36.2%;  Pred. No. 7.6e-75;
  Matches  366;  Conservative  147;  Mismatches  359;  Indels  140;  Gaps   31;

Qy         24 QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVT 83
Db         33 ELSPPSIQPAKSELIVSAGDEIRLFCTDPGSVKWTFETLGQLS--------ENTHAEWI- 83

Qy         84 VLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDD 143
Db         84 ---VEKAEAMNTGNYTC------TNEGGLSS-SIYVFVRDPEKLF----LVDPPLYGKED 129

Qy        144 DSAIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI-------------- 188
Db        130 NDALVRCPLTDPEVTNYSLTGCEG-KPLPKDL------TFVADPKAGITIKNVKREYHRL 182

Qy        189 ---CEATVKGKKFQTIPFNVYALKATSELDLEMEALKTV--------YKSGETIVVTCAV 237
Db        183 CLHCSANQGGK-------SVLSKKFTLKVRAAIRAVPVVAVSKASYLLREGEEFAVMCLI 235

Qy        238 FN-NEVVDLQW-----TYPGEVKGKG-----ITMLEEIKVPSIKLVYTLTVPEATVKDSG 286
Db        236 KDVSSSVDSMWIRENSQTKAQVKRNSWHQGDFNFLRQER---------LTISSARVNDSG 286

Qy        287 DYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PP 345
Db        287 VFMCYANNTFGSAN--VTTTLEVVDKGFINIFPMMNTTVFVNDGEDVDLIVEYEAYPKPE 344

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
Db        345 HRQWIYMNRTATDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNADVNSSV 403

Qy        406 TFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDI-KKCNNETSWTI 464
Db        404 TFNVYVNTKPEILT-----HDRLMNGMLQCVAAGFPEPTIDWYFCPGTEQRCSVP----- 453

Qy        465 LANNVSNIITEIHSRDRS-----TVEGRVTFAKVEETIAVRCLAKNLLGAENR------E 513
Db        454 ----VGPVDVQIQNSSVSPFGKLVIHSSIDYSAFKHNGTVECRAYNDVGKSSAFFNFAFK 509

Qy        514 LKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYI 573
Db        510 EQIHAHTLFTPLLIGFVIAAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYV 565

Qy        574 YVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTA 633
Db        566 YIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSA 625

Qy        634 RSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSF 693
Db        626 HLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSF 685

Qy        694 LSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSK 753
Db        686 ICSKQEDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPT 730

Qy        754 YSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKN 813
Db        731 KADKRRSA--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKN 783

Qy        814 CVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYT 873
Db        784 CIHRDLAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYT 843

Qy        874 TLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCW 933
Db        844 FESDVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCW 903

Qy        934 NSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR-MRVDS 984
Db        904 DADPLKRPTFKQIVQLIEKQISESTNHIYSNLANCSPHRENPAVDHSVRINS 955


RESULT 49
US-10-099-895-32
; Sequence 32, Application US/10099895
; Publication No. US20020177166A1
; GENERAL INFORMATION:
;  APPLICANT: BERNDT, Michael C
;  APPLICANT:  STOMSKI, Frank C
;  APPLICANT:  LOPEZ, Angel F
;  APPLICANT:  GUTHRIDGE, Mark A
;  TITLE OF INVENTION: A BINDING MOTIF OF A RECEPTOR
;  FILE REFERENCE: 3991/0K379
;  CURRENT APPLICATION NUMBER: US/10/099,895
;  CURRENT FILING DATE:  2002-03-14
;  PRIOR APPLICATION NUMBER: PCT/AU00/01118
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-099-895-32

  Query Match             25.7%;  Score 1454.5;  DB 4;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 8.6e-74;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

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; Publication No. US20030084466A1
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;  APPLICANT: BLUME-JENSEN, Peter
;  APPLICANT:  HUNTER, Tony
;  TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY
;  FILE REFERENCE: SALKINS.002C1
;  CURRENT APPLICATION NUMBER: US/10/192,867
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: US 60/175,625
;    2000-01-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00573
;    2001-01-08
;  NUMBER OF SEQ ID NOS: 6
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; SEQ ID NO 4
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US-10-192-867-4

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GenCore version 5.1.8
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OM protein - protein search, using sw model

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(without alignments)
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Searched: 250354 seqs, 46948837 residues

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Minimum DB seq length: 0
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5652	100.0	1089	9	US-10-517-905-2	Sequence 2, Appli
2	5652	100.0	1089	11	US-11-148-770-32	Sequence 32, Appl
3	5652	100.0	1089	11	US-11-076-427A-14	Sequence 14, Appl
4	5652	100.0	1089	11	US-11-075-047A-117	Sequence 117, App
5	5652	100.0	1089	11	US-11-177-894-26	Sequence 26, Appl
6	5652	100.0	1089	11	US-11-177-894-27	Sequence 27, Appl
7	5652	100.0	1089	11	US-11-177-894-28	Sequence 28, Appl
8	5652	100.0	1089	11	US-11-177-894-29	Sequence 29, Appl
9	5652	100.0	1089	11	US-11-233-510-28	Sequence 28, Appl
10	5652	100.0	1451	9	US-10-995-561-829	Sequence 829, App
11	5645	99.9	1089	9	US-10-517-905-21	Sequence 21, Appl
12	5643	99.8	1089	9	US-10-517-905-4	Sequence 4, Appli
13	5640	99.8	1089	9	US-10-517-905-25	Sequence 25, Appl
14	5637	99.7	1090	9	US-10-517-905-10	Sequence 10, Appl
15	5617.5	99.4	1084	9	US-10-517-905-23	Sequence 23, Appl
16	5617	99.4	1085	9	US-10-517-905-6	Sequence 6, Appli
17	5614.5	99.3	1086	9	US-10-517-905-8	Sequence 8, Appli
18	5602.5	99.1	1084	9	US-10-517-905-12	Sequence 12, Appl
19	5533	97.9	1089	9	US-10-517-905-27	Sequence 27, Appl
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21	2351.5	41.6	1106	11	US-11-075-047A-119	Sequence 119, App
22	2008	35.5	383	11	US-11-092-168-7	Sequence 7, Appli
23	1457.5	25.8	972	11	US-11-177-894-17	Sequence 17, Appl
24	1454.5	25.7	976	8	US-10-511-937-2423	Sequence 2423, Ap
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30	1454.5	25.7	976	11	US-11-177-894-21	Sequence 21, Appl
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37	1287	22.8	1338	8	US-10-505-928-634	Sequence 634, App
38	1287	22.8	1338	8	US-10-505-928-857	Sequence 857, App
39	1287	22.8	1338	9	US-10-821-234-1622	Sequence 1622, Ap
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43	1218.5	21.6	1356	9	US-10-995-561-906	Sequence 906, App
44	1214	21.5	1362	11	US-11-043-693-33	Sequence 33, Appl
45	1214	21.5	1368	11	US-11-043-693-34	Sequence 34, Appl
46	1188	21.0	1343	9	US-10-541-814-2	Sequence 2, Appli
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148	429.5	7.6	976	9	US-10-966-483-2	Sequence 2, Appli
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150	429.5	7.6	976	11	US-11-233-796-2	Sequence 2, Appli
151	429.5	7.6	976	11	US-11-203-251A-77	Sequence 77, Appl
152	428.5	7.6	1035	9	US-10-966-483-20	Sequence 20, Appl
153	428.5	7.6	1035	11	US-11-021-441-4	Sequence 4, Appli
154	428.5	7.6	1055	11	US-11-072-175-139	Sequence 139, App
155	428.5	7.6	1055	11	US-11-203-251A-86	Sequence 86, Appl
156	428	7.6	998	11	US-11-203-251A-83	Sequence 83, Appl
157	427.5	7.6	1055	11	US-11-169-041-155	Sequence 155, App
158	427.5	7.6	1055	11	US-11-051-720-1417	Sequence 1417, Ap
159	422.5	7.5	985	11	US-11-113-424-61	Sequence 61, Appl
160	417	7.4	998	9	US-10-510-524-1	Sequence 1, Appli
161	417	7.4	998	11	US-11-203-251A-88	Sequence 88, Appl
162	415.5	7.4	980	9	US-10-330-773-507	Sequence 507, App
163	415.5	7.4	995	9	US-10-330-773-505	Sequence 505, App
164	414	7.3	456	9	US-10-966-483-34	Sequence 34, Appl
165	414	7.3	456	11	US-11-021-441-18	Sequence 18, Appl
166	414	7.3	1259	10	US-11-223-945-40	Sequence 40, Appl
167	413.5	7.3	1001	9	US-10-330-773-510	Sequence 510, App
168	410	7.3	987	9	US-10-949-720-395	Sequence 395, App
169	410	7.3	987	11	US-11-203-251A-89	Sequence 89, Appl
170	409.5	7.2	1255	9	US-10-770-726-62	Sequence 62, Appl
171	409.5	7.2	1255	11	US-11-113-202-10	Sequence 10, Appl
172	409.5	7.2	1255	11	US-11-202-516-4	Sequence 4, Appli
173	409.5	7.2	1255	11	US-11-175-405-2	Sequence 2, Appli
174	408.5	7.2	1255	8	US-10-538-066-364	Sequence 364, App
175	408.5	7.2	1255	10	US-11-223-945-43	Sequence 43, Appl
176	408.5	7.2	1255	11	US-11-022-562-213	Sequence 213, App
177	408.5	7.2	1255	11	US-11-033-039-553	Sequence 553, App
178	408.5	7.2	1255	11	US-11-155-288-9	Sequence 9, Appli
179	408.5	7.2	1258	11	US-11-033-039-930	Sequence 930, App
180	407	7.2	990	9	US-10-821-234-1201	Sequence 1201, Ap
181	406	7.2	620	8	US-10-511-937-2959	Sequence 2959, Ap
182	403	7.1	479	9	US-10-966-483-36	Sequence 36, Appl
183	403	7.1	479	11	US-11-021-441-20	Sequence 20, Appl
184	403	7.1	490	9	US-10-966-483-42	Sequence 42, Appl
185	403	7.1	490	11	US-11-021-441-26	Sequence 26, Appl
186	403	7.1	497	9	US-10-966-483-38	Sequence 38, Appl
187	403	7.1	497	9	US-10-966-483-40	Sequence 40, Appl
188	403	7.1	497	11	US-11-021-441-22	Sequence 22, Appl
189	403	7.1	497	11	US-11-021-441-24	Sequence 24, Appl
190	401	7.1	617	11	US-11-218-020-7	Sequence 7, Appli
191	401	7.1	1400	9	US-10-501-035-274	Sequence 274, App
192	389	6.9	1154	9	US-10-330-773-867	Sequence 867, App
193	387.5	6.9	1142	9	US-10-501-035-376	Sequence 376, App
194	387.5	6.9	1142	11	US-11-109-156-22	Sequence 22, Appl
195	387	6.8	764	11	US-11-104-110-8	Sequence 8, Appli
196	387	6.8	764	11	US-11-104-111-28	Sequence 28, Appl
197	387	6.8	764	11	US-11-075-047A-4	Sequence 4, Appli
198	387	6.8	767	11	US-11-043-693-2	Sequence 2, Appli
199	387	6.8	1052	11	US-11-113-424-22	Sequence 22, Appl
200	384.5	6.8	1035	11	US-11-113-424-20	Sequence 20, Appl
201	384.5	6.8	1036	9	US-10-242-586-104	Sequence 104, App
202	384.5	6.8	1036	9	US-10-242-902-104	Sequence 104, App
203	384.5	6.8	1036	9	US-10-243-116-104	Sequence 104, App
204	384.5	6.8	1036	9	US-10-243-136-104	Sequence 104, App
205	384.5	6.8	1036	9	US-10-243-189-104	Sequence 104, App
206	384.5	6.8	1036	9	US-10-243-215-104	Sequence 104, App
207	384.5	6.8	1036	9	US-10-243-236-104	Sequence 104, App
208	384.5	6.8	1036	9	US-10-243-298-104	Sequence 104, App
209	384.5	6.8	1036	9	US-10-243-304-104	Sequence 104, App
210	384.5	6.8	1036	9	US-10-243-338-104	Sequence 104, App
211	384.5	6.8	1036	9	US-10-243-345-104	Sequence 104, App
212	384.5	6.8	1036	9	US-10-243-357-104	Sequence 104, App
213	384.5	6.8	1036	9	US-10-245-083-104	Sequence 104, App
214	384.5	6.8	1036	9	US-10-247-015-104	Sequence 104, App
215	383.5	6.8	391	10	US-11-223-945-38	Sequence 38, Appl
216	383	6.8	550	8	US-10-538-066-757	Sequence 757, App
217	383	6.8	1342	9	US-10-770-726-63	Sequence 63, Appl
218	383	6.8	1342	11	US-11-113-202-12	Sequence 12, Appl
219	383	6.8	1342	11	US-11-113-202-14	Sequence 14, Appl
220	378.5	6.7	612	11	US-11-218-020-9	Sequence 9, Appli
221	370	6.5	256	9	US-10-877-346-74	Sequence 74, Appl
222	356.5	6.3	546	9	US-10-661-966-18	Sequence 18, Appl
223	355	6.3	1005	11	US-11-203-251A-84	Sequence 84, Appl
224	351.5	6.2	1012	9	US-10-979-095-3	Sequence 3, Appli
225	349	6.2	777	11	US-11-043-693-3	Sequence 3, Appli
226	341.5	6.0	382	11	US-11-096-568A-17025	Sequence 17025, A
227	341.5	6.0	394	11	US-11-096-568A-17024	Sequence 17024, A
228	341.5	6.0	423	11	US-11-096-568A-17023	Sequence 17023, A
229	321.5	5.7	1000	9	US-10-455-772-274	Sequence 274, App
230	320.5	5.7	1124	11	US-11-195-197-9	Sequence 9, Appli
231	317.5	5.6	1124	11	US-11-114-979-1	Sequence 1, Appli
232	317	5.6	1006	8	US-10-511-937-2425	Sequence 2425, Ap
233	317	5.6	1006	11	US-11-203-251A-90	Sequence 90, Appl
234	310	5.5	525	11	US-11-096-568A-18655	Sequence 18655, A
235	303.5	5.4	518	11	US-11-226-701-13	Sequence 13, Appl
236	303.5	5.4	579	11	US-11-261-346-2	Sequence 2, Appli
237	303	5.4	1019	9	US-10-455-772-1120	Sequence 1120, Ap
238	300	5.3	277	11	US-11-151-601-4	Sequence 4, Appli
239	298	5.3	1170	9	US-10-330-773-864	Sequence 864, App
240	296.5	5.2	567	11	US-11-016-503-10	Sequence 10, Appl

241	294.5	5.2	272	11	US-11-096-568A-18656	Sequence 18656, A
242	294.5	5.2	567	11	US-11-016-503-2	Sequence 2, Appli
243	292.5	5.2	278	8	US-10-370-959-17	Sequence 17, Appl
244	292.5	5.2	278	8	US-10-370-959-31	Sequence 31, Appl
245	292.5	5.2	278	9	US-10-055-877-149	Sequence 149, App
246	292.5	5.2	278	11	US-11-103-065-4	Sequence 4, Appli
247	292.5	5.2	278	11	US-11-151-601-10	Sequence 10, Appl
248	291.5	5.2	285	11	US-11-096-568A-6170	Sequence 6170, Ap
249	291.5	5.2	295	11	US-11-096-568A-6169	Sequence 6169, Ap
250	291.5	5.2	557	11	US-11-016-503-4	Sequence 4, Appli
251	291.5	5.2	1024	9	US-10-455-772-784	Sequence 784, App
252	291.5	5.2	1024	9	US-10-455-772-788	Sequence 788, App
253	291.5	5.2	1071	11	US-11-043-752-44	Sequence 44, Appl
254	291	5.1	338	11	US-11-096-568A-30980	Sequence 30980, A
255	291	5.1	346	11	US-11-096-568A-30979	Sequence 30979, A
256	290.5	5.1	272	8	US-10-370-959-27	Sequence 27, Appl
257	288	5.1	269	9	US-10-455-772-786	Sequence 786, App
258	287.5	5.1	571	11	US-11-096-568A-19952	Sequence 19952, A
259	287.5	5.1	677	11	US-11-096-568A-19951	Sequence 19951, A
260	287.5	5.1	792	11	US-11-096-568A-19950	Sequence 19950, A
261	287	5.1	1018	9	US-10-455-772-272	Sequence 272, App
262	286.5	5.1	659	9	US-10-661-966-14	Sequence 14, Appl
263	286	5.1	394	11	US-11-043-752-2	Sequence 2, Appli
264	282.5	5.0	352	11	US-11-096-568A-7450	Sequence 7450, Ap
265	280.5	5.0	765	9	US-10-661-966-10	Sequence 10, Appl
266	280.5	5.0	765	9	US-10-661-966-15	Sequence 15, Appl
267	280.5	5.0	778	11	US-11-096-568A-27680	Sequence 27680, A
268	280.5	5.0	783	9	US-10-661-966-2	Sequence 2, Appli
269	280.5	5.0	835	11	US-11-096-568A-27679	Sequence 27679, A
270	280.5	5.0	963	11	US-11-096-568A-27678	Sequence 27678, A
271	277.5	4.9	648	9	US-10-661-966-16	Sequence 16, Appl
272	276	4.9	707	9	US-10-453-372-998	Sequence 998, App
273	276	4.9	1902	9	US-10-453-372-1004	Sequence 1004, Ap
274	276	4.9	5636	11	US-11-065-695-20	Sequence 20, Appl
275	275	4.9	4495	9	US-10-453-372-1002	Sequence 1002, Ap
276	274	4.8	424	11	US-11-096-568A-17960	Sequence 17960, A
277	274	4.8	429	11	US-11-096-568A-17959	Sequence 17959, A
278	274	4.8	430	11	US-11-096-568A-17958	Sequence 17958, A
279	273.5	4.8	344	8	US-10-511-814-2	Sequence 2, Appli
280	273.5	4.8	648	11	US-11-109-156-17	Sequence 17, Appl
281	273.5	4.8	648	11	US-11-219-264-2	Sequence 2, Appli
282	273.5	4.8	668	11	US-11-219-264-7	Sequence 7, Appli
283	272.5	4.8	648	8	US-10-511-814-14	Sequence 14, Appl
284	272.5	4.8	648	9	US-10-661-966-12	Sequence 12, Appl
285	272.5	4.8	648	9	US-10-661-966-17	Sequence 17, Appl
286	272	4.8	712	9	US-10-453-372-1000	Sequence 1000, Ap
287	270.5	4.8	446	11	US-11-096-568A-27457	Sequence 27457, A
288	270.5	4.8	454	11	US-11-096-568A-27456	Sequence 27456, A
289	270.5	4.8	475	11	US-11-096-568A-27455	Sequence 27455, A
290	270.5	4.8	486	11	US-11-096-568A-28698	Sequence 28698, A
291	270.5	4.8	494	11	US-11-096-568A-28697	Sequence 28697, A
292	270.5	4.8	515	11	US-11-096-568A-28696	Sequence 28696, A
293	270	4.8	274	11	US-11-096-568A-7451	Sequence 7451, Ap
294	270	4.8	606	10	US-11-251-465-19	Sequence 19, Appl
295	269	4.8	847	9	US-10-501-035-327	Sequence 327, App
296	268.5	4.8	231	9	US-10-455-772-1124	Sequence 1124, Ap
297	268	4.7	389	11	US-11-096-568A-21738	Sequence 21738, A
298	268	4.7	392	11	US-11-096-568A-21737	Sequence 21737, A
299	268	4.7	420	11	US-11-096-568A-21736	Sequence 21736, A
300	265.5	4.7	368	11	US-11-096-568A-15485	Sequence 15485, A
301	259.5	4.6	731	11	US-11-096-568A-28611	Sequence 28611, A
302	259.5	4.6	748	11	US-11-096-568A-28610	Sequence 28610, A
303	259.5	4.6	880	11	US-11-096-568A-28609	Sequence 28609, A
304	257.5	4.6	813	8	US-10-511-814-16	Sequence 16, Appl
305	257.5	4.6	813	9	US-10-661-966-19	Sequence 19, Appl
306	257	4.5	730	11	US-11-096-568A-28246	Sequence 28246, A
307	257	4.5	747	11	US-11-096-568A-28245	Sequence 28245, A
308	257	4.5	879	11	US-11-096-568A-28244	Sequence 28244, A
309	251	4.4	256	9	US-10-877-346-72	Sequence 72, Appl
310	251	4.4	256	11	US-11-113-424-183	Sequence 183, App
311	251	4.4	276	11	US-11-096-568A-30981	Sequence 30981, A
312	251	4.4	685	9	US-10-661-966-3	Sequence 3, Appli
313	250	4.4	276	11	US-11-096-568A-15486	Sequence 15486, A
314	250	4.4	835	11	US-11-186-283-8	Sequence 8, Appli
315	249.5	4.4	851	11	US-11-096-568A-29030	Sequence 29030, A
316	249	4.4	215	11	US-11-096-568A-6171	Sequence 6171, Ap
317	248.5	4.4	378	11	US-11-096-568A-27938	Sequence 27938, A
318	248.5	4.4	440	11	US-11-096-568A-27937	Sequence 27937, A
319	247	4.4	71	11	US-11-114-979-5	Sequence 5, Appli
320	245.5	4.3	753	11	US-11-096-568A-29031	Sequence 29031, A
321	244.5	4.3	370	11	US-11-096-568A-23307	Sequence 23307, A
322	244	4.3	570	11	US-11-075-047A-8	Sequence 8, Appli
323	244	4.3	635	11	US-11-096-568A-34256	Sequence 34256, A
324	244	4.3	684	11	US-11-096-568A-34255	Sequence 34255, A
325	244	4.3	850	11	US-11-096-568A-34254	Sequence 34254, A
326	243	4.3	835	11	US-11-186-283-2	Sequence 2, Appli
327	242.5	4.3	371	11	US-11-096-568A-24782	Sequence 24782, A
328	242.5	4.3	378	11	US-11-096-568A-24781	Sequence 24781, A
329	242	4.3	739	9	US-10-661-966-20	Sequence 20, Appl
330	242	4.3	838	11	US-11-087-099-829	Sequence 829, App
331	241	4.3	885	11	US-11-096-568A-29228	Sequence 29228, A
332	240.5	4.3	858	11	US-11-087-099-11449	Sequence 11449, A
333	240	4.2	499	11	US-11-096-568A-29032	Sequence 29032, A
334	240	4.2	1307	11	US-11-087-099-4253	Sequence 4253, Ap
335	239.5	4.2	438	11	US-11-096-568A-23781	Sequence 23781, A
336	239	4.2	1303	11	US-11-087-099-10526	Sequence 10526, A
337	239	4.2	1478	11	US-11-188-298-6040	Sequence 6040, Ap
338	239	4.2	1478	11	US-11-188-298-8632	Sequence 8632, Ap
339	239	4.2	1478	11	US-11-188-298-13053	Sequence 13053, A
340	238.5	4.2	714	11	US-11-096-568A-29230	Sequence 29230, A
341	238.5	4.2	720	11	US-11-096-568A-29229	Sequence 29229, A
342	238	4.2	654	11	US-11-188-298-13949	Sequence 13949, A
343	238	4.2	676	11	US-11-096-568A-28836	Sequence 28836, A
344	237.5	4.2	856	11	US-11-096-568A-29938	Sequence 29938, A
345	237	4.2	425	9	US-10-455-772-1104	Sequence 1104, Ap
346	237	4.2	550	11	US-11-096-568A-28837	Sequence 28837, A
347	237	4.2	847	11	US-11-087-099-10994	Sequence 10994, A
348	236.5	4.2	592	11	US-11-188-298-2229	Sequence 2229, Ap
349	236.5	4.2	923	11	US-11-087-099-8023	Sequence 8023, Ap
350	236.5	4.2	923	11	US-11-188-298-22194	Sequence 22194, A
351	236	4.2	633	11	US-11-188-298-782	Sequence 782, App
352	235.5	4.2	344	11	US-11-188-298-4616	Sequence 4616, Ap
353	235	4.2	451	11	US-11-188-298-6556	Sequence 6556, Ap
354	235	4.2	1299	11	US-11-087-099-9446	Sequence 9446, Ap
355	234.5	4.1	98	11	US-11-086-482-6	Sequence 6, Appli
356	234.5	4.1	807	11	US-11-096-568A-30427	Sequence 30427, A
357	234.5	4.1	821	11	US-11-096-568A-30426	Sequence 30426, A
358	234.5	4.1	860	11	US-11-087-099-6246	Sequence 6246, Ap
359	234	4.1	489	11	US-11-188-298-9657	Sequence 9657, Ap
360	234	4.1	513	11	US-11-087-099-11726	Sequence 11726, A
361	234	4.1	577	11	US-11-124-368A-232	Sequence 232, App
362	234	4.1	852	11	US-11-096-568A-29011	Sequence 29011, A
363	234	4.1	865	11	US-11-096-568A-29010	Sequence 29010, A
364	234	4.1	1062	11	US-11-188-298-7278	Sequence 7278, Ap
365	233.5	4.1	186	8	US-10-370-959-14	Sequence 14, Appl
366	233.5	4.1	309	11	US-11-096-568A-27939	Sequence 27939, A
367	233.5	4.1	435	11	US-11-204-709-19	Sequence 19, Appl
368	233.5	4.1	506	9	US-10-455-772-1100	Sequence 1100, Ap
369	233	4.1	223	11	US-11-096-568A-15487	Sequence 15487, A
370	233	4.1	454	11	US-11-096-568A-28838	Sequence 28838, A
371	232.5	4.1	278	11	US-11-188-298-19368	Sequence 19368, A
372	232	4.1	631	11	US-11-188-298-4923	Sequence 4923, Ap
373	231	4.1	489	9	US-10-455-772-1098	Sequence 1098, Ap
374	231	4.1	489	9	US-10-455-772-1110	Sequence 1110, Ap
375	231	4.1	572	11	US-11-075-047A-44	Sequence 44, Appl
376	230.5	4.1	583	11	US-11-075-047A-125	Sequence 125, App
377	230.5	4.1	583	11	US-11-075-047A-128	Sequence 128, App
378	230.5	4.1	631	11	US-11-188-298-21358	Sequence 21358, A
379	230.5	4.1	652	11	US-11-096-568A-18260	Sequence 18260, A
380	230	4.1	489	9	US-10-455-772-1106	Sequence 1106, Ap
381	230	4.1	489	9	US-10-455-772-1108	Sequence 1108, Ap
382	230	4.1	584	11	US-11-096-568A-12723	Sequence 12723, A
383	230	4.1	619	11	US-11-096-568A-12722	Sequence 12722, A
384	230	4.1	644	11	US-11-096-568A-12721	Sequence 12721, A
385	228.5	4.0	438	11	US-11-096-568A-18262	Sequence 18262, A
386	228.5	4.0	451	11	US-11-096-568A-18261	Sequence 18261, A

387	228	4.0	506	11	US-11-188-298-8068	Sequence 8068, Ap
388	228	4.0	872	11	US-11-096-568A-30927	Sequence 30927, A
389	228	4.0	885	11	US-11-096-568A-30926	Sequence 30926, A
390	228	4.0	1338	11	US-11-087-099-11043	Sequence 11043, A
391	228	4.0	1338	11	US-11-188-298-21213	Sequence 21213, A
392	227.5	4.0	318	11	US-11-188-298-7355	Sequence 7355, Ap
393	227.5	4.0	654	11	US-11-046-668-4	Sequence 4, Appli
394	227.5	4.0	683	11	US-11-046-668-2	Sequence 2, Appli
395	227	4.0	601	11	US-11-188-298-17935	Sequence 17935, A
396	226.5	4.0	1320	11	US-11-188-298-19369	Sequence 19369, A
397	226	4.0	226	9	US-10-469-469-275	Sequence 275, App
398	226	4.0	823	11	US-11-188-298-6352	Sequence 6352, Ap
399	226	4.0	893	11	US-11-096-568A-29014	Sequence 29014, A
400	225.5	4.0	513	11	US-11-087-099-7631	Sequence 7631, Ap
401	225.5	4.0	714	11	US-11-096-568A-29012	Sequence 29012, A
402	225.5	4.0	714	11	US-11-096-568A-30928	Sequence 30928, A
403	225	4.0	182	11	US-11-096-568A-7452	Sequence 7452, Ap
404	225	4.0	413	11	US-11-188-298-18832	Sequence 18832, A
405	225	4.0	489	9	US-10-455-772-1102	Sequence 1102, Ap
406	225	4.0	566	11	US-11-188-298-13476	Sequence 13476, A
407	224	4.0	416	11	US-11-188-298-7491	Sequence 7491, Ap
408	224	4.0	440	11	US-11-188-298-20398	Sequence 20398, A
409	224	4.0	461	11	US-11-188-298-11399	Sequence 11399, A
410	223.5	4.0	114	11	US-11-072-512-2659	Sequence 2659, Ap
411	223.5	4.0	285	11	US-11-188-298-7544	Sequence 7544, Ap
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413	223.5	4.0	847	11	US-11-087-099-3302	Sequence 3302, Ap
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415	223	3.9	413	11	US-11-096-568A-5905	Sequence 5905, Ap
416	223	3.9	414	11	US-11-096-568A-5904	Sequence 5904, Ap
417	223	3.9	654	11	US-11-096-568A-30428	Sequence 30428, A
418	223	3.9	660	11	US-11-188-298-4604	Sequence 4604, Ap
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422	222.5	3.9	748	11	US-11-096-568A-29940	Sequence 29940, A
423	222.5	3.9	783	11	US-11-096-568A-29939	Sequence 29939, A
424	222.5	3.9	1133	9	US-10-821-234-1219	Sequence 1219, Ap
425	222	3.9	146	11	US-11-086-482-5	Sequence 5, Appli
426	222	3.9	483	11	US-11-188-298-4164	Sequence 4164, Ap
427	221.5	3.9	821	11	US-11-096-568A-30590	Sequence 30590, A
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431	220.5	3.9	698	11	US-11-096-568A-30741	Sequence 30741, A
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476	215.5	3.8	855	11	US-11-096-568A-29018	Sequence 29018, A
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487	214	3.8	654	11	US-11-096-568A-27740	Sequence 27740, A
488	214	3.8	804	11	US-11-096-568A-27739	Sequence 27739, A
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494	213.5	3.8	738	11	US-11-188-298-1583	Sequence 1583, Ap
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496	213.5	3.8	1070	9	US-10-537-002-14	Sequence 14, Appl
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ALIGNMENTS

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RESULT 1
US-10-517-905-2
; Sequence 2, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-2
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Qy       1081 SDLVEDSFL 1089
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RESULT 2
US-11-148-770-32
; Sequence 32, Application US/11148770
; Publication No. US20060019280A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LEI L.
; APPLICANT: FRAZIER, MARSHA L.
; TITLE OF INVENTION: MUTATIONS IN KIT CONFER IMATINIB RESISTANCE IN
; TITLE OF INVENTION: GASTROINTESTINAL STROMAL TUMORS
; FILE REFERENCE: UTXC:869US
; CURRENT APPLICATION NUMBER: US/11/148,770
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/578,403
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-148-770-32

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  Query Match           100.0%;  Score 5652;  DB 11;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-11-076-427A-14
; Sequence 14, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-14

Query Match 100.0%; Score 5652; DB 11; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
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Db       1081 SDLVEDSFL 1089
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RESULT 4
US-11-075-047A-117
; Sequence 117, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.

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;  TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
;  FILE REFERENCE: 28967/39700A
;  CURRENT APPLICATION NUMBER: US/11/075,047A
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/550,907
;  PRIOR FILING DATE: 2004-03-07
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-075-047A-117

  Query Match           100.0%;  Score 5652;  DB 11;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 5
US-11-177-894-26
; Sequence 26, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: PDGFRA amino acid sequence
US-11-177-894-26

  Query Match           100.0%;  Score 5652;  DB 11;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Qy       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Db       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy      1081 SDLVEDSFL 1089
Db      1081 SDLVEDSFL 1089
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RESULT 6
US-11-177-894-27
; Sequence 27, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: PDGFRA amino acid sequence
US-11-177-894-27

  Query Match           100.0%;  Score 5652;  DB 11;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db         1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy        61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db        61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy       121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db       121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy       181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db       181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Db       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 7
US-11-177-894-28
; Sequence 28, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PDGFRA amino acid sequence
US-11-177-894-28

Query Match 100.0%; Score 5652; DB 11; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

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Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
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RESULT 8
US-11-177-894-29
; Sequence 29, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PDGFRA amino acid sequence
US-11-177-894-29

Query Match 100.0%; Score 5652; DB 11; Length 1089;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
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Qy       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
Db       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
Db       841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
Db       901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
Db       961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
Db      1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy      1081 SDLVEDSFL 1089
Db      1081 SDLVEDSFL 1089

RESULT 9
US-11-233-510-28
; Sequence 28, Application US/11233510
; Publication No. US20060063190A1
; GENERAL INFORMATION:
;  APPLICANT: Fischer, Timothy J.
;  APPLICANT:  Whitehead, Clark M.
;  APPLICANT:  Malinowski, Douglas P.
;  APPLICANT:  Marcelpoil, Raphael
;  APPLICANT:  Morel, Didier
;  TITLE OF INVENTION: Methods and Compositions for Evaluating
;  TITLE OF INVENTION:  Breast Cancer Prognosis
;  FILE REFERENCE: 46143/296738
;  CURRENT APPLICATION NUMBER: US/11/233,510
;  CURRENT FILING DATE:  2005-09-22
;  PRIOR APPLICATION NUMBER: 60/612,073
;  PRIOR FILING DATE: 2004-09-22
;  PRIOR APPLICATION NUMBER: 60/611,965
;  PRIOR FILING DATE: 2004-09-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-233-510-28

  Query Match           100.0%;  Score 5652;  DB 11;  Length 1089;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db         1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy        61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db        61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy       121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
Db       121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy       181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
Db       181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
Db       241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
Db       301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
Db       361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
Db       421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
Db       481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
Db       541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
Db       601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
Db       661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
Db       721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy       781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089

Db       1081 SDLVEDSFL 1089


RESULT 10
US-10-995-561-829
; Sequence 829, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 829
;   LENGTH: 1451
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1451)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-10-995-561-829

  Query Match           100.0%;  Score 5652;  DB 9;  Length 1451;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1089;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089

Db       1081 SDLVEDSFL 1089


RESULT 11
US-10-517-905-21
; Sequence 21, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
```

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;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-21

  Query Match            99.9%;  Score 5645;  DB 9;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRDIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 12
US-10-517-905-4
; Sequence 4, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-4

  Query Match            99.8%;  Score 5643;  DB 9;  Length 1089;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
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Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RVIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 13
US-10-517-905-25
; Sequence 25, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2

; SEQ ID NO 25
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-25

  Query Match            99.8%;  Score 5640;  DB 9;  Length 1089;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1087;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              : ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 KIIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089


RESULT 14
US-10-517-905-10
; Sequence 10, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 1090
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-10

  Query Match            99.7%;  Score 5637;  DB 9;  Length 1090;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1088;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRW--RVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRV 598
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Db        541 SLIVLVVIWKQKPRYEIRWRERVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRV 600

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 660

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 720

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
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Db        721 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 780

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 840

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 900

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
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Db        901 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 960

Qy        959 KKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGY 1018
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Db        961 KKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGY 1020

Qy       1019 IIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGI 1078
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Db       1021 IIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGI 1080

Qy       1079 DSSDLVEDSF 1088
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Db       1081 DSSDLVEDSF 1090


RESULT 15
US-10-517-905-23
; Sequence 23, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
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;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 1084
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-10-517-905-23

  Query Match            99.4%;  Score 5617.5;  DB 9;  Length 1084;
  Best Local Similarity  99.5%;  Pred. No. 0;
  Matches 1084;  Conservative    0;  Mismatches    0;  Indels    5;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRW-----ISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 595

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        596 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 655

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 715

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 775

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
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Db        776 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 835

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        836 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 895

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 955

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1015

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1016 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1075

Qy       1081 SDLVEDSFL 1089
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Db       1076 SDLVEDSFL 1084


RESULT 16
US-10-517-905-6
; Sequence 6, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 1085
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-6

  Query Match            99.4%;  Score 5617;  DB 9;  Length 1085;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
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Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
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Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
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Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
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Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
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Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
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Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
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Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
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Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
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Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
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Db        841 R----DSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 896

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
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Db        897 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 956

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
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Db        957 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1016

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1017 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1076

Qy       1081 SDLVEDSFL 1089
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Db       1077 SDLVEDSFL 1085
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RESULT 17
US-10-517-905-8
; Sequence 8, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
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;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 1086
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-8
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  Query Match           99.3%;  Score 5614.5;  DB 9;  Length 1086;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1085;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RDIM---PYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 897

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 957

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1017

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
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Db       1018 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1077

Qy       1081 SDLVEDSFL 1089
                ||||||||
Db       1078 SDLVEDSFL 1086


RESULT 18
US-10-517-905-12
; Sequence 12, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 1084
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-517-905-12

  Query Match             99.1%;  Score 5602.5;  DB 9;  Length 1084;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1083;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              |||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWRVIESI-----PYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 595

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 655

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 715

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 775

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 835

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 895

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 955

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1015

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1075

Qy       1081 SDLVEDSFL 1089
                ||||||||
Db       1076 SDLVEDSFL 1084


RESULT 19
US-10-517-905-27
; Sequence 27, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 1089
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (560)..(560)
;   OTHER INFORMATION: The 'Xaa' at location 560 stands for Lys, Asn, Arg, Ser, Thr,
;   OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
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; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: The 'Xaa' at location 561 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (562)..(562)
; OTHER INFORMATION: The 'Xaa' at location 562 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (563)..(563)
; OTHER INFORMATION: The 'Xaa' at location 563 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (564)..(564)
; OTHER INFORMATION: The 'Xaa' at location 564 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (566)..(566)
; OTHER INFORMATION: The 'Xaa' at location 566 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (567)..(567)
; OTHER INFORMATION: The 'Xaa' at location 567 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: The 'Xaa' at location 568 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (569)..(569)
; OTHER INFORMATION: The 'Xaa' at location 569 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (570)..(570)
; OTHER INFORMATION: The 'Xaa' at location 570 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (571)..(571)
; OTHER INFORMATION: The 'Xaa' at location 571 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (841)..(841)
; OTHER INFORMATION: The 'Xaa' at location 841 stands for Lys, Arg, Thr, or Ile.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (842)..(842)
; OTHER INFORMATION: The 'Xaa' at location 842 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (843)..(843)
; OTHER INFORMATION: The 'Xaa' at location 843 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (844)..(844)
; OTHER INFORMATION: The 'Xaa' at location 844 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (845)..(845)
; OTHER INFORMATION: The 'Xaa' at location 845 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (846)..(846)
; OTHER INFORMATION: The 'Xaa' at location 846 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (847)..(847)
; OTHER INFORMATION: The 'Xaa' at location 847 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (848)..(848)
; OTHER INFORMATION: The 'Xaa' at location 848 stands for Asn, Ser, Thr, Ile, Asp,
; OTHER INFORMATION: Gly, Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe.
US-10-517-905-27

Query Match 97.9%; Score 5533; DB 9; Length 1089;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1070; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGTSHPAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120

Qy        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPASYDSRQGFNG 180

Qy        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFNN 240

Qy        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 EVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAARQATREVK 300

Qy        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTLIENL 360

Qy        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVPSSILDL 420

Qy        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIITEIHSRD 480

Qy        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        481 RSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVII 540

Qy        541 SLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600
              ||||||||||||||||||      |      |||||||||||||||||||||||||||||
Db        541 SLIVLVVIWKQKPRYEIRWXXXXXIXXXXXXYIYVDPMQLPYDSRWEFPRDGLVLGRVLG 600

Qy        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 SGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNL 660

Qy        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSY 720

Qy        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 VILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKN 780

Qy        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLA 840

Qy        841 RDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 XXXXXXXXYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMM 900

Qy        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKK 960

Qy        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 SYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYII 1020

Qy       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 PLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSSTFIKREDETIEDIDMMDDIGIDS 1080

Qy       1081 SDLVEDSFL 1089
              |||||||||
Db       1081 SDLVEDSFL 1089
```

RESULT 20
US-11-076-427A-16
; Sequence 16, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-16

Query Match 41.6%; Score 2351.5; DB 11; Length 1106;
Best Local Similarity 44.0%; Pred. No. 2.6e-143;
Matches 503; Conservative 196; Mismatches 341; Indels 103; Gaps 25;

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Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   ::  |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
```

```
                |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :      |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||| : :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||  | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
                | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: ||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| ||||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||  |||||:||||:|: :|| || :
Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |       |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:|||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:||||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  |  ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :        ||                |: ||||||  || ||  | |       |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :     ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
```

```
Db       1104 SFL 1106


RESULT 21
US-11-075-047A-119
; Sequence 119, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
;  APPLICANT: ALITALO, et al.
;  TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
;  FILE REFERENCE: 28967/39700A
;  CURRENT APPLICATION NUMBER: US/11/075,047A
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/550,907
;  PRIOR FILING DATE: 2004-03-07
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
;   LENGTH: 1106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-075-047A-119

  Query Match             41.6%;  Score 2351.5;  DB 11;  Length 1106;
  Best Local Similarity   44.0%;  Pred. No. 2.6e-143;
  Matches  503;  Conservative  196;  Mismatches  341;  Indels  103;  Gaps   25;

Qy          6 PAFLVLGCLLTGLSLILC---QLSLPSIL-PNENEKVVQLNSSFSLRCFGESEVSWQYPM 61
              ||  : | ||  |||:|    |:|   ::  |   | |: ::|:| | | | : | |:  |
Db          8 PALALKGELLL-LSLLLLLEPQISQGLVVTPPGPELVLNVSSTFVLTCSGSAPVVWE-RM 65

Qy         62 SEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121
              |:|   ::     :   | | :|| ::: :   || | | :| ::  | : | : :||:|
Db         66 SQEPPQEM----AKAQDGTFSSVLTLTNLTGLDTGEYFCTHNDSRGLETD-ERKRLYIFV 120

Qy        122 PDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEG--VVPASYDSRQGFN 179
              ||| | |:|    :  : : :     |||| |||:  |||| :|   :|  || ::||:
Db        121 PDPTVGFLPNDAEELFIFLTEITEITIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFS 180

Qy        180 GTFTVGPYICEATVKGKKFQTIPFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN 239
              | |    |||: |:  ::  :  : || |: :| ::: : |::|| : || | : | |
Db        181 GIFEDRSYICKTTIGDREVDSDAYYVYRLQVSS-INVSVNAVQTVVRQGENITLMCIVIG 239

Qy        240 NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVY----TLTVPEATVKDSGDYECAARQA 295
              |:||: :|||| :  |:   ::| :    : : |     | :| | ::||| | |   ::
Db        240 NDVVNFEWTYPRKESGR---LVEPVTDFLLDMPYHIRSILHIPSAELEDSGTYTCNVTES 296

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLT 355
              : :: | : |:| | |:: :     |:   ||  :   |   ||||| : | |:| |
Db        297 VNDHQDEKAINITVVESGYVRLLGEVGTLQFAELHRSRTLQVVFEAYPPPTVLWFKDNRT 356

Qy        356 LIENLT-EITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLTQVP 414
              | ::   ||      : | || |:| |:| |  ::|||: | :|||    :|:|   ||
Db        357 LGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVP 416

Qy        415 SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANNVSNIIT 474
              :|:| : |  | | |||||   | | |:| |  |:|:|:|  |   |:| |:
Db        417 VRVLELSESHPDS-GEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPTLLGNS------ 469

Qy        475 EIHSRDRSTVEGRVTF--------------AKVEETIAVRCLAKNLLGAENRELKLVAP 519
              | : | :|  ||:                |:  ::|||  :| :| : :|: :|
Db        470 ---SEEESQLETNVTYWEEEQEFEVVSTLRLQHVDRPLSVRCTLRNAVGQDTQEVIVVPH 526

Qy        520 TLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQ 579
              :|  :: | :|:| |:|: |||||:|:::|::|||||||:||||:| ||||||||||||
Db        527 SLPFKVVVISAILALVVLTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMQ 586

Qy        580 LPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQ 639
              ||||| || ||| |||| |||||||:||| ||:||| ||  |||||||| ||||||||
Db        587 LPYDSTWELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQ 646

Qy        640 ALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPE 699
              |||||||||:|||||||:|||||||| |||||||||| |||||:|||:|: :|| || :

Db        647 ALMSELKIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSD 706

Qy        700 K---PKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSD 756
              |   |  ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:|
Db        707 KRRPPSAELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYAD 765

Qy        757 IQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVH 816
              |: | |  |      |  :   :  | :: |  |: :||: |:|||| ||||||||||||
Db        766 IESSNYMAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVH 824

Qy        817 RDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLS 876
              |||||||||: :||:|||||||||||||| ||||:||||||||:|||||||::||||||
Db        825 RDLAARNVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLS 884

Qy        877 DVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSE 936
              ||||:|||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  :
Db        885 DVWSFGILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEK 944

Qy        937 PEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMR-----------VDS 984
              | || |  | ::| ||   ||| |:::  :||:|||||: | :           :|:
Db        945 FEIRPPFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDT 1004

Qy        985 DNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQT 1044
              :           ||                  |: ||||||  || ||  | |      |
Db       1005 SSVLYTAVQPNE----------------GDNDYIIPLP--DPKPEVADEGPLEGSPSLA 1045

Qy       1045 SEESAIETGSSSSTF-----IKREDE---------TIE---DIDMMDDIGIDSSDL-VED 1086
              |  | :   ::|||      :: :||          :|   ::: : | |  :    ||
Db       1046 S--STLNEVNTSSTISCDSPLEPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAED 1103

Qy       1087 SFL 1089
              |||
Db       1104 SFL 1106


RESULT 22
US-11-092-168-7
; Sequence 7, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
;  APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
;  APPLICANT:  Montigen Pharmaceuticals, Inc.
;  APPLICANT:  Hurley, Laurence H.
;  APPLICANT:  Mahadevan, Daruka
;  APPLICANT:  Han, Haiyong
;  APPLICANT:  Bearss, David J.
;  APPLICANT:  Vankayalapati, Hariprasad
;  APPLICANT:  Bashyam, Sridevi
;  APPLICANT:  Munoz, Ruben M.
;  APPLICANT:  Warner, Steven L.
;  APPLICANT:  Della Croce, Kimiko
;  APPLICANT:  Von Hoff, Daniel D.
;  APPLICANT:  Grand, Cory L.
;  TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
;  FILE REFERENCE: 920214.00003CONT3
;  CURRENT APPLICATION NUMBER: US/11/092,168
;  CURRENT FILING DATE:  2005-03-29
;  PRIOR APPLICATION NUMBER: US 10/965,313
;    US 60/608,529
;    US 60/511,486
;    US 60/511,489
;  PRIOR FILING DATE: 2004-10-14
;    2004-09-09
;    2003-10-14
;    2003-10-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-092-168-7
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  Query Match           35.5%;  Score 2008;  DB 11;  Length 383;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-122;
  Matches  383;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        599 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIV 60

Qy        659 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTR 120

Qy        719 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEV 180

Qy        779 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFG 240

Qy        839 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPG 300

Qy        899 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQY 360

Qy        959 KKSYEKIHLDFLKSDHPAVARMR 981
              |||||||||||||||||||||||
Db        361 KKSYEKIHLDFLKSDHPAVARMR 383


RESULT 23
US-11-177-894-17
; Sequence 17, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 972
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-17

  Query Match           25.8%;  Score 1457.5;  DB 11;  Length 972;
  Best Local Similarity  36.1%;  Pred. No. 8.8e-86;
  Matches  354;  Conservative  147;  Mismatches  359;  Indels  121;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::: :|::     | |     | | : : :|          ||    ::|
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                 | | :|| |||   |  :          ||::| ||   |    : |  :  ::|:
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               ::  |  |||| |  :|   :|  |   | |       |   |
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
                |    :||   :  | :    | ||   : :   :   : : ||   ||| : :
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
                    |    ||  |      |             : :   |||:  | | ||| : | |
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
                        |: | :|||| | |  :     ||  |    :||  |:| |     |:
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
               | |  :   :      |    ||| |:| | | |  : | || :  | |   :  | :
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
                  ||    ||:          ::| | | | | |:|  |   ::     | ::|  :
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAPTLRSELTVA 528
               |  : :      :  |:  :  :  :    | | | | :|  :                |:
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKEQIHPHTLF 518

Qy        529 AAVLVLLVIV--IISLIVLVVIWK--QKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDS 584
              :|:  |||  :: :||::: :|  ||| ||::|:|:| |  :|: |:|:|| |||||
Db        519 TPLLIGFVIVAGMMCIIVMILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPTQLPYDH 576

Qy        585 RWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSE 644
              :|||||: | |: ||:|||||||| ||||| :|   | |||||||:|  :|::|||||
Db        577 KWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSE 636

Qy        645 LKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKE 704
              ||::::|| |:|||||||||  ||  :|||| ||||:|:| : ||||:    |   :
Db        637 LKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHAEA 696

Qy        705 LDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDR 764
                  | : ||: |      ::  :|||||      ||       |   :| :||:  |
Db        697 ALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKRRSV--R 739

Qy        765 PASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNV 824
                ||     :: :|   : :|:   | | ||||||||||:|| |||||||:||||||||:
Db        740 IGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNI 794

Qy        825 LLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGIL 884
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Qy        885 LWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFY 944
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Db        855 LWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFK 914

Qy        945 HLSEIVENLLPGQYKKSYEKI 965
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Db        915 QIVQLIEKQISESTNHIYSNL 935


RESULT 24
US-10-511-937-2423
; Sequence 2423, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
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;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2423
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-2423

  Query Match             25.7%;  Score 1454.5;  DB 8;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-85;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939


RESULT 25
US-11-148-770-31
; Sequence 31, Application US/11148770
; Publication No. US20060019280A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, LEI L.
;  APPLICANT:  FRAZIER, MARSHA L.
;  TITLE OF INVENTION: MUTATIONS IN KIT CONFER IMATINIB RESISTANCE IN
;  TITLE OF INVENTION:  GASTROINTESTINAL STROMAL TUMORS
;  FILE REFERENCE: UTXC:869US
;  CURRENT APPLICATION NUMBER: US/11/148,770
;  CURRENT FILING DATE:  2005-06-09
;  PRIOR APPLICATION NUMBER: 60/578,403
;  PRIOR FILING DATE: 2004-06-09
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-148-770-31

  Query Match             25.7%;  Score 1454.5;  DB 11;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-85;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518
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Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
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Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

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RESULT 26
US-11-177-894-15
; Sequence 15, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-15

Query Match 25.7%; Score 1454.5; DB 11; Length 976;
Best Local Similarity 35.7%; Pred. No. 1.4e-85;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;

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Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAPNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
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Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
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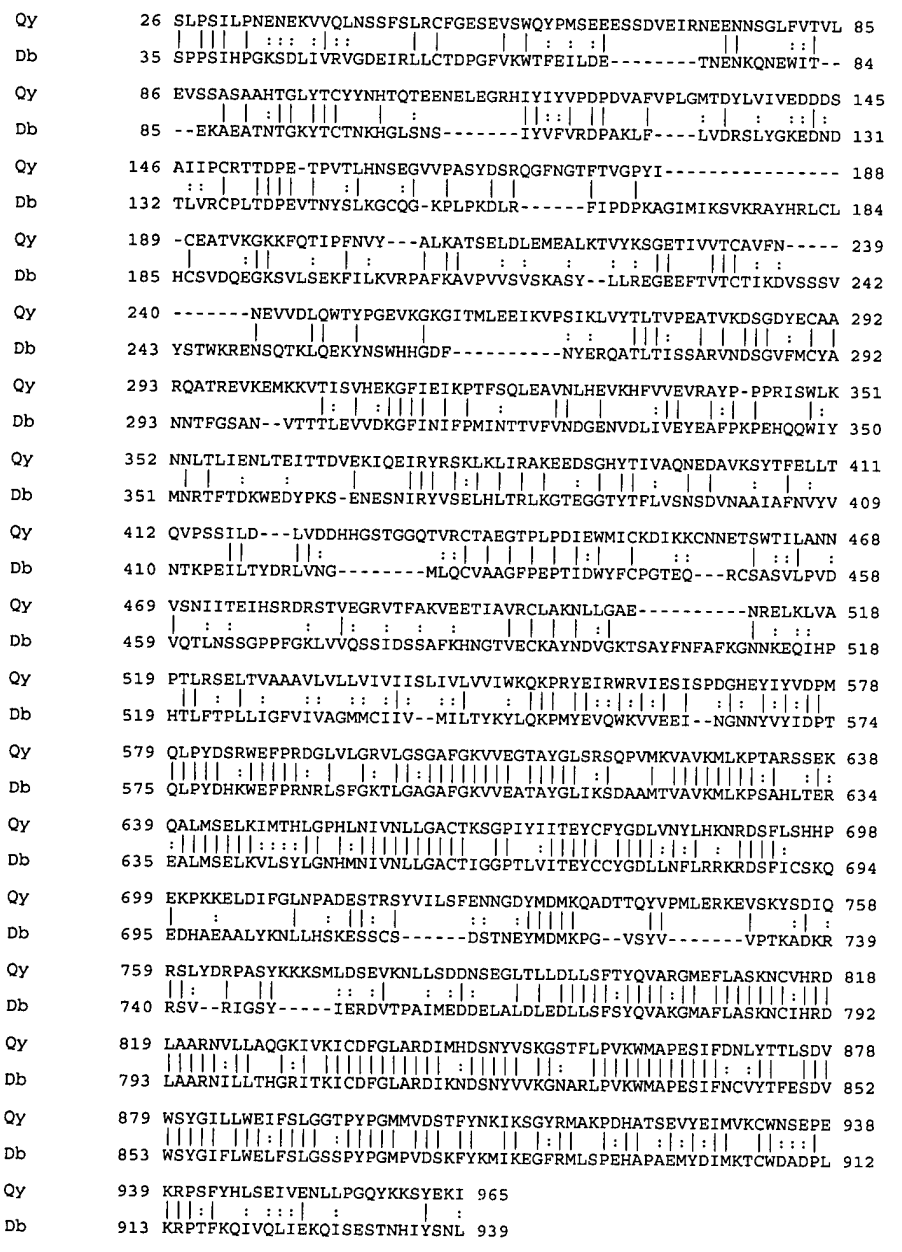
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Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
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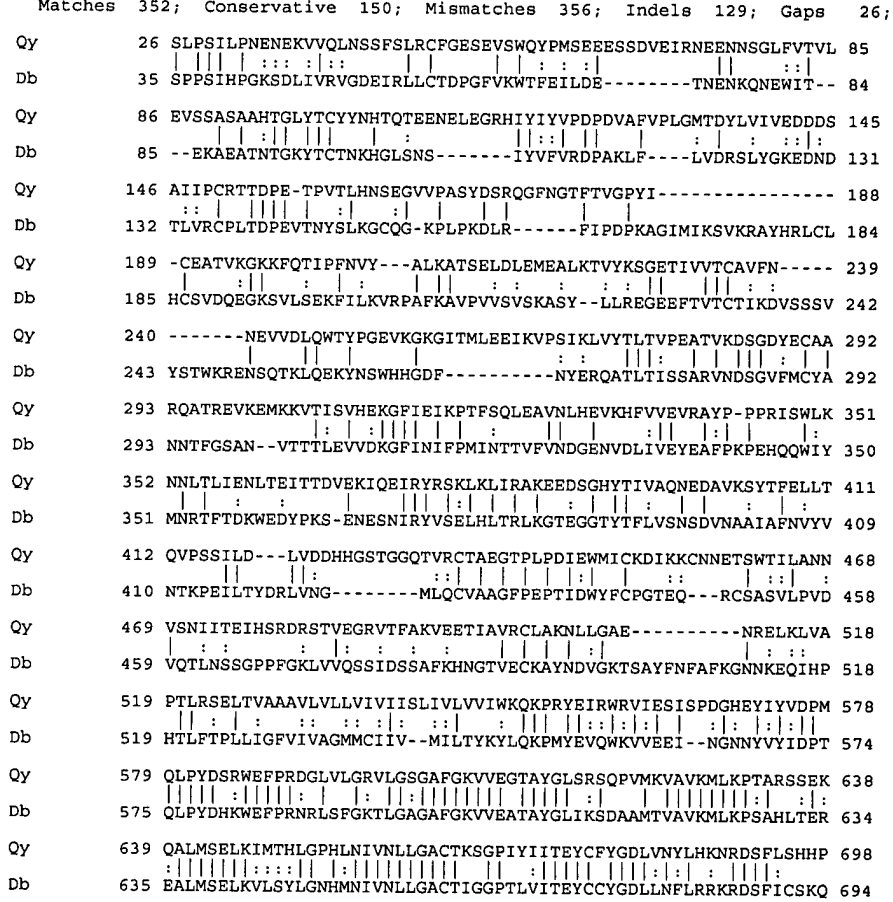
RESULT 27
US-11-177-894-16
; Sequence 16, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-16

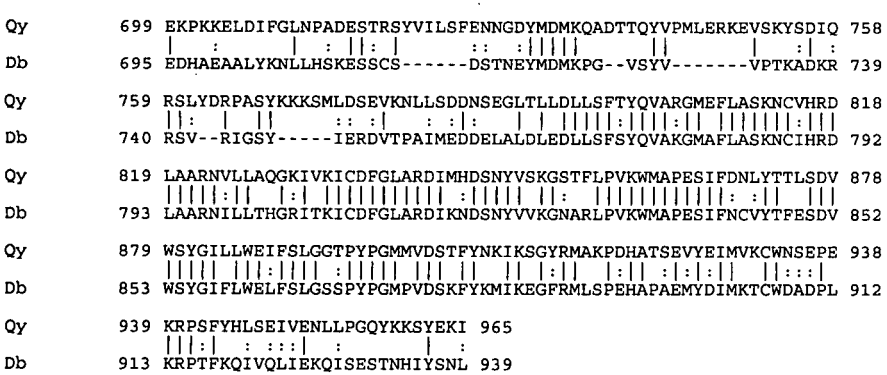
Query Match 25.7%; Score 1454.5; DB 11; Length 976;
Best Local Similarity 25.7%; Pred. No. 1.4e-85;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;



RESULT 28
US-11-177-894-18
; Sequence 18, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-18

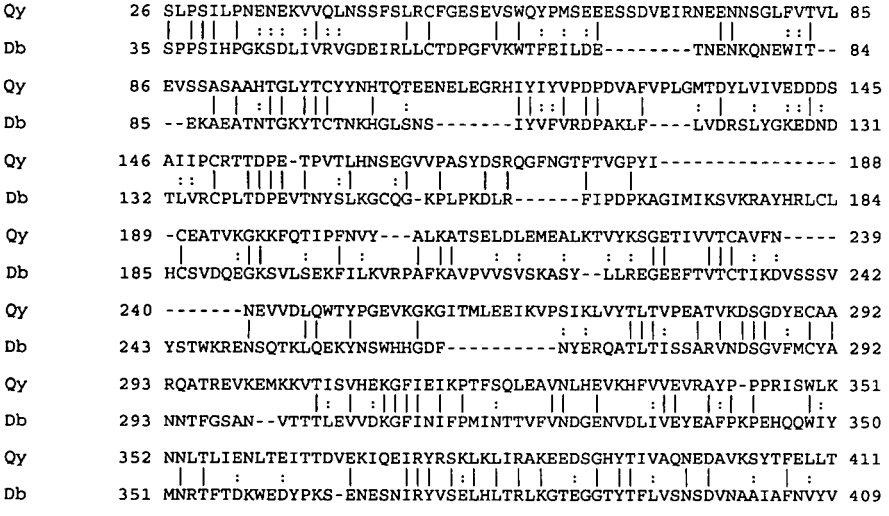
Query Match 25.7%; Score 1454.5; DB 11; Length 976;
Best Local Similarity 35.7%; Pred. No. 1.4e-85;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;

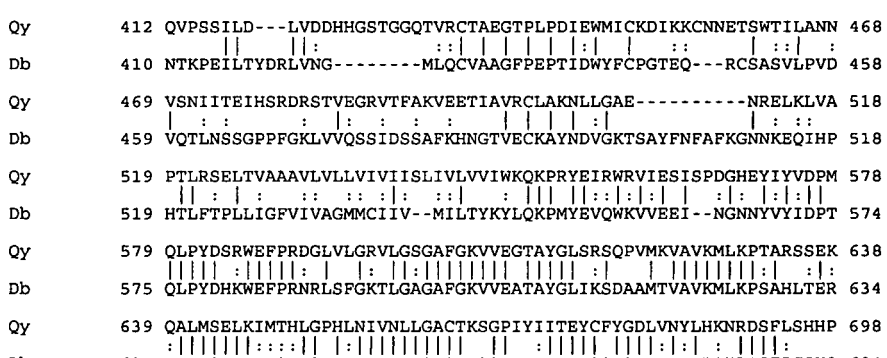




RESULT 29
US-11-177-894-20
; Sequence 20, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-20

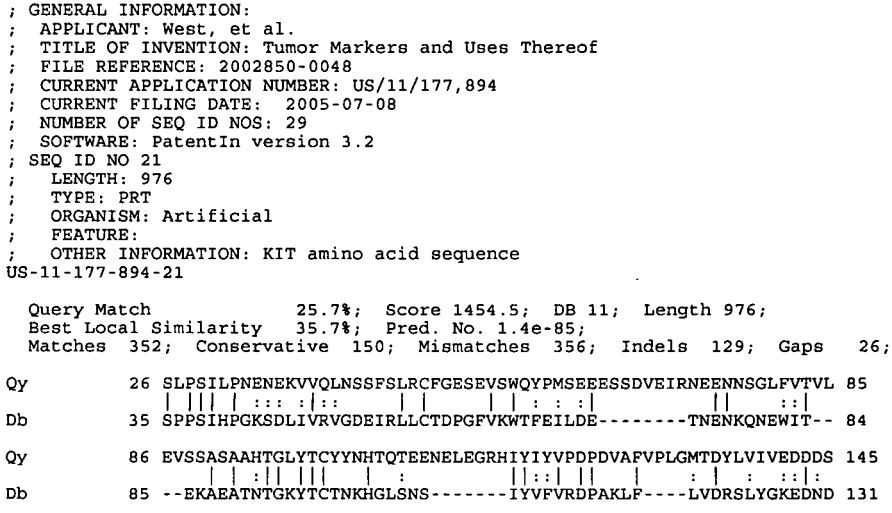
Query Match 25.7%; Score 1454.5; DB 11; Length 976;
Best Local Similarity 35.7%; Pred. No. 1.4e-85;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;





RESULT 30
US-11-177-894-21
; Sequence 21, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-21

Query Match 25.7%; Score 1454.5; DB 11; Length 976;
Best Local Similarity 35.7%; Pred. No. 1.4e-85;
Matches 352; Conservative 150; Mismatches 356; Indels 129; Gaps 26;



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Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939
```

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RESULT 31
US-11-154-287-1
; Sequence 1, Application US/11154287
; Publication No. US20060058339A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA N.
;  APPLICANT:  HURT, CLARENCE R.
;  APPLICANT:  ZHANG, CHAO
;  APPLICANT:  ZHANG, JIAZHONG
;  TITLE OF INVENTION: COMPOUNDS MODULATING C-KIT ACTIVITY AND USES THEREFOR
;  FILE REFERENCE: 039363-2155
;  CURRENT APPLICATION NUMBER: US/11/154,287
;  CURRENT FILING DATE:  2005-06-16
;  PRIOR APPLICATION NUMBER: 60/682,076
;  PRIOR FILING DATE: 2005-05-17
;  PRIOR APPLICATION NUMBER: 60/682,058
;  PRIOR FILING DATE: 2005-05-17
;  PRIOR APPLICATION NUMBER: 60/580,898
;  PRIOR FILING DATE: 2004-06-17
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-154-287-1

  Query Match             25.7%;  Score 1454.5;  DB 11;  Length 976;
  Best Local Similarity   35.7%;  Pred. No. 1.4e-85;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;
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Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF----------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
Db        459 VQTLNSSGPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
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Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
              |||||:||  |:| |||||||||||| :||||| ||:  |||||||||||: :||  |||
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
              ||||| |||:|||| :||||| ||| ||  || |:||  |:|| :|:|:||  ||:::|
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
              |||:|  : :::|  :       |  :
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939


RESULT 32
US-11-154-988-1
; Sequence 1, Application US/11154988
; Publication No. US20060058340A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA N.
;  APPLICANT:  HURT, CLARENCE R.
;  APPLICANT:  ZHANG, CHAO
;  APPLICANT:  ZHANG, JIAZHONG
;  TITLE OF INVENTION: COMPOUNDS MODULATING C-KIT ACTIVITY
;  FILE REFERENCE: 039363-2121
;  CURRENT APPLICATION NUMBER: US/11/154,988
;  CURRENT FILING DATE:  2005-06-16
;  PRIOR APPLICATION NUMBER: 60/580,898
;  PRIOR FILING DATE: 2004-06-17
;  PRIOR APPLICATION NUMBER: 60/682,076
;  PRIOR FILING DATE: 2005-05-17
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-154-988-1

  Query Match            25.7%;  Score 1454.5;  DB 11;  Length 976;
  Best Local Similarity  35.7%;  Pred. No. 1.4e-85;
  Matches  352;  Conservative  150;  Mismatches  356;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::: :|::     | |     | | : : :|          ||    ::|
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                 | | :|| |||   |  :          ||::| ||   |    : |  :  ::|:
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
               ::  |  |||| |  :|   :|  |  | |      |  |
Db        132 TLVRCPLTDPEVTNYSLKGCQG-KPLPKDLR------FIPDPKAGIMIKSVKRAYHRLCL 184

Qy        189 -CEATVKGKKFQTIPFNVY---ALKATSELDLEMEALKTVYKSGETIVVTCAVFN----- 239
               |    :||   :  | :    | ||   : :   :   : : ||   ||| : :
Db        185 HCSVDQEGKSVLSEKFILKVRPAFKAVPVVSVSKASY--LLREGEEFTVTCTIKDVSSSV 242

Qy        240 -------NEVVDLQWTYPGEVKGKGITMLEEIKVPSIKLVYTLTVPEATVKDSGDYECAA 292
                    |   ||  |     |            : :   |||:  | | ||| : | |
Db        243 YSTWKRENSQTKLQEKYNSWHHGDF---------NYERQATLTISSARVNDSGVFMCYA 292

Qy        293 RQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYP-PPRISWLK 351
                     |: | :|||| | |  :    ||  |    :||  |:| |    |:
Db        293 NNTFGSAN--VTTTLEVVDKGFINIFPMINTTVFVNDGENVDLIVEYEAFPKPEHQQWIY 350

Qy        352 NNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSYTFELLT 411
               | |  :   :     |    ||| |:| | | |  : | || :  | |   :  | :
Db        351 MNRTFTDKWEDYPKS-ENESNIRYVSELHLTRLKGTEGGTYTFLVSNSDVNAAIAFNVYV 409

Qy        412 QVPSSILD---LVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKDIKKCNNETSWTILANN 468
                    ||    ||:          ::| | | | | |:|  |   ::     | ::|  :
Db        410 NTKPEILTYDRLVNG--------MLQCVAAGFPEPTIDWYFCPGTEQ---RCSASVLPVD 458

Qy        469 VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAE----------NRELKLVA 518
              |  : :       :  |:  : :  :    | | | | :|            | : ::
Db        459 VQTLNSSGPPPFGKLVVQSSIDSSAFKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHP 518

Qy        519 PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPM 578
              || : | :   ::  :: :|:  ::|   : ||| ||::|:|:| |  :|: |:|:||
Db        519 HTLFTPLLIGFVIVAGMMCIIV--MILTYKYLQKPMYEVQWKVVEEI--NGNNYVYIDPT 574

Qy        579 QLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEK 638
              ||||| :|||||: |  |: ||:|||||||| ||||| :|   | ||||||||:|  :|:
Db        575 QLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTER 634

Qy        639 QALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHP 698
              :|||||||:::||  |:||||||||||  ||  :|||||  ||||:|:|  : ||||:
Db        635 EALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQ 694

Qy        699 EKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQ 758
              |    :     |  : ||: |       ::  :|||||          ||       |   :| :
Db        695 EDHAEAALYKNLLHSKESSCS------DSTNEYMDMKPG--VSYV-------VPTKADKR 739

Qy        759 RSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRD 818
              ||:  |  ||     :: :|   : :|:   | | |||||:||||:|| |||||||:|||
Db        740 RSV--RIGSY-----IERDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRD 792

Qy        819 LAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDV 878
              |||||:||  |:| |||||||||||| :||||| ||:  |||||||||||: :||  |||
Db        793 LAARNILLTHGRITKICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDV 852

Qy        879 WSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPE 938
              ||||| |||:|||| :||||| ||| ||  || |:||  |:|| :|:|:||  ||:::|
Db        853 WSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPL 912

Qy        939 KRPSFYHLSEIVENLLPGQYKKSYEKI 965
              |||:|  : :::|  :       |  :
Db        913 KRPTFKQIVQLIEKQISESTNHIYSNL 939

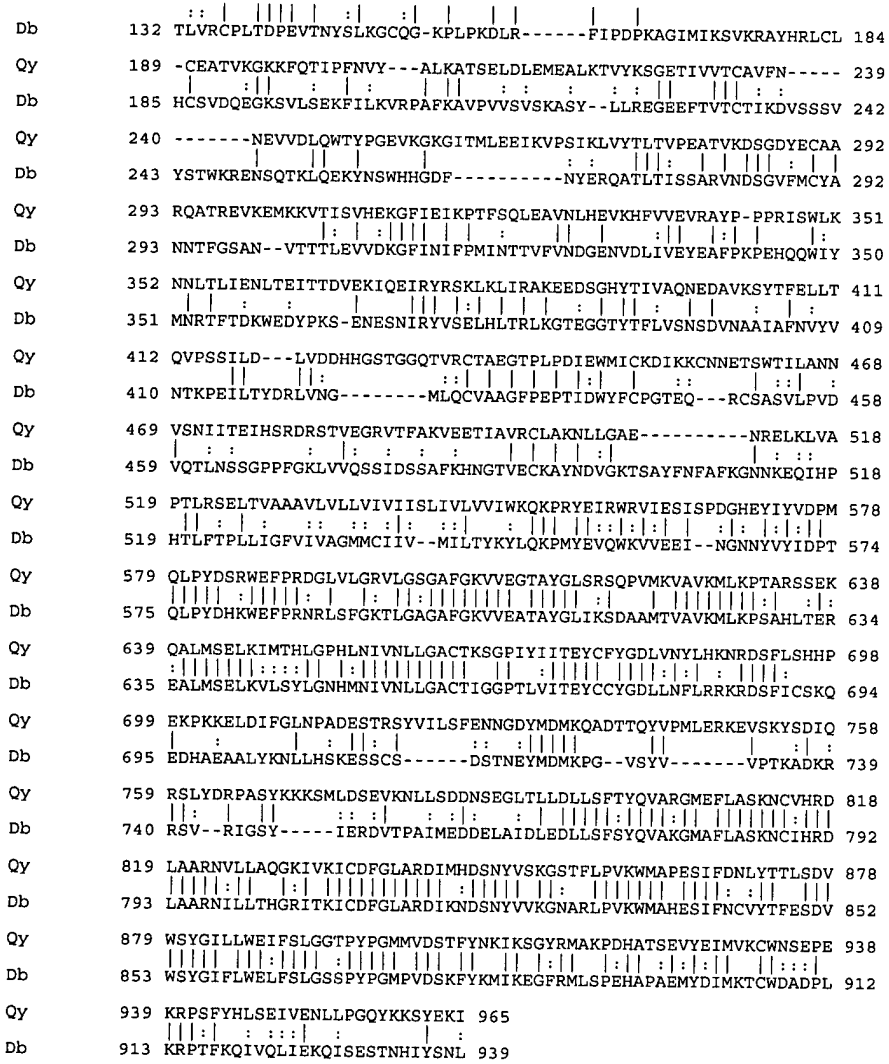

RESULT 33
US-11-177-894-19
; Sequence 19, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 976
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: KIT amino acid sequence
US-11-177-894-19

  Query Match            25.5%;  Score 1443.5;  DB 11;  Length 976;
  Best Local Similarity  35.5%;  Pred. No. 7.1e-85;
  Matches  350;  Conservative  151;  Mismatches  357;  Indels  129;  Gaps   26;

Qy         26 SLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVL 85
              | ||| | ::: :|::     | |     | | : : :|          ||    ::|
Db         35 SPPSIHPGKSDLIVRVGDEIRLLCTDPGFVKWTFEILDE--------TNENKQNEWIT-- 84

Qy         86 EVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIVEDDDS 145
                 | | :|| |||   |  :          ||::| ||   |    : |  :  ::|:
Db         85 --EKAEATNTGKYTCTNKHGLSNS-------IYVFVRDPAKLF----LVDRSLYGKEDND 131

Qy        146 AIIPCRTTDPE-TPVTLHNSEGVVPASYDSRQGFNGTFTVGPYI---------------- 188
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RESULT 34
US-10-821-234-1587
; Sequence 1587, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1587
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1587

Query Match 23.8%; Score 1346.5; DB 9; Length 972;
Best Local Similarity 34.0%; Pred. No. 1.3e-78;
Matches 335; Conservative 164; Mismatches 334; Indels 151; Gaps 31;

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Qy        868 FDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYE 927
              || :||  |||||||||||||||||  ||||::|:| ||  :| ||:||:|  |   :|
Db        828 FDCVYTVQSDVWSYGILLWEIFSLGLNPYPGILVNSKFYKLVKDGYQMAQPAFAPKNIYS 887

Qy        928 IMVKCWNSEPEKRPSFYHLSEIVE 951
              ||  ||  ||  ||:|  :   ::
Db        888 IMQACWALEPTHRPTFQQICSFLQ 911


RESULT 35
US-11-255-147-8
; Sequence 8, Application US/11255147
; Publication No. US20060094081A1
; GENERAL INFORMATION:
;  APPLICANT: SCHUBERT, CARSTEN
;  APPLICANT:  SPRINGER, BARRY A.
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  PATCH, RAYMOND J.
;  APPLICANT:  STRUBLE, GEOFFREY T.
;  APPLICANT:  MA, HONGCHANG
;  APPLICANT:  SCHALK-HIHI, CELINE
;  APPLICANT:  BRANDT, BENJAMIN M.
;  APPLICANT:  PETROUNIA, IOANNA
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE C-FMS KINASE DOMAIN:
;  TITLE OF INVENTION:  APPLICATIONS AND USE OF HETEROLOGOUS SUBSTITUTIONS OF
;  TITLE OF INVENTION:  KINASE INSERT DOMAINS FOR CRYSTALLIZATION
;  FILE REFERENCE: PRD2389USNP
;  CURRENT APPLICATION NUMBER: US/11/255,147
;  CURRENT FILING DATE:  2005-10-20
;  PRIOR APPLICATION NUMBER: 60/620,698
;  PRIOR FILING DATE: 2004-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
;   LENGTH: 972
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-255-147-8

  Query Match           23.8%;  Score 1346.5;  DB 10;  Length 972;
  Best Local Similarity   34.0%;  Pred. No. 1.3e-78;
  Matches  335;  Conservative  164;  Mismatches  334;  Indels  151;  Gaps   31;

Qy         27 LPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLE 86
              :| | |:  | ||:  :: :||| |   | |  | |   :    : :: ::|     :|
Db         20 IPVIEPSVPELVVKPGATVTLRCVGNGSVEWDGPPSPHWT----LYSDGSSS-----ILS 70

Qy         87 VSSASAAHTGLYTCYYNHTQTEENELEG--RHIYIYVPDPDVAFVPLGMTDYLVIVEDDD 144
              ::|:  :|| | |       ||  :  |    |::|| ||      |  :    |:| :|
Db         71 TNNATFQNTGTYRC------TEPGDPLGGSAAIHLYVKDP---ARPWNVLAQEVVVFEDQ 121

Qy        145 SAIIPCRTTDP--ETPVTLHNSEGVVPASYDSRQGFN--GTFTV--------GPYICEAT 192
              |::||  |||  |  |:|    |  |    :  |:    ||:          | | |
Db        122 DALLPCLLTDPVLEAGVSLVRVRG-RPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSAL 180

Qy        193 VKGKKFQTIPFNVYALK------ATSELDLEMEALKTVYKSGETIVVTCAVFNNEV---V 243
              : |:|  :|   :   |      | : :  |:  ::     ||   : |:  : :|   |
Db        181 MGGRKVMSISIRLKVQKVIPGPPALTLVPAELVRIR-----GEAAQIVCSASSVDVNFDV 235

Qy        244 DLQWTYPGEVKGKGITMLEEIKVPS--------IKLVYTLTVPEATVKDSGDYECAARQA 295
              ||                :: :|          : | || : :   : :|:| | |
Db        236 FLQHNN------------TKLAIPQQSDFHNNRYQKVLTLNLDQVDFQHAGNYSCVASNV 283

Qy        296 TREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPR-ISWLKNNL 354
              : |    :   | |  :: :    : :: | : |  :  | | |||  :  :|
Db        284 --QGKHSTSMFFRVVESAYLNLSSEQNLIQEVTVGEGLNLKVMVEAYPGLQGFNW----- 336

Qy        355 TLI---------ENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAVKSY 405
              | :         |   ||        |:   | | |  ::| |: :|:|    ::
Db        337 TYLGPFSDHQPEPKLANATTK----DTYRHTFTLSLPRLKPSEAGRYSFLARNPGGWRAL 392

Qy        406 TFELLTQVP---SSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICK-DIKKCNNETS 461
              |||| : |   | |   ::      |  |: | | | | |:: |: |     :|:
Db        393 TFELTLRYPPEVSVIWTFIN------GSGTLLCAASGYPQPNVTWLQCSGHTDRCDEAQV 446

Qy        462 WTILANNVSNIITE--IHSRDRSTVEGRVTFAKVEETIAVRCLAKNLLGAENRELKLVAP 519
              :  :   :::   |   : ||:  :|   :|      | | | :|: :     ::
Db        447 LQVWDDPYPEVLSQEPFH---KVTVQSLLTVETLEHNQTYECRAHNSVGSGSWAFIPISA 503

Qy        520 TLRSE-------LTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWRVIESISPDGHEY 572
              :           |  | : :: :::: |::|:  :||||:|::||::|||   :|: |
Db        504 GAHTHPPDEFLFTPVVVACMSIMALLLLLLLLLYKYKQKPKYQVRWKIIESY--EGNSY 561

Qy        573 IYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPT 632
              ::|| ||||: :|||||: |  |: ||:|||||||| ||:|| :   |:||||||| |
Db        562 TFIDPTQLPYNEKWEFPRNNLQFGKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLKST 621

Qy        633 ARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDS 692
              | : ||:|||||||||:||| | ||||||||||  ||: :||||| ||||:|:| :  ::
Db        622 AHADEKEALMSELKIMSHLGQHENIVNLLGACTHGGPVLVITEYCCYGDLLNFLRRKAEA 681

Qy        693 FLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVS 752
              |              |:|  :          |   || ::            ||:| |
Db        682 MLGP------------SLSPGQDP---------EGGVDYKNIH----------LEKKYVR 710

Qy        753 KYSDIQRSLYD-----RPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGME 807
              : |        |     || |    |  ||  :  |  ::   | | ||| |: |||:||
Db        711 RDSGPSSQGVDTYVEMRPVS---TSSNDSFSEQDLDKEDGRPLELRDLLHFSSQVAQGMA 767

Qy        808 FLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESI 867
              |||||||:|||:|||||||  | : || |||||||||:||||: ||:  ||||||||||
Db        768 FLASKNCIHRDVAARNVLLTNGHVAKIGDFGLARDIMNDSNYIVKGNARLPVKWMAPESI 827

Qy        868 FDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYE 927
              || :||  |||||||||||||||||  ||||::|:| ||  :| ||:||:|  |   :|
Db        828 FDCVYTVQSDVWSYGILLWEIFSLGLNPYPGILVNSKFYKLVKDGYQMAQPAFAPKNIYS 887

Qy        928 IMVKCWNSEPEKRPSFYHLSEIVE 951
              ||  ||  ||  ||:|  :   ::
Db        888 IMQACWALEPTHRPTFQQICSFLQ 911


RESULT 36
US-11-092-168-8
; Sequence 8, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
;  APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
;  APPLICANT:  Montigen Pharmaceuticals, Inc.
;  APPLICANT:  Hurley, Laurence H.
;  APPLICANT:  Mahadevan, Daruka
;  APPLICANT:  Han, Haiyong
;  APPLICANT:  Bearss, David J.
;  APPLICANT:  Vankayalapati, Hariprasad
;  APPLICANT:  Bashyam, Sridevi
;  APPLICANT:  Munoz, Ruben M.
;  APPLICANT:  Warner, Steven L.
;  APPLICANT:  Della Croce, Kimiko
;  APPLICANT:  Von Hoff, Daniel D.
;  APPLICANT:  Grand, Cory L.
;  TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
;  FILE REFERENCE: 920214.00003CONT3
;  CURRENT APPLICATION NUMBER: US/11/092,168
;  CURRENT FILING DATE:  2005-03-29
;  PRIOR APPLICATION NUMBER: US 10/965,313
;    US 60/608,529
;    US 60/511,486
;    US 60/511,489
;  PRIOR FILING DATE: 2004-10-14
;    2004-09-09
;    2003-10-14
;    2003-10-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
```

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;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-092-168-8

  Query Match             22.9%;  Score 1296.5;  DB 11;  Length 411;
  Best Local Similarity   64.0%;  Pred. No. 5.9e-76;
  Matches  254;  Conservative   51;  Mismatches   87;  Indels    5;  Gaps    3;

Qy        586 WEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSEL 645
              || ||| ||||| |||||||:||| ||:||| ||  |||||||||| ||||||||||||||
Db          2 WELPRDQLVLGRTLGSGAFGQVVEATAHGLSHSQATMKVAVKMLKSTARSSEKQALMSEL 61

Qy        646 KIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEK---PK 702
              |||:|||||||:|||||||| |||||||| ||||:|||:|: :|| || :|   |
Db         62 KIMSHLGPHLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHHSDKRRPPS 121

Qy        703 KELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLY 762
              ||    | |      |:| |: |::| |||| : ::  |||||: |   ||:||: | |
Db        122 AELYSNAL-PVGLPLPSHVSLTGESDGGYMDMSKDESVDYVPMLDMKGDVKYADIESSNY 180

Qy        763 DRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAAR 822
              |     |  :   :  | :: |  |: :||: |:|||| ||||||||||||||||||
Db        181 MAPYDNYVPSAPERTCRATLINE-SPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAAR 239

Qy        823 NVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYG 882
              |||: :||:|||||||||||| ||||:|||||||:|||||||::|||||||||:|
Db        240 NVLICEGKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFG 299

Qy        883 ILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPS 942
              |||||||:|||||| : ::  ||| || |||||:| ||: |:|||| |||  : | ||
Db        300 ILLWEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPP 359

Qy        943 FYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
              |  |  ::| ||   ||| |:::  :||:|||||: |
Db        360 FSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILR 396


RESULT 37
US-10-505-928-634
; Sequence 634, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 634
;   LENGTH: 1338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-634

  Query Match             22.8%;  Score 1287;  DB 8;  Length 1338;
  Best Local Similarity   28.8%;  Pred. No. 1.4e-74;
  Matches  393;  Conservative  176;  Mismatches  390;  Indels  404;  Gaps   51;

Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSEEESSD 68
              :| |||    |    :|  | :      : ::|    :  |:| ||:    |  | |  :||
Db         14 LLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESER 73

Qy         69 VEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDV 126
              : |      |   | : | :::| | ||| |:| |    | : :     |||:: |
Db         74 LSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGR 133

Qy        127 AFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDSRQGF- 178
              || :      :: : :    :|||| | |   |||      : ::|      :|||:||
Db        134 PFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFI 193

Qy        179 --NGTF-TVGPYICEATVKGKKFQTIPFNVYYALKATSE-LDLEMEALKTV-YKSGETIVV 233
                | |:  :|   ||||| |  ::|   |    : |:  :|:::   : |    | |:|:
Db        194 ISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVL 250

Qy        234 TCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVKDSGDY 288
              |      |  | : |:|| | | |  ::   |   :    : |: ||: :   || | |
Db        251 NCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLY 309

Qy        289 ECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQ-LEAVNLHEVKHFVVEVRAYPPP 345
              | |          | |  |||  :| || :|    | || |          ::|:|:| |
Db        310 TCRVRSG----PSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSP 365

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSK---LKLIRAKEEDSGHYTIV--AQNED 400
              : |||: |   |          :  || ::   | :    |||:|:|||:   :  :
Db        366 EVVWLKDGLPATE-----------KSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSN 413

Qy        401 AVKSYTFELLTQVPSSILDLVDDHH--------GSTGGQTVRCTAEGTPLPDIEWM---- 448
              |: |  |:  |   | :                ||   | : ||| | | | |:|
Db        414 VFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSR--QILTCTAYGIPQPTIKWFWHPC 471

Qy        449 ----------ICKDIKKCNNETSWTILA-NNVSNIITEIHSRDRSTVEGRVTFAKVEETI 497
                       |      ||| |: : | :|: | |  |  |  : :||:    |:  |:
Db        472 NHNHSEARCDFCS-----NNEESFILDADSNMGNRIESITQR-MAIIEGK---NKMASTL 522

Qy        498 AVR---------CLAKNLLGAENRELKLV--------------APTLRSELTVAAAVLVL 534
              |           |:| | :|    | :                ||   :| ::  |
Db        523 VVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKF 582

Qy        535 LVIVIISLIVLVV--------IWKQK-------------------------------- 552
              |   :  :::  |         | |||
Db        583 LYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVY 642

Qy        553 ---------------------------------------------PRYEIRW-------- 559
                                                          |  :| |
Db        643 TGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQ 702

Qy        560 -----------------RVIE---------------------------------------- 563
                              || |
Db        703 QEPGIILGPGSSTLFIERVTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITL 762

Qy        564 ----------------------SISPDGHEY--IYVDP---------MQLPYD-SRWEF 588
                                   | |    :|  | :||          :|||| |:|||
Db        763 TCTCVAATLFWLLLTLLIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEF 822

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
              |: | ||: || ||||||| :|:|: :|      |||||||  | :|| :|||:||||:
Db        823 ARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKIL 882

Qy        649 THLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF-------LSHHPEK 700
              ||:| |||:|||||||||  ||: :| ||| ||:| |||   || |       |   |:|
Db        883 THIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKK 942

Qy        701 PKKELDI-FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
              | | :  |  | :|  |    || ::|   |   :|       :| :|
Db        943 EKMEPGLEQGKKPRLDSVTSSE--SFASSGFQEDKSLSD-------VEEEE--------- 984

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
              |    ||                | :|: ||:|:::|||||||||:|: |:||||
Db        985 ---DSDGFYK-----------------EPITMEDLISYSFQVARGMEFLSSRKCIHRDL 1023

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
              ||||:||::  :|||||||||||  : :|| || | ||:|||||||||| :|:| ||||
Db       1024 AARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVW 1083

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
              |||:|||||||||:|||| :|  | :::: | ||  |:::| |:|:||: ||: :|::
Db       1084 SYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKE 1143

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDK 999
              || |  | | : :||                    | :: |  : || :
Db       1144 RPRFAELVEKLGDLLQ--------------------ANVQQDGKD-YIPI-------- 1172
```

```
Qy       1000 LKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSST- 1058
Db       1173 ---------NAILTGNSGFTYSTPAF-----SEDFFK------ESISAPKFNSGSSDDVR 1212

Qy       1059 ------FIKRED-ETIEDI-----DMMDDIGIDSSDLVEDSFL 1089
Db       1213 YVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPML 1255


RESULT 38
US-10-505-928-857
; Sequence 857, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 857
;   LENGTH: 1338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-857

  Query Match             22.8%;  Score 1287;  DB 8;  Length 1338;
  Best Local Similarity   28.8%;  Pred. No. 1.4e-74;
  Matches  393;  Conservative  176;  Mismatches  390;  Indels  404;  Gaps   51;

Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSEEESSD 68
Db         14 LLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESER 73

Qy         69 VEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDV 126
Db         74 LSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGR 133

Qy        127 AFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDSRQGF- 178
Db        134 PFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFI 193

Qy        179 --NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKTV-YKSGETIVV 233
Db        194 ISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVL 250

Qy        234 TCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVKDSGDY 288
Db        251 NCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLY 309

Qy        289 ECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQ-LEAVNLHEVKHFVVEVRAYPPP 345
Db        310 TCRVRSG----PSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSP 365

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSK---LKLIRAKEEDSGHYTIV--AQNED 400
Db        366 EVVWLKDGLPATE-----------KSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSN 413

Qy        401 AVKSYTFELLTQVPSSILDLVDDHH--------GSTGGQTVRCTAEGTPLPDIEWM---- 448
Db        414 VFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSR--QILTCTAYGIPQPTIKWFWHPC 471

Qy        449 ----------ICKDIKKCNNETSWTILA-NNVSNIITEIHSRDRSTVEGRVTFAKVEETI 497
Db        472 NHNHSEARCDFCS-----NNEESFILDADSNMGNRIESITQR-MAIIEGK---NKMASTL 522

Qy        498 AVR---------CLAKNLLGAENRELKLV--------------APTLRSELTVAAAVLVL 534
Db        523 VVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKF 582

Qy        535 LVIVIISLIVLVV--------IWKQK---------------------------------- 552
Db        583 LYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVY 642

Qy        553 ------------------------------------------------PRYEIRW-------- 559
Db        643 TGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQ 702

Qy        560 -----------------RVIE---------------------------------------- 563
Db        703 QEPGIILGPGSSTLFIERVTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITL 762

Qy        564 ----------------------SISPDGHEY--IYVDP---------MQLPYD-SRWEF 588
Db        763 TCTCVAATLFWLLLTLLIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEF 822

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
Db        823 ARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKIL 882

Qy        649 THLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF-------LSHHPEK 700
Db        883 THIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKK 942

Qy        701 PKKELDI-FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
Db        943 EKMEPGLEQGKKPRLDSVTSSE--SFASSGFQEDKSLSD-------VEEEE--------- 984

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
Db        985 ---DSDGFYK-----------------EPITMEDLISYSFQVARGMEFLSSRKCIHRDL 1023

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
Db       1024 AARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVW 1083

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
Db       1084 SYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKE 1143

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDK 999
Db       1144 RPRFAELVEKLGDLLQ----------------------ANVQQDGKD-YIPI-------- 1172

Qy       1000 LKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSST- 1058
Db       1173 ---------NAILTGNSGFTYSTPAF-----SEDFFK------ESISAPKFNSGSSDDVR 1212

Qy       1059 ------FIKRED-ETIEDI-----DMMDDIGIDSSDLVEDSFL 1089
Db       1213 YVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPML 1255


RESULT 39
US-10-821-234-1622
; Sequence 1622, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1622
;   LENGTH: 1338
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-10-821-234-1622

  Query Match             22.8%;  Score 1287;  DB 9;  Length 1338;
  Best Local Similarity   28.8%;  Pred. No. 1.4e-74;
  Matches  393;  Conservative  176;  Mismatches  390;  Indels  404;  Gaps   51;

Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSEEESSD 68
              :| |||    |    :|  | :     : ::|    :  |:| ||:    |  | | :||
Db         14 LLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESER 73

Qy         69 VEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDV 126
              : |        |   | : | :::| | ||| |:| |    | : :     |||:: |
Db         74 LSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGR 133

Qy        127 AFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDSRQGF- 178
              || :    :: : :    :|||| | |   |||     : ::|      :|||:||
Db        134 PFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFI 193

Qy        179 --NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKTV-YKSGETIVV 233
                | |:  :|  |||||  |  ::|   |     : |:  :|:::   :  |    | |:|:
Db        194 ISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVL 250

Qy        234 TCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVKDSGDY 288
              |       |  | : |:|| | | |  ::    |   :    : |: ||: :   || | |
Db        251 NCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLY 309

Qy        289 ECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQ-LEAVNLHEVKHFVVEVRAYPPP 345
              |  |          | |  |||  :| || :|    | || |          ::|:|:| |
Db        310 TCRVRSG----PSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSP 365

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSK---LKLIRAKEEDSGHYTIV--AQNED 400
              : |||: |  |          :  || ::   | :    |||:|:|||:   :  :
Db        366 EVVWLKDGLPATE-----------KSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSN 413

Qy        401 AVKSYTFELLTQVPSSILDLVDDHH--------GSTGGQTVRCTAEGTPLPDIEWM---- 448
              |: |  |: |   | :              ||   | : ||| | | | |:|
Db        414 VFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSR--QILTCTAYGIPQPTIKWFWHPC 471

Qy        449 ----------ICKDIKKCNNETSWTILA-NNVSNIITEIHSRDRSTVEGRVTFAKVEETI 497
                       |      ||| |: : | :|: | |  |  |  : :||:    |:  |:
Db        472 NHNHSEARCDFCS-----NNEESFILDADSNMGNRIESITQR-MAIIEGK---NKMASTL 522

Qy        498 AVR---------CLAKNLLGAENRELKLV-------------APTLRSELTVAAAVLVL 534
              |           |:| | :|   | :                    ||   :| ::  |
Db        523 VVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKF 582

Qy        535 LVIVIISLIVLVV--------IWKQK---------------------------------- 552
              |   :  :::  |        | |||
Db        583 LYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVY 642

Qy        553 ----------------------------------------------PRYEIRW-------- 559
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Db        643 TGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQ 702

Qy        560 -----------------RVIE-------------------------------------- 563
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Db        703 QEPGIILGPGSSTLFIERVTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITL 762

Qy        564 ----------------------SISPDGHEY--IYVDP---------MQLPYD-SRWEF 588
                                   | |    :|  | :||          :|||| |:|||
Db        763 TCTCVAATLFWLLLTLFIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEF 822

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
              |: | ||: || |||||||: :|:|: :|     |||||||  | :|| :|||:||||:
Db        823 ARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKIL 882

Qy        649 THLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF-------LSHHPEK 700
              ||:| |||:|||||||||  ||: :| ||| ||:| |||   || |       |   |:|
Db        883 THIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKK 942

Qy        701 PKKELDI-FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
              | |  :  |  |  :|  |    || ::|   |   :|       :| :|

Db        943 EKMEPGLEQGKKPRLDSVTSSE--SFASSGFQEDKSLSD-------VEEEE--------- 984

Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
                |    ||                  | :|: ||:|:::|||||||||:|: |:|||
Db        985 ---DSDGFYK-----------------EPITMEDLISYSFQVARGMEFLSSRKCIHRDL 1023

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
              ||||:||::  :|||||||||||  : :|| || | ||:|||||||||| :|:| ||||
Db       1024 AARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVW 1083

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
              |||:||||||||||:||||: :|  | :::: | ||  |:::| |:|:||: ||: :|::
Db       1084 SYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKE 1143

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDK 999
              || |  | | : :||                    | :: |  : || :
Db       1144 RPRFAELVEKLGDLLQ---------------------ANVQQDGKD-YIPI-------- 1172

Qy       1000 LKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSST- 1058
                    |: :||:    |        ||  |      ::       :|||
Db       1173 ---------NAILTGNSGFTYSTPAF-----SEDFFK------ESISAPKFNSGSSDDVR 1212

Qy       1059 ------FIKRED-ETIEDI-----DMMDDIGIDSSDLVEDSFL 1089
                   |:  |  :| |::       | ||   ||| |:    |
Db       1213 YVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPML 1255


RESULT 40
US-11-109-156-23
; Sequence 23, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
;  APPLICANT: Toshio Ota
;  APPLICANT:  Takao Isogai
;  APPLICANT:  Tetsuo Nishikawa
;  APPLICANT:  Koji Hayashi
;  APPLICANT:  Kaoru Otsuka
;  APPLICANT:  Jun-Ichi Yamamoto
;  APPLICANT:  Shizuko Ishii
;  APPLICANT:  Tomoyasu Sugiyama
;  APPLICANT:  Ai Wakamatsu
;  APPLICANT:  Keiichi Nagai
;  APPLICANT:  Tetsuji Otsuki
;  APPLICANT:  Shin-Ichi Funahashi
;  APPLICANT:  Chiaki Senoo
;  APPLICANT:  Jun-Ichi Nezu
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
;  TITLE OF INVENTION:  PHOSPHATASE
;  FILE REFERENCE: 06501-099002
;  CURRENT APPLICATION NUMBER: US/11/109,156
;  CURRENT FILING DATE:  2005-04-19
;  PRIOR APPLICATION NUMBER: US/10/060,065
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/JP00/05061
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/159,590
;  PRIOR FILING DATE: 1999-10-18
;  PRIOR APPLICATION NUMBER: US 60/183,322
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: JP 11-248036
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: JP 2000-118776
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: JP 2000-183767
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: JP 2000-241899
;  PRIOR FILING DATE: 2000-06-09
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1338
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-11-109-156-23

Query Match 22.8%; Score 1287; DB 11; Length 1338;
Best Local Similarity 28.8%; Pred. No. 1.4e-74;
Matches 393; Conservative 176; Mismatches 390; Indels 404; Gaps 51;

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Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSEEESSD 68
              :| |||    |    :|  | :     : ::|    :  |:| ||:    |  | |  :||
Db         14 LLSCLLLTGSSSGSKLKDPELSLKGTQHIMQAGQTLHLQCRGEAAHKWSLPEMVSKESER 73

Qy         69 VEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDV 126
              : |       |   | : | :::| | ||| |:| |    | : :          |||:: |
Db         74 LSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGR 133

Qy        127 AFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDSRQGF- 178
               || :      :: : :    :|||| | |   |||     : ::|      :|||:||
Db        134 PFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFI 193

Qy        179 --NGTF-TVGPYICEATVKGKKFQTIPFNVYYALKATSE-LDLEMEALKTV-YKSGETIVV 233
                | |:  :|   ||||| |  ::|    |    : |:  :|:::   : |    | |:|:
Db        194 ISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVL 250

Qy        234 TCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVKDSGDY 288
               |      |  | :|:|| | | |  ::    |   :    : |: ||: :   || | |
Db        251 NCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLY 309

Qy        289 ECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQ-LEAVNLHEVKHFVVEVRAYPPP 345
               | |           | |  |||  :| || :|    | || |          ::|:|:| |
Db        310 TCRVRSG----PSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSP 365

Qy        346 RISWLKNNLTLIENLTEITTDVEKIQEIRYRSK---LKLIRAKEEDSGHYTIV--AQNED 400
               : |||: |   |          :  || ::   | :    |||:|:|||:   :  :
Db        366 EVVWLKDGLPATE-----------KSARYLTRGYSLIIKDVTEEDAGNYTILLSIKQSN 413

Qy        401 AVKSYTFELLTQVPSSILDLVDDHH--------GSTGGQTVRCTAEGTPLPDIEWM---- 448
               |: |  |:  |   | :              ||   | : ||| | | | |:|
Db        414 VFKNLTATLIVNVKPQIYEKAVSSFPDPALYPLGSR--QILTCTAYGIPQPTIKWFWHPC 471

Qy        449 ----------ICKDIKKCNNETSWTILA-NNVSNIITEIHSRDRSTVEGRVTFAKVEETI 497
                        |      ||| |: : | :|: | |  |  |  : :||:    |:  |:
Db        472 NHNHSEARCDFCS-----NNEESFILDADSNMGNRIESITQR-MAIIEGK---NKMASTL 522

Qy        498 AVR---------CLAKNLLGAENRELKLV-------------APTLRSELTVAAAVLVL 534
               |          |:| | :|   | :                ||   :| ::  |
Db        523 VVADSRISGIYICIASNKVGTVGRNISFYITDVPNGFHVNLEKMPTEGEDLKLSCTVNKF 582

Qy        535 LVIVIISLIVLVV--------IWKQK-------------------------------- 552
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Db        583 LYRDVTWILLRTVNNRTMHYSISKQKMAITKEHSITLNLTIMNVSLQDSGTYACRARNVY 642

Qy        553 ------------------------------------------------PRYEIRW-------- 559
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Db        643 TGEEILQKKEITIRDQEAPYLLRNLSDHTVAISSSTTLDCHANGVPEPQITWFKNNHKIQ 702

Qy        560 -----------------RVIE---------------------------------------- 563
                              || |
Db        703 QEPGIILGPGSSTLFIERVTEEDEGVYHCKATNQKGSVESSAYLTVQGTSDKSNLELITL 762

Qy        564 ----------------------SISPDGHEY--IYVDP---------MQLPYD-SRWEF 588
                                   | |   :|  | :||          :|||| |:|||
Db        763 TCTCVAATLFWLLLTLLIRKMKRSSSEIKTDYLSIIMDPDEVPLDEQCERLPYDASKWEF 822

Qy        589 PRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIM 648
               |: | ||: || |||||||: :|:|: :|     |||||||  | :|| :|||:||||:
Db        823 ARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKALMTELKIL 882

Qy        649 THLGPHLNIVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSF-------LSHHPEK 700
               ||:| |||:|||||||||  ||: :| ||| ||:| |||    || |       |   |:|
Db        883 THIGHHLNVVNLLGACTKQGGPLMVIVEYCKYGNLSNYLKSKRDLFFLNKDAALHMEPKK 942

Qy        701 PKKELDI-FGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQR 759
               | |  :  |  |  :|  |    || ::|   |   :|         :| :|
Db        943 EKMEPGLEQGKKPRLDSVTSSE--SFASSGFQEDKSLSD-------VEEEE--------- 984
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Qy        760 SLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDL 819
                 |    ||                | :|: ||:|:::|||||||||:|: |:||||
Db        985 ---DSDGFYK-----------------EPITMEDLISYSFQVARGMEFLSSRKCIHRDL 1023

Qy        820 AARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVW 879
              ||||:||::  :|||||||||||  : :|| || | ||:||||||||| :|:| ||||
Db       1024 AARNILLSENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKWMAPESIFDKIYSTKSDVW 1083

Qy        880 SYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEK 939
              |||:|||||||||:||||: :|  | :::: | ||  |:::| |:|:||: ||: :|::
Db       1084 SYGVLLWEIFSLGGSPYPGVQMDEDFCSRLREGMRMRAPEYSTPEIYQIMLDCWHRDPKE 1143

Qy        940 RPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDK 999
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Db       1144 RPRFAELVEKLGDLLQ---------------------ANVQQDGKD-YIPI-------- 1172

Qy       1000 LKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSSQTSEESAIETGSSSST- 1058
                        |: :||:    |        ||  |      ::       :|||
Db       1173 ---------NAILTGNSGFTYSTPAF-----SEDFFK------ESISAPKFNSGSSDDVR 1212

Qy       1059 ------FIKRED-ETIEDI-----DMMDDIGIDSSDLVEDSFL 1089
                    |:  |  :| |::      | ||   ||| |:    |
Db       1213 YVNAFKFMSLERIKTFEELLPNATSMFDDYQGDSSTLLASPML 1255
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RESULT 41
US-11-075-047A-2
; Sequence 2, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-2

Query Match 22.8%; Score 1287; DB 11; Length 1338;
Best Local Similarity 28.8%; Pred. No. 1.4e-74;
Matches 393; Conservative 176; Mismatches 390; Indels 404; Gaps 51;

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Qy         10 VLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSEEESSD 68
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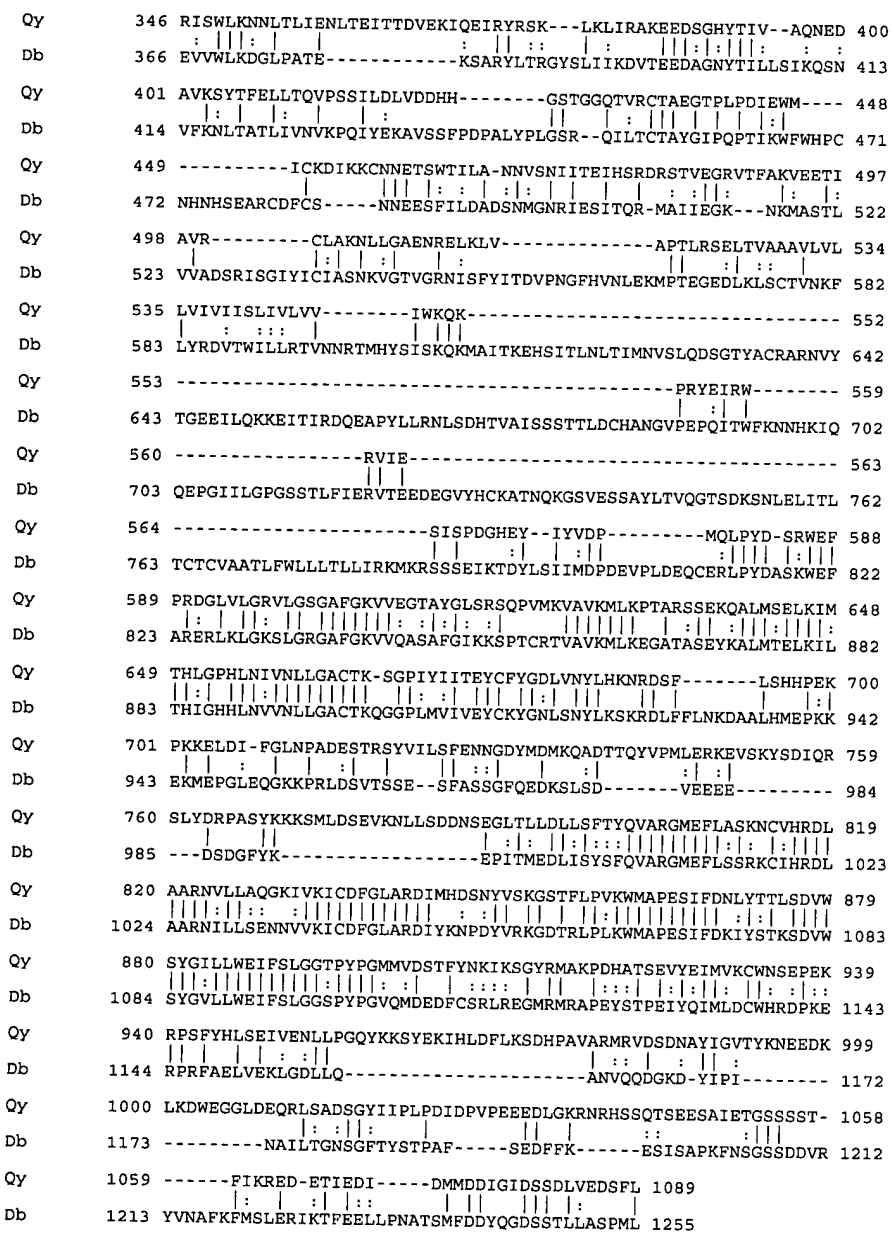
Qy         69 VEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDV 126
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Db         74 LSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFISDTGR 133

Qy        127 AFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDSRQGF- 178
               || :      :: : :    :|||| | |   |||     : ::|      :|||:||
Db        134 PFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFI 193

Qy        179 --NGTF-TVGPYICEATVKGKKFQTIPFNVYYALKATSE-LDLEMEALKTV-YKSGETIVV 233
                | |:  :|   ||||| |  ::|    |    : |:  :|:::   : |    | |:|:
Db        194 ISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRGHTLVL 250

Qy        234 TCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVKDSGDY 288
               |      |  | :|:|| | | |  ::    |   :    : |: ||: :   || | |
Db        251 NCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNKDKGLY 309

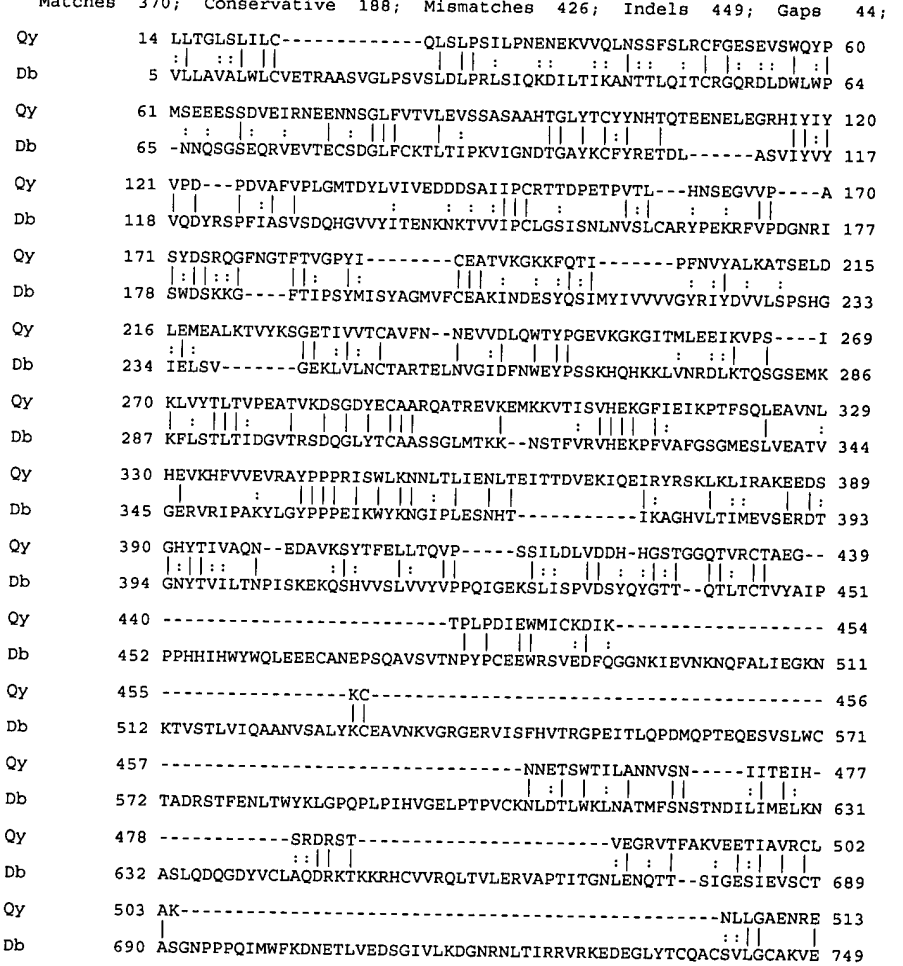
Qy        289 ECAARQATREVKEMKKVTISVH--EKGFIEIKPTFSQ-LEAVNLHEVKHFVVEVRAYPPP 345
               | |           | |  |||  :| || :|    | || |          ::|:|:| |
Db        310 TCRVRSG----PSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKVKAFPSP 365
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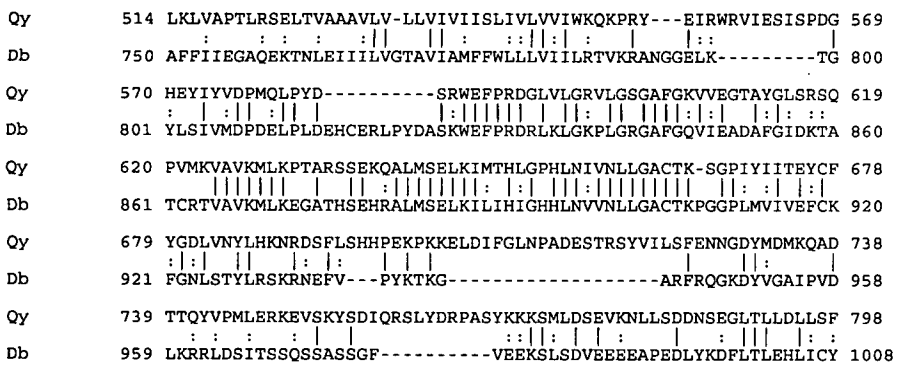


RESULT 42
US-10-995-561-904
; Sequence 904, Application US/10995561

; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-904

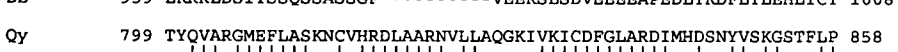
Query Match 21.6%; Score 1218.5; DB 9; Length 1356;
Best Local Similarity 25.8%; Pred. No. 3.6e-70;
Matches 370; Conservative 188; Mismatches 426; Indels 449; Gaps 44;

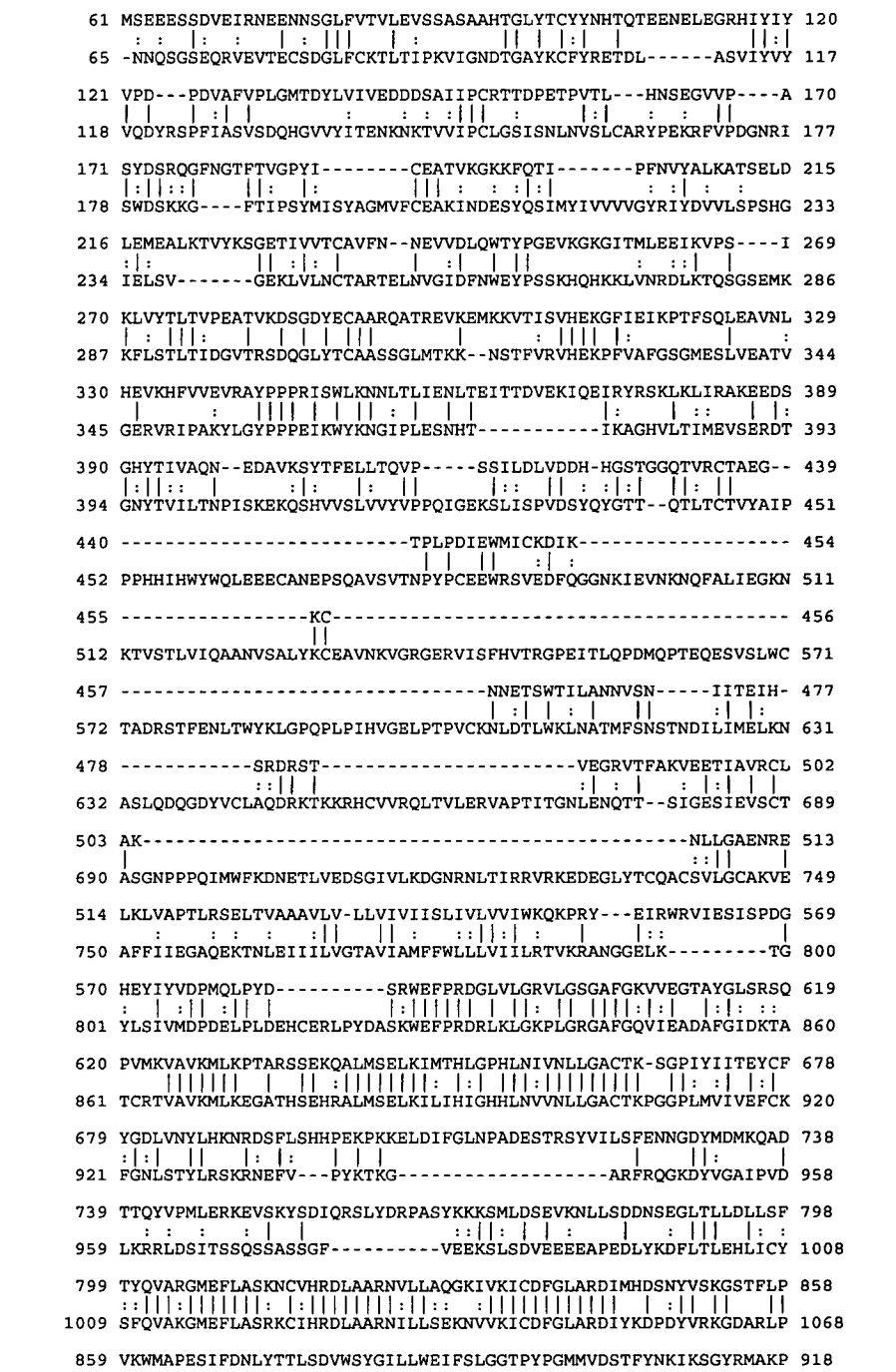




RESULT 43
US-10-995-561-906
; Sequence 906, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 906
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-906

Query Match 21.6%; Score 1218.5; DB 9; Length 1356;
Best Local Similarity 25.8%; Pred. No. 3.6e-70;
Matches 370; Conservative 188; Mismatches 426; Indels 449; Gaps 44;





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Db       1069 LKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAP 1128

Qy        919 DHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPG---QYKKSY------------ 962

Db       1129 DYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEE 1188

Qy        963 --------------------EKIHLD-------FLKS------------------DHPA 976

Db       1189 DSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPE 1248

Qy        977 VARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGK 1036

Db       1249 V-KVIPDDNQTDSGMVLASEE--LKTLE---DRTKLSPSFGGMVPSKSRESVASE----- 1297

Qy       1037 RNRHSSQTS-EESAIETGSSSST-FIKREDETIEDIDMMDDIGIDSSDLVEDS 1087

Db       1298 ---GSNQTSGYQSGYHSDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDS 1347
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RESULT 44
US-11-043-693-33
; Sequence 33, Application US/11043693
; Publication No. US20050281831A1
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dorsey & Whitney LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/043,693
; FILING DATE: 26-Jan-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,901
; FILING DATE: 20-Mar-2002
; APPLICATION NUMBER: 09/348,886
; FILING DATE: 01-JUL-1999
; APPLICATION NUMBER: US 08/643,839
; FILING DATE: 07-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard F. Trecartin
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1362 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-11-043-693-33

Query Match 21.5%; Score 1214; DB 11; Length 1362;
Best Local Similarity 27.6%; Pred. No. 7.2e-70;
Matches 378; Conservative 188; Mismatches 383; Indels 420; Gaps 53;

```
Qy          8 FLVLGC---LLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP-MSE 63

Db         12 WLCLGLLDGLVSGYSMTPPTLSLKG-----TQHIMQAGQTLHLQCRGEAAHKWSLPEMVS 66

Qy         64 EESSDVEIRNEE--NNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIYV 121

Db         67 KESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKETESAIYIFI 126

Qy        122 PDPDVAFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS----YDS 174

Db        127 SDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDS 186

Qy        175 RQGF---NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSE-LDLEMEALKTV-YKSG 228

Db        187 RKGFIISNATYKEIGLLTCEATVNGHLYKT---NYLTHRQTNTIIDVQISTPRPVKLLRG 243

Qy        229 ETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS--IKLVYT-LTVPEATVK 283

Db        244 HTLVLNCTATTPLNTRVQMTWSYPDE-KNKRASVRRRIDQSNSHANIFYSVLTIDKMQNK 302

Qy        284 DSGDYECAARQATREVKEMKKV--TISVHEKGFIEIK----PTFSQLEAVNLHEVKHFVV 337

Db        303 DKGLYTCRVRSG----PSFKSVNTSVRVHENPFISVEWLKGPI---LEATAGDELVKLPV 355

Qy        338 EVRAYPPPRISWLKNNLTLIEN-------LTEITTDVEKIQEIRYRSKLKLIRAKEEDSG 390

Db        356 KLAAYPPPEFQWYKDGKALSGRHSPHALVLKEVT--------------------EASTG 394

Qy        391 HYTIVAQNEDA--VKSYTFELLTQVPSSILD------LVDDHHGSTGGQTVRCTAEGTPL 442

Db        395 TYTLALWNSAAGLRRNISLELVVNVPPQIHEKEASSPSIYSRHSR---QALTCTAYGVPL 451

Qy        443 P-DIEW-------------------------MICKD---------IKKCNNETSWT---- 463

Db        452 PLSIQWHWRPWTPCKMFAQRSLRRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVE 511

Qy        464 ----------------------ILANNVSN-------IITEIHSRDRSTVEGRVTFAKVE 494

Db        512 GKNKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYFYVTTI--PDGFTIESKPSEELLE 569

Qy        495 -ETIAVRCLA-----------------------------KNL---------------LG 508

Db        570 GQPVLLSCQADSYKYEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATPLAASLEEVAPG 629

Qy        509 AENRELKLVAPTLRSE----------------------LTVAAAVLVLLVIVIISLIVL 545

Db        630 ARHATLSLSIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLLVN 689

Qy        546 V-----------------VIWK----------------------QKPRYEIRWRVIESI 565

Db        690 VSDSLEMQCLVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLCSV 749

Qy        566 -----------------SPD------------------------------------- 568

Db        750 CNAKGCVNSSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKT 809

Qy        569 GHEYIYVDPMQLP---------YD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRS 618

Db        810 GYLSIIMDPGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIHKG 869

Qy        619 QPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYC 677

Db        870 SSCDTVAVKMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPQGPLMVIVEFC 929

Qy        678 FYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQA 737

Db        930 KYGNLSNFLRAKRDAF----------------SPCAEK-------SPEQRGRFRAMVE- 964

Qy        738 DTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNL-LSDDNSEGLTLLDLL 796
```

```
Db        965 -----LARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSP-----LTMEDLV 1014

Qy        797 SFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTF 856

Db       1015 CYSFQVARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGSAR 1074

Qy        857 LPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMA 916

Db       1075 LPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTRMR 1134

Qy        917 KPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHL--------- 967

Db       1135 APELATPAIRRIMLNCWSGDPKARPAFSELVEILGDLLQGRGLQEEEEVCMAPRSSQSSE 1194

Qy        968 --DFLKSDHPAVARMRVDSDNA-------YIGVTYKN--------------EEDKLKDW 1003

Db       1195 EGSFSQVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMKTF 1254

Qy       1004 E----------GGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSS 1042

Db       1255 EEFPMTPTTYKGSVDNQ---TDSGMVL------ASEEFEQIESRHRQES 1294


RESULT 45
US-11-043-693-34
; Sequence 34, Application US/11043693
; Publication No. US20050281831A1
;  GENERAL INFORMATION:
;    APPLICANT:  Davis-Smyth, Terri L.
;    APPLICANT:  Chen, Helen H.
;    APPLICANT:  Presta, Leonard
;    APPLICANT:  Ferrara, Napoleone
;    TITLE OF INVENTION:  NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
;    TITLE OF INVENTION:  PRODUCTION
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dorsey & Whitney LLP
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/043,693
;      FILING DATE:  26-Jan-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/105,901
;      FILING DATE:  20-Mar-2002
;      APPLICATION NUMBER:  09/348,886
;      FILING DATE:  01-JUL-1999
;      APPLICATION NUMBER:  US 08/643,839
;      FILING DATE:  07-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard F. Trecartin
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-63291-3/RFT/NBC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1368 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-11-043-693-34

  Query Match             21.5%;  Score 1214;  DB 11;  Length 1368;
  Best Local Similarity   27.4%;  Pred. No. 7.2e-70;
  Matches  375;  Conservative  190;  Mismatches  388;  Indels  418;  Gaps   50;

Qy          8 FLVLGC---LLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEE 64

Db         12 WLCLGLLDGLVSGYSMTPPTLSITT----EESHVIDTGDSLSISCRGQHPLEWAWPGAQE 67

Qy         65 -------ESSDVEIRN--EENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGR 115

Db         68 APATGDKDSEDTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARIEGTTAA 127

Qy        116 HIYIYVPDPDVAFVPL-GMTDYLVIVEDDDSAIIPCRTTDPETPVTLHN--SEGVVPAS- 171

Db        128 SIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGK 187

Qy        172 ---YDSRQGF---NGTF-TVGPYICEATVKGKKFQTIPFNVYALKATSEL-DLEMEALKT 223

Db        188 RIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKT---NYLTHRTGNELYDIQLLPRKS 244

Qy        224 V-YKSGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLE-EIKVPSIKLVYTLTVPE 279

Db        245 LELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHN 304

Qy        280 ATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIK----PTFSQLEAVNLHEVKHF 335

Db        305 VSQHDLGSYVCKANNGIQRFRESTEV--RVHENPFISVEWLKGPI---LEATAGDELVKL 359

Qy        336 VVEVRAYPPPRISWLKNNLTLIEN-------LTEITTDVEKIQEIRYRSKLKLIRAKEED 388

Db        360 PVKLAAYPPPEFQWYKDGKALSGRHSPHALVLKEVT--------------------EAS 398

Qy        389 SGHYTIVAQNEDA--VKSYTFELLTQVPSSILD------LVDDHHGSTGGQTVRCTAEGT 440

Db        399 TGTYTLALWNSAAGLRRNISLELVVNVPPQIHEKEASSPSIYSRHSR---QALTCTAYGV 455

Qy        441 PLP-DIEW------------------------MICKD---------IKKCNNETSWT-- 463

Db        456 PLPLSIQWHWRPWTPCKMFAQRSLRRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEF 515

Qy        464 ------------------------ILANNVSN-------IITEIHSRDRSTVEGRVTFAK 492

Db        516 VEGKNKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYFYVTTI--PDGFTIESKPSEEL 573

Qy        493 VE-ETIAVRCLA------------------------------KNL--------------- 506

Db        574 LEGQPVLLSCQADSYKYEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATPLAASLEEVA 633

Qy        507 LGAENRELKLVAPTLRSE----------------------LTVAAAVLVLLVIVIISLI 543

Db        634 PGARHATLSLSIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLL 693

Qy        544 VLV-----------------VIWK----------------------QKPRYEIRWRVIE 563

Db        694 VNVSDSLEMQCLVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLC 753

Qy        564 SI-----------------SPD------------------------------------ 568

Db        754 SVCNAKGCVNSSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADI 813

Qy        569 --GHEYIYVDPMQLP---------YD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLS 616

Db        814 KTGYLSIIMDPGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIH 873

Qy        617 RSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITE 675

Db        874 KGSSCDTVAVKMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPQGPLMVIVE 933

Qy        676 YCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMK 735
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Db        934 FCKYGNLSNFLRAKRDAF----------------SPCAEK-------SPEQRGRFRAMV 969

Qy        736 QADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNL-LSDDNSEGLTLLD 794
Db        970 E------LARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSP-----LTMED 1018

Qy        795 LLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGS 854
Db       1019 LVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGS 1078

Qy        855 TFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYR 914
Db       1079 ARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTR 1138

Qy        915 MAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHL------- 967
Db       1139 MRAPELATPAIRRIMLNCWSGDPKARPAFSELVEILGDLLQGRGLQEEEEVCMAPRSSQS 1198

Qy        968 ----DFLKSDHPAVARMRVDSDNA-------YIGVTYKN---------------EEDKLK 1001
Db       1199 SEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMK 1258

Qy       1002 DWE----------GGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSS 1042
Db       1259 TFEEFPMTPTTYKGSVDNQ---TDSGMVL------ASEEFEQIESRHRQES 1300


RESULT 46
US-10-541-814-2
; Sequence 2, Application US/10541814
; Publication No. US20060057694A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth A. Thomas, Jr.
;  APPLICANT:  Bo-Sheng Pan
;  APPLICANT:  Georgia B. McGaughey
;  TITLE OF INVENTION: RAT RECEPTOR TYROSINE KINASE, KDR
;  FILE REFERENCE: 20803P
;  CURRENT APPLICATION NUMBER: US/10/541,814
;  CURRENT FILING DATE:  2005-07-06
;  PRIOR APPLICATION NUMBER: 60/443,335
;  PRIOR FILING DATE: 2003-01-29
;  PRIOR APPLICATION NUMBER: PCT/US2004/001928
;  PRIOR FILING DATE: 2004-01-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1343
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-541-814-2

  Query Match             21.0%;  Score 1188;  DB 9;  Length 1343;
  Best Local Similarity   25.2%;  Pred. No. 3.3e-68;
  Matches  346;  Conservative  203;  Mismatches  420;  Indels  404;  Gaps   42;

Qy         28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEV 87
Db         32 PKLSTQKDILTILANTTLQITCRGQRDLDWLWPNTPRDSEERVLVTECGDS-IFCKTLTV 90

Qy         88 SSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIV---EDDD 144
Db         91 PRVVGNDTGAYKCFYRDTDVSS------IVYVYVQDHRSPFIASVSDEHGIVYITENKNK 144

Qy        145 SAIIPCRTTDPETPVTL---HNSEGVVP----ASYDSRQGFNGTFTVGPYI--------C 189
Db        145 TVVIPCRGSISNLNVSLCARYPEKRFVPDGNRISWDSEKG----FTIPSYMISYAGMVFC 200

Qy        190 EATVKGKKFQTI-------PFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN--N 240
Db        201 EAKINDETYQSIMYIVLVVGYRIYDVVLSPPHEIELSA-------GEKLVLNCTARTELN 253

Qy        241 EVVDLQWTYP-GEVKGKGITMLEEIKVPSI---KLVYTLTVPEATVKDSGDYECAARQAT 296

Db        254 VGLDFSWQFPSSKHQHKKIVNRDVKSLPGTVAKMFLSTLTIDSVTKSDQGEYTCTAYSGL 313

Qy        297 REVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTL 356
Db        314 MTKK--NKTFVRVHTKPFIAFGSGMKSLVEATVGSQVRIPVKYLSYPAPDIKWYRNGRPI 371

Qy        357 IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAV--KSYTFELLTQVP 414
Db        372 ESNYTMIVGD-----------ELTIMEVSERDAGNYTVILTNPISMEKQSHMVSLVVNVP 420

Qy        415 -----SSILDLVDDHHGSTGGQTVRCTA-EGTPLPDIEW----------------MICK 451
Db        421 PQIGEKALISPMDSYQYGT-MQTLTCTVYANPPLHHIQWYWQLEEACSYRPSQTNPYTCK 479

Qy        452 D---------------------------------------------IKKC---------- 456
Db        480 EWRHVKDFQGGNKIEVTKNQYALIEGKNKTVSTLVIQAANVSALYKCEAINKAGRGERVI 539

Qy        457 ---------------------------------------------------------- 456
Db        540 SFHVIRGPEITVQPATQPTEQESVSLLCTADRNTFENLTWYKLGSQATSVHMGESLTPVC 599

Qy        457 -NNETSW----TILANNVSNIIT-------------EIHSRDRST---------------- 483
Db        600 KNLDALWKLNGTVFSNSTNDILIVAFQNASLQDQGNYVCSAQDKKTKKRHCLVKQLVILE 659

Qy        484 -----VEGR-------------------------VTFAKVEETIA---------------- 498
Db        660 RMAPMITGNLENQTTTIGETIEVVCPTSGNPTPLITWFKDNETLVEDSGIVLKDGNRNLT 719

Qy        499 ---VR---------CLAKNLLGAENRELKLVAPTLRSELTVAAAVLV-LLVIVIISLIVLV 546
Db        720 IRRVRKEDGGLYTCQACNVLGCARAETLFIIEGAQEKTNLEVIILVGTAVIAMFFWLLLV 779

Qy        547 VIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYD----------SRWEFPRDGLVLG 596
Db        780 IVLRTVKRAN------EGELKTGYLSIVMDPDELPLDERCERLPYDASKWEFPRDRLKLG 833

Qy        597 RVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLN 656
Db        834 KPLGRGAFGQVIEADAFGIDKTATCKTVAVKMLKEGATHSEHRALMSELKILIHIGHHLN 893

Qy        657 IVNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADE 715
Db        894 VVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRGKRNEFV---PYKSKG------------ 938

Qy        716 STRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLD 775
Db        939 -------ARFRSGKDYVGELSVDLKRRLDSITSSQSSASSGF----------VEEKSLSD 981

Qy        776 SEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKIC 835
Db        982 VEEEEASEELYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKIC 1041

Qy        836 DFGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTP 895
Db       1042 DFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASP 1101

Qy        896 YPGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLP 955
Db       1102 YPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHEDPNQRPAFSELVEHLGNLLQ 1161

Qy        956 GQYKKSYEKIHLDFLKSDHPAVARMRVDS-----------------------DNAYIGV 991
Db       1162 ANAQQDGK----DYIVLPMSETLSMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNT-AGI 1216

Qy        992 TYKNEEDKLKDWEGGLDEQRLSADSGYIIPL--PDIDPVPEE-------------EDLG 1035
Db       1217 SHYLQNSKRK-------SRPVSVKTFEDIPLEEPEVKVIPDDSQTDSGMVLASEELKTLE 1269

Qy       1036 KRNRHS-------SQTSEESAIETGSSSSTFIK---REDETIEDIDMMDDIGI 1078
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Db       1270 DRNKLSPSFGGMMPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYSSDEAGL 1322


RESULT 47
US-10-541-814-15
; Sequence 15, Application US/10541814
; Publication No. US20060057694A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth A. Thomas, Jr.
;  APPLICANT:  Bo-Sheng Pan
;  APPLICANT:  Georgia B. McGaughey
;  TITLE OF INVENTION: RAT RECEPTOR TYROSINE KINASE, KDR
;  FILE REFERENCE: 20803P
;  CURRENT APPLICATION NUMBER: US/10/541,814
;  CURRENT FILING DATE:  2005-07-06
;  PRIOR APPLICATION NUMBER: 60/443,335
;  PRIOR FILING DATE: 2003-01-29
;  PRIOR APPLICATION NUMBER: PCT/US2004/001928
;  PRIOR FILING DATE: 2004-01-23
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 1343
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-541-814-15

  Query Match             20.9%;  Score 1183;  DB 9;  Length 1343;
  Best Local Similarity   25.1%;  Pred. No. 7e-68;
  Matches  344;  Conservative  205;  Mismatches  421;  Indels  402;  Gaps   41;

Qy          28 PSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEESSDVEIRNEENNSGLFVTVLEV 87
               |  :   ::   :  |::  : | |: :: | :| :  :| :  :  |  :| :|   | |
Db          32 PKLSTQKDILTILANTTLQITCRGQRDLDWLWPNTPRDSEERVLVTECGDS-IFCKTLTV 90

Qy          88 SSASAAHTGLYTCYYNHTQTEENELEGRHIYIYVPDPDVAFVPLGMTDYLVIV---EDDD 144
                  || | |:|  |           :|:|| |    |:     :: ::      :
Db          91 PRVVGNDTGAYKCFYRDTDVSS------IVYVYVQDHRSPFIASVSDEHGIVYITENKNK 144

Qy         145 SAIIPCRTTDPETPVTL---HNSEGVVP----ASYDSRQGFNGTFTVGPYI--------C 189
               : :|||| :     |:|   :  : ||     |:|| :|    ||:  |:         |
Db         145 TVVIPCRGSISNLNVSLCARYPEKRFVPDGNRISWDSEKG----FTIPSYMISYAGMVFC 200

Qy         190 EATVKGKKFQTI-------PFNVYALKATSELDLEMEALKTVYKSGETIVVTCAVFN--N 240
               || :  : :|:|        : :| :  :   ::|: |       || :|: |      |
Db         201 EAKINDETYQSIMYIVLVVGYRIYDVVLSPPHEIELSA-------GEKLVLNCTARTELN 253

Qy         241 EVVDLQWTYP-GEVKGKGITMLEEIKVPSI---KLVYTLTVPEATVKDSGDYECAARQAT 296
                 :|  | :|  : : | |   :   :|       : |||:   |  | |:| | |
Db         254 VGLDFSWQFPSSKHQHKKIVNRDVKSLPGTVAKMFLSTLTIDSVTKSDQGEYTCTAYSGL 313

Qy         297 REVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVRAYPPPRISWLKNNLTL 356
                  |   | : || | ||         |    :       |:  :|| | | | :|   :
Db         314 MTKK--NKTFVRVHTKPFIAFGSGMKSLVEATVGSQVRIPVKYLSYPAPDIKWYRNGRPI 371

Qy         357 IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTIVAQNEDAV--KSYTFELLTQVP 414
                | | |  |           :| ::   | |:|:||::  |  ::  :|:   |:  ||
Db         372 ESNYTMIVGD-----------ELTIMEVSERDAGNYTVILTNPISMEKQSHMVSLVVNVP 420

Qy         415 -----SSILDLVDDHHGSTGGQTVRCTA-EGTPLPDIEW----------------MICK 451
                    :::  :| :   |  ||: ||     ||  |:|                 ||
Db         421 PQIGEKALISPMDSYQYGT-MQTLTCTVYANPPLHHIQWYWQLEEACSYRPSQTNPYTCK 479

Qy         452 D----------------------------------------IKKC------------- 456
                :                                        : ||
Db         480 EWRHVKDFQGGNKIEVTKNQYALIEGKNKTVSTLVIQAAYVSALYKCEAINKAGRGERVI 539

Qy         457 ------------------------------------------------------------ 456

Db         540 SFHVIRGPEITVQPATQPTERESMSLLCTADRNTFENLTWYKLGSQATSVHMGESLTPVC 599

Qy         457 -NNETSW----TILANNVSNIIT--------------EIHSRDRST-------------- 483
                | :  |    |: :|: ::|:                  ::|: |

Db         600 KNLDALWKLNGTVFSNSTNDILIVAFQNASLQDQGNYVCSAQDKKTKKRHCLVKQLVILE 659

Qy         484 -----VEGR-------------------------VTFAKVEETIA--------------- 498
                     : |                        :|: |  ||:
Db         660 RMAPMITGNLENQTTTIGETIEVVCPTSGNPTPLITWFKDNETLVEDSGIVLKDGNRNLT 719

Qy         499 ---VR--------CLAKNLLGAENRELKLVAPTLRSELTVAAAVLVLLVIVIISLIVLVV 547
                  ||         | | |:||    |   :   :: :  :   :||   :: :   :|:|
Db         720 IRRVRKEDGGLYTCQACNVLGCARAETLFIIEGVQEKTNLEVIILVGTAVIAMFFWLLLV 779

Qy         548 IWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYD----------SRWEFPRDGLVLGR 597
               |  :  :    |  |     |:  | :|| :|| |          |:|||||| | ||:
Db         780 ILVRTVK-----RANEGELKTGYLSIVMDPDELPLDERCERLPYDASKWEFPRDRLKLGK 834

Qy         598 VLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNI 657
                || ||||:|:|  |:|: ::     |||||||  |  || :||||||||: |:| |||:
Db         835 PLGRGAFGQVIEADAFGIDKTATCKTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV 894

Qy         658 VNLLGACTK-SGPIYIITEYCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADES 716
               |||||||| ||: :| |:| :|:|  ||    |: |:   | | |
Db         895 VNLLGACTKPGGPLMVIVEFCKFGNLSTYLRGKRNEFV---PYKSKG------------- 938

Qy         717 TRSYVILSFENNGDYMDMKQADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDS 776
                     | :  ||:      |  : :  :   : | |  |                ::||: |
Db         939 ------ARFRSGKDYVGELSVDLKRRLDSITSSQSSASSGF----------VEEKSLSDV 982

Qy         777 EVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICD 836
               | :    :   : |||  |: :::|||:|||||||: |:|||||||:||::  :|||||
Db         983 EEEEASEELYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICD 1042

Qy         837 FGLARDIMHDSNYVSKGSTFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPY 896
               |||||||  | :|| ||   ||:||||||:||| :||  | |||:|:|||||||| :||
Db        1043 FGLARDIYKDPDYVRKGDPRLPLKWMAPETIFDRIYTIQSGVWSFGVLLWEIFSLGASPY 1102

Qy         897 PGMMVDSTFYNKIKSGYRMAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPG 956
               ||: :|  |  ::| | ||  ||: | |:|: |: ||: :| :||:|  | | : |||
Db        1103 PGVKIDEKFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHEDPNQRPAFSELVEHLGNLLQA 1162

Qy         957 QYKKSYEKIHLDFLKSDHPAVARMRVDS-----------------------DNAYIGVT 992
                 ::  :    |::         |  ||                      ||   |::
Db        1163 NAQQDGK----DYIVLPMSETLSMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNT-AGIS 1217

Qy         993 YKNEEDKLKDWEGGLDEQRLSADSGYIIPL--PDIDPVPEE-------------EDLGK 1036
               :  :  | |         : :|  :   |||  |::  :|::              : |
Db        1218 HYLQNSKRK-------SRPVSVKTFEDIPLEEPEVKVIPDDSQTDSGMVLASEELKTLED 1270

Qy        1037 RNRHS-------SQTSEESAIETGSSSSTFIK---REDETIEDIDMMDDIGI 1078
               ||: |       | ||    ||: ::  :     |:|   :   |: |:
Db        1271 RNKLSPSFGGMMPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYSSDEAGL 1322


RESULT 48
US-10-995-561-905
; Sequence 905, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 905
;   LENGTH: 1306
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-905

  Query Match             20.8%;  Score 1177.5;  DB 9;  Length 1306;
  Best Local Similarity   25.1%;  Pred. No. 1.5e-67;
```

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  Matches  360;  Conservative  181;  Mismatches  393;  Indels  499;  Gaps   44;

Qy         14 LLTGLSLILC------------QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
Db          5 VLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWP 64

Qy         61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
Db         65 -NNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDL------ASVIYVY 117

Qy        121 VPD---PDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTL---HNSEGVVP----A 170
Db        118 VQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRI 177

Qy        171 SYDSRQGFNGTFTVGPYI--------CEATVKGKKFQTI-------PFNVYALKATSELD 215
Db        178 SWDSKKG----FTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHG 233

Qy        216 LEMEALKTVYKSGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLEEIKVPS----I 269
Db        234 IELSV-------GEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMK 286

Qy        270 KLVYTLTVPEATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNL 329
Db        287 KFLSTLTIDGVTRSDQGLYTCAASSGLMTKK--NSTFVRVHEKPFVAFGSGMESLVEATV 344

Qy        330 HEVKHFVVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDS 389
Db        345 GERVRIPAKYLGYPPPEIKWYKNGIPLESNHT-----------IKAGHVLTIMEVSERDT 393

Qy        390 GHYTIVAQN--EDAVKSYTFELLTQVP-----SSILDLVDDH-HGSTGGQTVRCTAEG-- 439
Db        394 GNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTT--QTLTCTVYAIP 451

Qy        440 -------------------------TPLPDIEWMICKDIK------------------- 454
Db        452 PPHHIHWYWQLEEECANEPSQAVSVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEGKN 511

Qy        455 -----------------KC---------------------------------------- 456
Db        512 KTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPDMQPTEQESVSLWC 571

Qy        457 --------------------------------NNETSWTILANNVSN-----IITEIH- 477
Db        572 TADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTNDILIMELKN 631

Qy        478 ------------SRDRST----------------------VEGRVTFAKVEETIAVRCL 502
Db        632 ASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTT--SIGESIEVSCT 689

Qy        503 AK-------------------------------------------------NLLGAENRE 513
Db        690 ASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAKVE 749

Qy        514 LKLVAPTLRSELTVAAAVLV-LLVIVIISLIVLVVIWKQKPRY---EIRWRVIESISPDG 569
Db        750 AFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELK---------TG 800

Qy        570 HEYIYVDPMQLPYD----------SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQ 619
Db        801 YLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTA 860

Qy        620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCF 678
Db        861 TCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCK 920

Qy        679 YGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQAD 738
Db        921 FGNLSTYLRSKRNEFVP----------YKVSPED---------------------- 944

Qy        739 TTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSF 798
Db        945 -------------LYKDF-------------------------------LTLEHLICY 958

Qy        799 TYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLP 858
Db        959 SFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLP 1018

Qy        859 VKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKP 918
Db       1019 LKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAP 1078

Qy        919 DHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPG---QYKKSY------------ 962
Db       1079 DYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEE 1138

Qy        963 ---------------------EKIHLD-------FLKS-----------------DHPA 976
Db       1139 DSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPE 1198

Qy        977 VARMRVDSDNAYIGVTYKNEEDKLKDWEGGLDEQRLSADSGYIIPLPDIDPVPEEEDLGK 1036
Db       1199 V-KVIPDDNQTDSGMVLASEE--LKTLE---DRTKLSPSFGGMVPSKSRESVASE----- 1247

Qy       1037 RNRHSSQTS-EESAIETGSSSST-FIKREDETIEDIDMMDDIGIDSSDLVEDS 1087
Db       1248 ---GSNQTSGYQSGYHSDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDS 1297


RESULT 49
US-10-511-937-2463
; Sequence 2463, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2463
;   LENGTH: 993
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-2463

  Query Match           20.6%;  Score 1166;  DB 8;  Length 993;
  Best Local Similarity   30.3%;  Pred. No. 5.6e-67;
  Matches  336;  Conservative  165;  Mismatches  365;  Indels  242;  Gaps   36;

Qy          6 PAFLVLGCLLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEEE 65
Db         12 PLLVVFSAMIFG---TITNQDLPVI------KCVLINHKNNDSSVGKSS---SYPMVSES 59

Qy         66 SSDVEIRNEENNSGLFVTVLEVSS----ASAAHT--------GLYTCYYNHTQTEEN--- 110
Db         60 PEDLGCALRPQSSG---TVYEAAAVEVDVSASITLQVLVDAPGNISCLWVFKHSSLNCQP 116

Qy        111 --ELEGRHIYIYVPDPDVAFVPLGMT-----DYLVIVE---------------------- 141
Db        117 HFDLQNRGV--------VSMVILKMTETQAGEYLLFIQSEATNYTILFTVSIRNTLLYTL 168
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Qy        142 --------DDDSAIIPCRTTDPETPV--TLHNSEGVVPASYDSRQGFNGTFTVGPYIC-- 189
                      ::  |::    : ||  |   | :|:|                        |
Db        169 RRPYFRKMENQDALVCISESVPEPIVEWVLCDSQG--------------------ESCKE 208

Qy        190 EATVKGKKFQTIPFNVYALK----ATSELDLEMEALKTV--------------YKSGETI 231
              |:    || : :   ::       | :||  |   | |:                 | || :
Db        209 ESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRLFTIDLNQTPQTTLPQLFLKVGEPL 268

Qy        232 VVTC-AVFNNEVVDLQWTYPGEVKGKGITMLEE----------IKVPSIKLVYTLTVPEA 280
               : | ||  |    | |    |:: |    |||                |::::   |
Db        269 WIRCKAVHVNHGFGLTW----ELENKA---LEEGNYFEMSTYSTNRTMIRILFAF-VSSV 320

Qy        281 TVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNLHEVKHFVVEVR 340
              |:| | |:: :         :   ::: ||||    :    | :: :|   | |  :
Db        321 ARNDTGYYTCSSSK-----HPSQSALVTIVGKGFINATNSSEDYE-IDQYEEFCFSVRFK 374

Qy        341 AYPPPRISWLKNNLTL------IENLTEITTDVEKIQEIRYRSKLKLIRAKEEDSGHYTI 394
              |||  | :|  :  :        ::|   |:               |    | :  | |
Db        375 AYPQIRCTWTFSRKSFPCEQKGLDNGYSIS--------------KFCNHKHQ-PGEYIF 418

Qy        395 VAQNEDAVKSYTFELLTQVPSSILDLVDDHHGSTGGQTVRCTAEGTPLPDIEWMICKD-I 453
              |:|:||  :  | |  :    :|                | ::| |||   |  | |
Db        419 HAENDDAQFTKMFTLNIRRKPQVL-------AEASASQASCFSDGYPLPSWTWKKCSDKS 471

Qy        454 KKCNNETS---WTILANN------VSNIITEIHSRDRSTVEGRVTFAKVEETIAVRCLAK 504
              |  | :   |   ||       ||:                :  :: :   |:| |
Db        472 PNCTEEITEGVWNRKANRKVFGQWVSS-------------STLNMSEAIKGFLVKCCAY 517

Qy        505 NLLGAENRELKLVA----PTLRSELTVAAAVLVLLVIVIISLIVLVVIWKQKPRYEIRWR 560
              | ||     : | :    | ::  ::  | : | |: ::: :::   :|:: ||| : :
Db        518 NSLGTSCETILLNSPGPFPFIQDNISFYATIGVCLLFIVVLTLLICHKYKKQFRYESQLQ 577

Qy        561 VIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQP 620
              :::      :|| |||  :  || :|||||: |  |:|||||||||:  ||||:|::
Db        578 MVQVTGSSDNEYFYVDFREYEYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGV 637

Qy        621 VMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYG 680
               ::|||||||  | |||::|||||||:|| || | ||||||||| |||||:| ||| ||
Db        638 SIQVAVKMLKEKADSSEREALMSELKMMTQLGSHENIVNLLGACTLSGPIYLIFEYCCYG 697

Qy        681 DLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTT 740
              ||:|||   |: |                      |::  :  |:|  :    |:
Db        698 DLLNYLRSKREKF----------------------HRTWTEIFKEHNFSFYPTFQSHPN 734

Qy        741 QYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSE-VKNLLSDDNSEGLTLLDLLSFT 799
               :|     ::   ||    |:  :  :: |  | |  :::   ||  ||| |
Db        735 SSMPGSREVQIHPDSDQISGLHGN--SFHSEDEIEYENQKRLEEEEDLNVLTFEDLLCFA 792

Qy        800 YQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPV 859
              ||||:|||||  |:|||||||||||:  ||:|||||||||||||| ||||| :|:  |||
Db        793 YQVAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNYVVRGNARLPV 852

Qy        860 KWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPD 919
              |||||||:|: :||  ||||||||||||||||  ||||: ||: ||  |::|::| :|
Db        853 KWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPYPGIPVDANFYKLIQNGFKMDQPF 912

Qy        920 HATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVAR 979
              :|| |:| ||  ||  :  ||||| :|:  :   |    :  |: :  |   | :|
Db        913 YATEEIYIIMQSCWAFDSRKRPSFPNLTSFLGCQLADAEEAMYQNV--DGRVSECPH--- 967

Qy        980 MRVDSDNAYIGVTYKNEEDKLKDWEGGL 1007
                      ||:|     :: : ||
Db        968 ------------TYQNRRPFSREMDLGL 983


RESULT 50
US-11-076-427A-12
; Sequence 12, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, et al.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
;  TITLE OF INVENTION:  VESSEL ARTERIALIZATION
;  FILE REFERENCE: 28967/40008A
;  CURRENT APPLICATION NUMBER: US/11/076,427A
;  CURRENT FILING DATE:  2005-03-08
;  PRIOR APPLICATION NUMBER: US 60/551,581
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 1298
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-076-427A-12

  Query Match             20.6%;  Score 1163.5;  DB 11;  Length 1298;
  Best Local Similarity   26.6%;  Pred. No. 1.2e-66;
  Matches  365;  Conservative  190;  Mismatches  393;  Indels  423;  Gaps   48;

Qy          8 FLVLGC---LLTGLSLILCQLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYPMSEE 64
              :| ||    |::| |     :: |::   |   |:    | |: | |:  : | :| ::|
Db         12 WLCLGLLDGLVSGYS-----MTPPTLNITEESHVIDTGDSLSISCRGQHPLEWAWPGAQE 66

Qy         65 -------ESSDVEIRN--EENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGR 115
                     :| |  :    |  ::  :  || :    |  || | ||| : :
Db         67 APATGDKDSEDTGVVRDCEGTDARPYCKVLLLHEVHANDTGSYVCYYKYIKARIEGTTAA 126

Qy        116 HIYIYVPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVV-----PA 170
              |::| | :  |:    |   ::|   |:  :||  : |   ||| :   |:
Db        127 SSYVFVRDFEQPFINKPDT---LLVNRKDAMWVPCLVSIPGLNVTLRSQSSVLWPDGQEV 183

Qy        171 SYDSRQGFNGTFTVGPYI-------CEATVKGKKFQTIPFNVYALKATSELDLEMEALKT 223
              :| |:|         | :        || |   : | : || |: :      |:::   |:
Db        184 VWDDRRGM---LVSTPLLHDALYLQCETTWGDQDFLSNPFLVH-ITGNELYDIQLLPRKS 239

Qy        224 V-YKSGETIVVTCAVFN--NEVVDLQWTYPGEVKGKGITMLE-EIKVPSIKLVYTLTVPE 279
              :   || :|: | |:   |  |   | |||:   :|  : |   :    :|   ||:
Db        240 LELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHTELSSILTIHN 299

Qy        280 ATVKDSGDYECAARQATREVKEMKKVTISVHEKGFIEIK----PTFSQLEAVNLHEVKHF 335
              :  | | | | |     :  :|  :|   |||  || ::     |    |||    |:
Db        300 VSQHDLGSYVCKANNGIQRFRESTEVI--VHENPFISVEWLKGPI---LEATAGDELVKL 354

Qy        336 VVEVRAYPPPRISWLKNNLTLIEN-------LTEITTDVEKIQEIRYRSKLKLIRAKEED 388
              |:: |||||   | |:  |          | |:|                        |
Db        355 PVKLAAYPPPEFQWYKDGKALSGRHSPHALVLKEVT--------------------EAS 393

Qy        389 SGHYTIVAQNEDA--VKSYTFELLTQVPSSILD------LVDDHHGSTGGQTVRCTAEGT 440
              :| ||:   |  |   :: : ||:  ||  | :       :    |     | : ||| |
Db        394 TGTYTLALWNSAAGLRRNISLELVVNVPPQIHEKEASSPSIYSRHSR---QALTCTAYGV 450

Qy        441 PLP-DIEW-------------------------MICKD---------IKKCNNETSWT-- 463
              |||  |:|                        |:|         :    :  :||
Db        451 PLPLSIQWHWRPWTPCKMFAQRSLRRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEF 510

Qy        464 ------------------------ILANNVSN-------IITEIHSRDRSTVEGRVTFAK 492
                                       :::| |          :| |    |  |:| : :
Db        511 VEGKNKTVSKLVIQNANVSAMYKCVVSNKVGQDERLIYFYVTTI--PDGFTIESKPSEEL 568

Qy        493 VE-ETIAVRCLA-----------------------------KNL---------------- 506
              :| : : : | |                            ||:
Db        569 LEGQPVLLSCQADSYKYEHLRWYRLNLSTLHDAHGNPLLLDCKNVHLFATPLAASLEEVA 628

Qy        507 LGAENRELKLVAPTLRSE----------------------LTVAAAVLVLLVIVIISLI 543
               || :  | |  | :  |                     |:| |      |   :  |:
Db        629 PGARHATLSLSIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLL 688

Qy        544 VLV-----------------VIWK----------------------QKPRYEIRWRVIE 563
              | |                  ::|                     |: | |   | :
Db        689 VNVSDSLEMQCLVAGAHAPSIVWYKDERLLEEKSGVDLADSNQKLSIQRVREEDAGRYLC 748

Qy        564 SI-----------------SPD----------------------------------- 568
              |:                 | |
Db        749 SVCNAKGCVNSSASVAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADI 808
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Qy        569 --GHEYIYVDPMQLP---------YD-SRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLS 616
Db        809 KTGYLSIIMDPGEVPLEEQCEYLSYDASQWEFPRERLHLGRVLGYGAFGKVVEASAFGIH 868

Qy        617 RSQPVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITE 675
Db        869 KGSSCDTVAVKMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPQGPLMVIVE 928

Qy        676 YCFYGDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMK 735
Db        929 FCKYGNLSNFLRAKRDAF-----------------SPCAEK-------SPEQRGRFRAMV 964

Qy        736 QADTTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNL-LSDDNSEGLTLLD 794
Db        965 E------LARLDRRRPGSSDRVLFARFSKTEGGARRASPDQEAEDLWLSP-----LTMED 1013

Qy        795 LLSFTYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGS 854
Db       1014 LVCYSFQVARGMEFLASRKCIHRDLAARNILLSESDVVKICDFGLARDIYKDPDYVRKGS 1073

Qy        855 TFLPVKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYR 914
Db       1074 ARLPLKWMAPESIFDKVYTTQSDVWSFGVLLWEIFSLGASPYPGVQINEEFCQRLRDGTR 1133

Qy        915 MAKPDHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHL------- 967
Db       1134 MRAPELATPAIRRIMLNCWSGDPKARPAFSELVEILGDLLQGRGLQEEEEVCMAPRSSQS 1193

Qy        968 ----DFLKSDHPAVARMRVDSDNA-------YIGVTYKN---------------EEDKLK 1001
Db       1194 SEEGSFSQVSTMALHIAQADAEDSPPSLQRHSLAARYYNWVSFPGCLARGAETRGSSRMK 1253

Qy       1002 DWE----------GGLDEQRLSADSGYIIPLPDIDPVPEEEDLGKRNRHSS 1042
Db       1254 TFEEFPMTPTTYKGSVDNQ---TDSGMVL------ASEEFEQIESRHRQES 1295
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Search completed: May 15, 2006, 09:07:22
Job time : 139 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 08:49:40 ; Search time 20715 Seconds
(without alignments)
17597.734 Million cell updates/sec

Title: US-08-439-095-2
Perfect score: 6413
Sequence: 1 ccattactgttggagctaca.....aaaaaaaaaaaaaaaaaaa 6413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6399.4	99.8	6412	6	AR437544	AR437544 Sequence
2	6373.2	99.4	6428	6	CQ414643	CQ414643 Sequence
3	6364.4	99.2	6378	6	AR380649	AR380649 Sequence
4	6364.4	99.2	6378	6	AR575515	AR575515 Sequence
5	6364.4	99.2	6378	6	AX330200	AX330200 Sequence
6	6364.4	99.2	6378	6	AX336347	AX336347 Sequence
7	6364.4	99.2	6378	8	HUMPDGFRAA	M21574 Human plate
8	6364.4	99.2	6633	6	CS079378	CS079378 Sequence
9	4777	74.5	6373	6	AR206726	AR206726 Sequence
10	4765.6	74.3	6375	6	AR036472	AR036472 Sequence
11	4765.6	74.3	6375	6	AR069431	AR069431 Sequence
12	4765.6	74.3	6375	6	BD166138	BD166138 Platelet-
13	4765.6	74.3	6375	6	I73453	I73453 Sequence 5
14	4765.6	74.3	6375	8	HUMPDGFARA	M22734 Human plate
15	4037.2	63.0	4100	6	AR036471	AR036471 Sequence
16	4037.2	63.0	4100	6	AR069430	AR069430 Sequence
17	4037.2	63.0	4100	6	BD166137	BD166137 Platelet-
18	4037.2	63.0	4100	6	I73452	I73452 Sequence 3
19	3838.8	59.9	4054	6	AR007257	AR007257 Sequence
20	3838.8	59.9	4054	6	AR062461	AR062461 Sequence
21	3838.8	59.9	4054	6	AR170043	AR170043 Sequence
22	3838.8	59.9	4054	6	AR170470	AR170470 Sequence
23	3838.8	59.9	4054	6	I27747	I27747 Sequence 35
24	3838.8	59.9	4054	6	AR262570	AR262570 Sequence
25	3838.8	59.9	4054	6	AR369685	AR369685 Sequence
26	3585	55.9	6576	9	MUSPDGFAR	M84607 Mus musculu
27	3270	51.0	3270	6	AR441854	AR441854 Sequence
28	3268.4	51.0	3270	6	AR441855	AR441855 Sequence
29	3268.4	51.0	3270	6	AR441857	AR441857 Sequence
30	3268.4	51.0	3270	6	AR441858	AR441858 Sequence
31	3266.8	50.9	3270	6	AR441856	AR441856 Sequence
32	3260.6	50.8	6264	9	RATAPDGFR	M63837 Rat alpha-p
33	3176.8	49.5	3199	6	AR322283	AR322283 Sequence
34	3101.6	48.4	132164	8	AC098587	AC098587 Homo sapi
35	2883.6	45.0	4238	9	BC053036	BC053036 Mus muscu
36	2779.2	43.3	3240	4	AY525124	AY525124 Canis fam
37	2655.6	41.4	3564	9	MUSMPDGAA	M57683 M.musculus
38	2253.8	35.1	3032	8	BC063414	BC063414 Homo sapi
39	2024	31.6	2717	6	CQ719900	CQ719900 Sequence
40	1995.4	31.1	3614	5	AF188842	AF188842 Gallus ga
c 41	1767.2	27.6	202012	14	AC160350	AC160350 Bos tauru
42	1767	27.6	1767	6	AR441859	AR441859 Sequence
43	1687.4	26.3	4049	5	XELPDGFAR	M80798 Xenopus lae
44	1676	26.1	6114	5	BC043948	BC043948 Xenopus l
45	1535.8	23.9	2550	8	AY229892	AY229892 Homo sapi
46	1239.6	19.3	3788	5	AF200951	AF200951 Danio rer
47	1094.6	17.1	244565	9	AC120348	AC120348 Mus muscu
c 48	1094.6	17.1	264425	9	AC019028	AC019028 Mus muscu
49	1073	16.7	1474	9	RNPDGFACE	Z14118 R.norvegicu
c 50	1060	16.5	235304	14	AC114072	AC114072 Rattus no
51	1043	16.3	1578	9	BC037467	BC037467 Mus muscu
52	836.8	13.0	231589	14	AC118944	AC118944 Rattus no
53	808.2	12.6	2060	5	AB121073	AB121073 Oryzias l
54	773.4	12.1	3052	5	BRPDGFRA	Z32814 B.rerio mRN
55	736	11.5	2225	8	BC015186	BC015186 Homo sapi
56	700.8	10.9	777	10	BV166582	BV166582 PDGFRA _1
57	667.6	10.4	3321	6	AR441864	AR441864 Sequence
58	667.6	10.4	5427	6	AR036470	AR036470 Sequence
59	667.6	10.4	5427	6	AR069429	AR069429 Sequence
60	667.6	10.4	5427	6	BD166136	BD166136 Platelet-
61	667.6	10.4	5427	6	I73451	I73451 Sequence 1
62	667.6	10.4	5427	6	AR206727	AR206727 Sequence
63	667.6	10.4	5427	8	HUMPDGFR	M21616 Human plate
64	667.6	10.4	5720	6	I07567	I07567 Sequence 1
65	666	10.4	3321	6	AR441860	AR441860 Sequence
66	666	10.4	3321	11	AY893116	AY893116 Synthetic
67	666	10.4	4465	6	AR007225	AR007225 Sequence
68	666	10.4	4465	6	AR062429	AR062429 Sequence
69	666	10.4	4465	6	AR170011	AR170011 Sequence
70	666	10.4	4465	6	AR170438	AR170438 Sequence
71	666	10.4	4465	6	I27715	I27715 Sequence 1
72	666	10.4	4465	6	AR262538	AR262538 Sequence
73	666	10.4	4465	6	AR369653	AR369653 Sequence
74	666	10.4	4544	6	I06337	I06337 Sequence 20
75	666	10.4	5570	6	AR380648	AR380648 Sequence
76	666	10.4	5570	6	AX587739	AX587739 Sequence
77	666	10.4	5570	8	HUMPDGFRA	J03278 Human plate
78	666	10.4	5598	6	CS079370	CS079370 Sequence
79	666	10.4	5707	6	CQ870288	CQ870288 Sequence
80	666	10.4	5727	6	AR322282	AR322282 Sequence
81	666	10.4	5742	8	BC032224	BC032224 Homo sapi
82	664.4	10.4	3321	6	AR441861	AR441861 Sequence
83	664.4	10.4	3321	6	AR441863	AR441863 Sequence
84	664.4	10.4	3321	11	AY890635	AY890635 Synthetic
85	662.8	10.3	3321	6	AR441862	AR441862 Sequence
86	661.4	10.3	5084	6	CQ870284	CQ870284 Sequence
87	624.2	9.7	3859	8	AB209657	AB209657 Homo sapi
88	622	9.7	3739	6	CQ870279	CQ870279 Sequence
89	622	9.7	5111	6	CQ870281	CQ870281 Sequence
90	620.4	9.7	5110	6	AX306191	AX306191 Sequence
91	620.4	9.7	5110	9	MMPDGFRE	X04367 Mouse pre-P

92	615.4	9.6	5435	9	BC055311	BC055311 Mus muscu
93	614.8	9.6	3805	4	AY532634	AY532634 Canis fam
94	604.8	9.4	5403	9	AY090783	AY090783 Rattus no
95	573	8.9	2463	6	E27633	E27633 Novel DNA a
96	549.6	8.6	1690	9	AF359356	AF359356 Rattus no
97	539.4	8.4	1176	6	AR380859	AR380859 Sequence
98	539.4	8.4	1176	8	HSPDGF	X76079 H.sapiens m
99	539.4	8.4	1176	8	HUMPDGFRAX	L25829 Human plate
100	526.4	8.2	528	6	AX481430	AX481430 Sequence
101	475	7.4	475	6	CQ697602	CQ697602 Sequence
102	461	7.2	461	6	CS134813	CS134813 Sequence
103	418	6.5	561	6	CQ672138	CQ672138 Sequence
104	406.2	6.3	506	6	CQ411236	CQ411236 Sequence
105	404.8	6.3	490	6	CQ673908	CQ673908 Sequence
106	366	5.7	366	6	CQ666245	CQ666245 Sequence
107	366	5.7	392	6	CQ686692	CQ686692 Sequence
108	360.4	5.6	420	6	CQ708233	CQ708233 Sequence
109	346	5.4	2960	9	AY536430	AY536430 Mus muscu
110	346	5.4	3891	9	BC075716	BC075716 Mus muscu
111	346	5.4	5164	9	BC052457	BC052457 Mus muscu
112	344.4	5.4	2960	9	AY536431	AY536431 Mus muscu
113	344.4	5.4	5098	6	AX195906	AX195906 Sequence
114	344.4	5.4	5098	9	MMCKIT	Y00864 Mouse c-kit
115	344.4	5.4	5132	6	CS104364	CS104364 Sequence
116	344.4	5.4	5132	6	CS117950	CS117950 Sequence
117	342.8	5.3	3154	4	AF044249	AF044249 Canis fam
118	342.2	5.3	2919	8	AB097502	AB097502 Callithri
119	341.2	5.3	2979	4	AF448148	AF448148 Canis fam
120	341.2	5.3	2992	4	AY313776	AY313776 Canis fam
121	341.2	5.3	3004	4	AY296484	AY296484 Canis fam
122	340.2	5.3	2937	4	AF099030	AF099030 Canis fam
123	335.2	5.2	369	6	CQ680565	CQ680565 Sequence
124	333.8	5.2	3705	9	RRCKITRTK	X62491 R.rattus mR
125	333.8	5.2	3816	6	CS117952	CS117952 Sequence
126	333.8	5.2	3816	9	RATCKITPO	D12524 Rattus norv
127	331.6	5.2	5084	6	CQ981615	CQ981615 Sequence
128	331.6	5.2	5084	6	CS031773	CS031773 Sequence
129	331.6	5.2	5084	6	CS040725	CS040725 Sequence
130	331.6	5.2	5084	6	CS117948	CS117948 Sequence
131	331.6	5.2	5084	6	I96184	I96184 Sequence 21
132	331.6	5.2	5084	6	AR380790	AR380790 Sequence
133	331.6	5.2	5084	6	AX195908	AX195908 Sequence
134	331.6	5.2	5084	6	AX331941	AX331941 Sequence
135	331.6	5.2	5084	6	AX335913	AX335913 Sequence
136	331.6	5.2	5084	8	HSKITCR	X06182 Human c-kit
137	331.4	5.2	2150	4	AY829238	AY829238 Bubalus b
138	330.6	5.2	341	6	CQ705458	CQ705458 Sequence
139	328.4	5.1	5179	8	BC071593	BC071593 Homo sapi
140	327.4	5.1	4222	4	S76596	S76596 c-kit=recep
141	323.2	5.0	2176	4	AF263826	AF263826 Bos tauru
142	323.2	5.0	2176	4	AF263827	AF263827 Bos tauru
143	323.2	5.0	3069	4	BOVCKR	D16680 Bos primige
144	322.8	5.0	2919	6	A82459	A82459 Sequence 47
145	322.8	5.0	2919	6	BD135505	BD135505 Methods f
146	322.8	5.0	2960	4	SSAJ3228	AJ223228 Sus scrof
147	322.6	5.0	17087	8	D50017	D50017 Homo sapien
148	322.6	5.0	132003	8	AC138779	AC138779 Homo sapi
149	322.6	5.0	163404	14	AC009614	AC009614 Homo sapi
c 150	322.6	5.0	164084	14	AC026580	AC026580 Homo sapi
151	321.4	5.0	2894	4	ECA224645	AJ224645 Equus cab
152	321.2	5.0	2960	4	SSAJ3229	AJ223229 Sus scrof
153	321.2	5.0	2960	4	SSAJ3230	AJ223230 Sus scrof
154	321.2	5.0	3771	4	GOTCKIT	D45168 Goat mRNA f
155	320.6	5.0	500	6	CQ671407	CQ671407 Sequence
156	320.6	5.0	5044	5	CHKCKITP	D13225 Gallus gall
157	320	5.0	4588	5	OMY417832	AJ417832 Oncorhync
158	319.8	5.0	2894	4	ECA224643	AJ224643 Equus cab
159	319.8	5.0	2894	4	ECA224644	AJ224644 Equus cab
160	319.8	5.0	2973	4	ECA224642	AJ224642 Equus cab
161	319.6	5.0	3952	6	CQ898728	CQ898728 Sequence
162	319.4	5.0	495	6	BD027931	BD027931 Sequence
163	319.4	5.0	495	6	AX892398	AX892398 Sequence
164	319	5.0	320	6	CQ706662	CQ706662 Sequence
165	318.6	5.0	2821	4	AY874543	AY874543 Equus cab
166	317.8	5.0	2933	4	AF055037	AF055037 Equus cab
167	314.6	4.9	2924	4	AF131209	AF131209 Trichosur
168	310.6	4.8	2473	13	REFESKIT	X03711 Hardy-Zucke
169	309.4	4.8	355	6	CQ705423	CQ705423 Sequence
170	307.2	4.8	3545	5	AF153446	AF153446 Danio rer
171	307.2	4.8	3826	5	XLXKRK1	Z48770 X.laevis c-
172	304.2	4.7	3425	5	AY536523	AY536523 Carassius
173	304	4.7	2940	5	AM050293	AM050293 Sparus au
174	302.6	4.7	2982	6	AX695523	AX695523 Sequence
175	302.6	4.7	3422	6	CS104350	CS104350 Sequence
176	302.6	4.7	3422	8	HSFLT3RTK	Z26652 Homo sapien
177	302.6	4.7	3475	6	I44733	I44733 Sequence 3
178	302.6	4.7	3475	6	AX695522	AX695522 Sequence
179	302.6	4.7	3475	8	HSU02687	U02687 Human growt
180	302.6	4.7	3476	6	I40109	I40109 Sequence 1
181	302.6	4.7	3501	6	AR005212	AR005212 Sequence
182	302.6	4.7	3501	6	AR071704	AR071704 Sequence
183	302.6	4.7	3501	6	I25170	I25170 Sequence 3
184	302.6	4.7	3501	6	I40601	I40601 Sequence 3
185	302.6	4.7	3501	6	AR452605	AR452605 Sequence
186	302.2	4.7	73760	14	AC101367	AC101367 Mus muscu
187	301.4	4.7	3581	5	AF240639	AF240639 Danio rer
188	301	4.7	2934	5	AF324481	AF324481 Danio nig
189	299.4	4.7	3120	6	I44518	I44518 Sequence 22
190	299.4	4.7	3120	6	AR262794	AR262794 Sequence
191	299.4	4.7	3120	6	AR447109	AR447109 Sequence
192	299.2	4.7	2934	5	AF324478	AF324478 Danio alb
c 193	298	4.6	73760	14	AC101367	AC101367 Mus muscu
194	297.2	4.6	2934	5	AF324480	AF324480 Danio ker
195	296	4.6	2982	4	DQ007998	DQ007998 Canis fam
196	295.8	4.6	2958	6	AR632468	AR632468 Sequence
197	294	4.6	302	6	CQ657040	CQ657040 Sequence
198	293.6	4.6	3521	6	I44732	I44732 Sequence 1
199	293.6	4.6	3521	9	MMFLT3	X59398 Mouse Flt3
200	290.8	4.5	2958	6	AR632466	AR632466 Sequence
201	290.8	4.5	2982	6	AR632465	AR632465 Sequence
202	290	4.5	291	10	G43580	G43580 WIAF-2453-S
203	290	4.5	85637	8	AL391002	AL391002 Human DNA
204	289.6	4.5	6024	5	BC061947	BC061947 Xenopus l
205	289.4	4.5	2977	5	AB091826	AB091826 Oncorhync
206	288.8	4.5	972	9	AF296695S2	AF296696 Rattus no
207	288.2	4.5	2949	6	AR632467	AR632467 Sequence
208	288	4.5	3795	8	HSM808750	BX648599 Homo sapi
209	288	4.5	3985	6	CS118311	CS118311 Sequence
210	288	4.5	3985	6	CS119721	CS119721 Sequence
211	288	4.5	3992	6	CQ873921	CQ873921 Sequence
212	288	4.5	3992	6	AR575630	AR575630 Sequence
213	288	4.5	3992	6	AX394288	AX394288 Sequence
214	288	4.5	3992	6	AX587822	AX587822 Sequence
215	288	4.5	3992	6	AX770566	AX770566 Sequence
216	288	4.5	3992	6	AX780018	AX780018 Sequence
217	288	4.5	3992	8	HSCFMS	X03663 Human mRNA
218	286.4	4.5	2823	11	AY890719	AY890719 Synthetic
219	286.4	4.5	2979	6	AX695520	AX695520 Sequence
220	286.4	4.5	3426	6	AX695519	AX695519 Sequence
221	286.4	4.5	3426	9	MUSFLK2	M64689 Mouse flk-2
222	286.4	4.5	3453	6	AR005211	AR005211 Sequence
223	286.4	4.5	3453	6	AR071703	AR071703 Sequence
224	286.4	4.5	3453	6	I25169	I25169 Sequence 1
225	286.4	4.5	3453	6	I40600	I40600 Sequence 1
226	286.4	4.5	3453	6	AR452604	AR452604 Sequence
227	286.4	4.5	3904	8	BC047521	BC047521 Homo sapi
228	285.4	4.5	2978	4	AY876383	AY876383 Bubalus b
229	282.2	4.4	2265	6	CQ719901	CQ719901 Sequence
230	280.8	4.4	2978	6	AR632464	AR632464 Sequence
231	279.6	4.4	972	9	AF296694S2	AF296693 Rattus no
232	278.8	4.3	3691	9	BC043054	BC043054 Mus muscu
233	278.8	4.3	3699	9	BC036343	BC036343 Mus muscu
234	278.6	4.3	3881	6	CQ727597	CQ727597 Sequence
235	277.2	4.3	3793	9	BC066863	BC066863 Mus muscu
236	276.2	4.3	781	4	AF347050S2	AF347051 Sus scrof
237	275.6	4.3	3679	9	RRCSF1	X61479 Rat mRNA fo

	238	274	4.3	4835	5	BC082504 BC082504 Xenopus t
	239	273.8	4.3	2925	5	AF324479 AF324479 Danio dan
	240	273.6	4.3	3113	5	AJ871269 AJ871269 Sparus au
	241	269.6	4.2	3828	4	CATFMSC J03149 Cat (F.dome
	242	269.2	4.2	3575	9	MMCFMS X68932 M.musculus
	243	268	4.2	4577	13	FCSSMONC K01643 Feline sarc
c	244	261	4.1	581	10	BV042977 BV042977 S212P6780
	245	260.4	4.1	467	6	CQ398565 CQ398565 Sequence
	246	260.4	4.1	467	6	CQ404852 CQ404852 Sequence
	247	258.2	4.0	1044	5	AB025556 AB025556 Lampetra
	248	258	4.0	3665	9	MMFMSCR X06368 Murine mRNA
c	249	254.4	4.0	3991	10	BV178925 BV178925 sqnm10318
c	250	251.6	3.9	248565	14	AC128841 AC128841 Rattus no
c	251	248	3.9	175628	9	AC138641 AC138641 Mus muscu
	252	246.4	3.8	400	6	CQ665889 CQ665889 Sequence
	253	243.8	3.8	1525	5	AF178759 AF178759 Danio rer
	254	243.8	3.8	4473	5	AY833404 AY833404 Danio rer
	255	243.8	3.8	4491	5	AY524001 AY524001 Danio rer
	256	243.6	3.8	1911	6	AX481431 AX481431 Sequence
	257	227.6	3.5	4617	5	CCQUEK2 X83287 C.coturnix
	258	226	3.5	1534	5	S65207 S65207 endothelial
	259	225.4	3.5	1983	5	S78748 S78748 Xenopus lae
	260	225	3.5	966	5	AB025555 AB025555 Lampetra
	261	224.4	3.5	248	6	CQ673336 CQ673336 Sequence
	262	222.6	3.5	1519	2	AB025557 AB025557 Branchios
	263	221.6	3.5	4450	6	BD261545 BD261545 Methods f
	264	221.6	3.5	4450	6	CS032708 CS032708 Sequence
	265	221.6	3.5	4450	6	CS041660 CS041660 Sequence
	266	221.6	3.5	4450	6	CS126002 CS126002 Sequence
	267	221.6	3.5	4450	6	AX671078 AX671078 Sequence
	268	221.6	3.5	4450	8	HSFLT4X X69878 H.sapiens F
	269	221.4	3.5	2231	5	AB121074 AB121074 Oryzias l
	270	220	3.4	3897	6	AX481482 AX481482 Sequence
	271	220	3.4	4111	6	AR564634 AR564634 Sequence
	272	220	3.4	4195	6	AR016568 AR016568 Sequence
	273	220	3.4	4195	6	AR106405 AR106405 Sequence
	274	220	3.4	4195	6	BD270836 BD270836 Flt4 (VER
	275	220	3.4	4195	6	CS067238 CS067238 Sequence
	276	220	3.4	4195	6	AR608967 AR608967 Sequence
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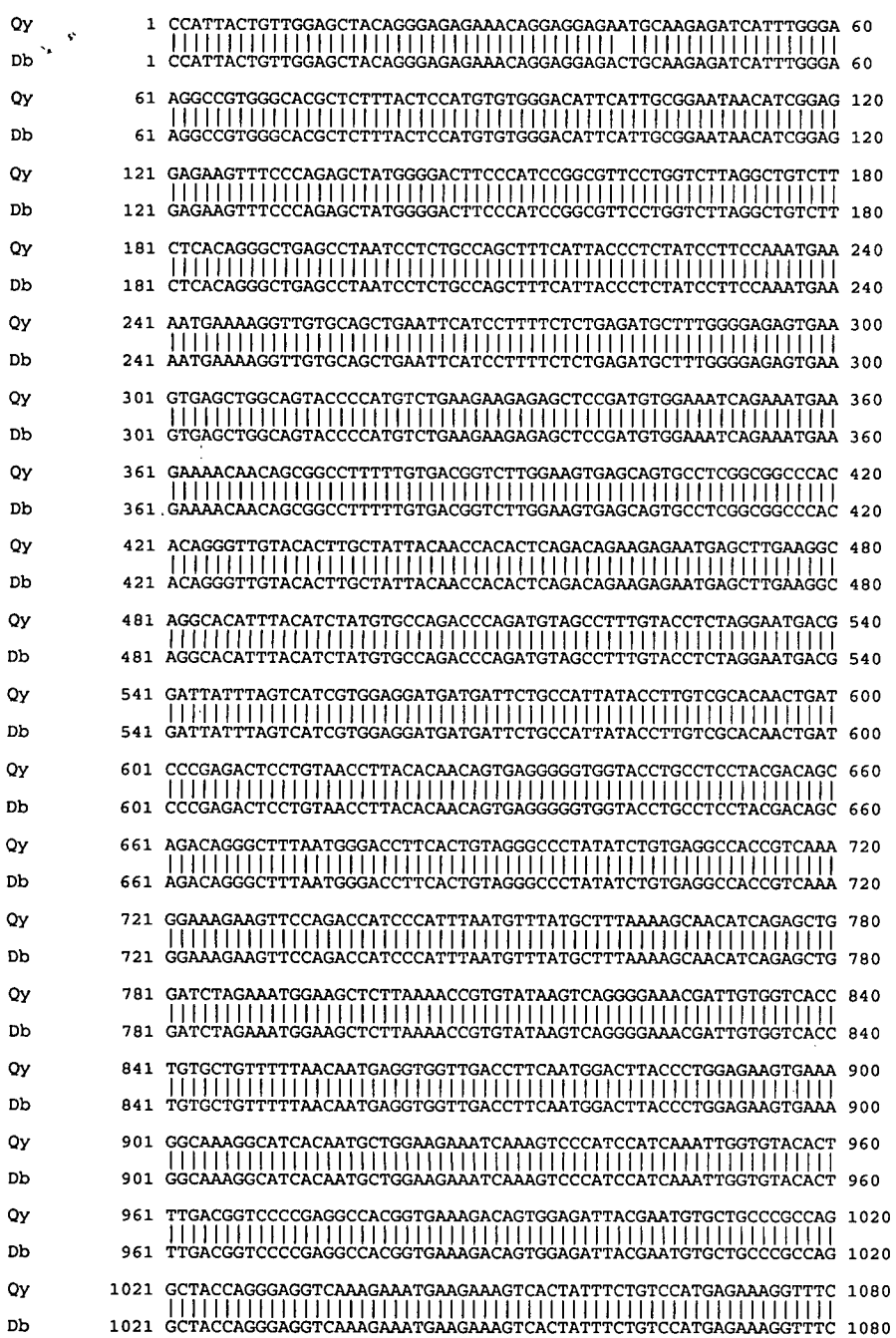
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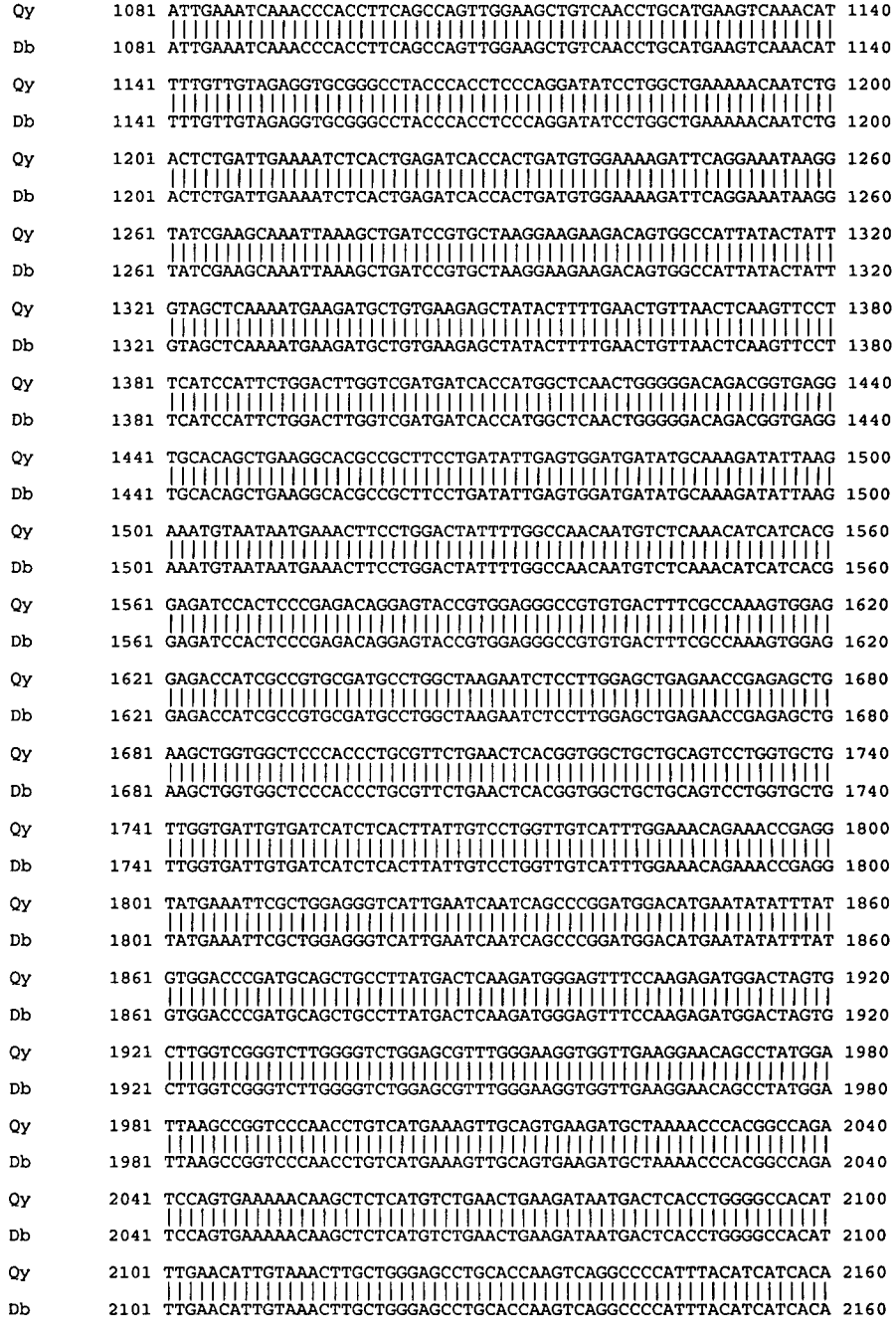
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VERSION AR437544.1 GI:40202638
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6412)
AUTHORS Matsui,T., Aaronson,S.A. and Pierce,J.H.
TITLE Antibodies for the alpha platelet-derived growth factor receptor
JOURNAL Patent: US 6660488-A 1 09-DEC-2003;
The United States of America as represented by the Department of Health & Human Services; Washington, DC
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Qy       3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
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Db       3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180

Qy       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
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Db       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240

Qy       3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
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Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Qy       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480

Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540

Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
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Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
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Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840

Qy       3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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Db       4080 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4139

Qy       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
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Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Db       4740 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4799

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6361 GATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6413
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RESULT 2
CQ414643
LOCUS       CQ414643               6428 bp    DNA     linear   PAT 23-JAN-2004
DEFINITION  Sequence 21714 from Patent WO0170979.
ACCESSION   CQ414643
VERSION     CQ414643.1  GI:41322424
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lee,J. and Lillie,J.
  TITLE     Genes, compositions, kits, and method for identification,
            assessment, prevention, and therapy of ovarian cancer
  JOURNAL   Patent: WO 0170979-A 21714 27-SEP-2001;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             99.4%;  Score 6373.2;  DB 6;  Length 6428;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6386;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          2 CATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAA 61
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          9 CATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGAA 68

Qy         62 GGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGG 128

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Db        249 ATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAG 308

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Db        669 GACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAG 728

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Db        729 GAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGG 788

Qy        782 ATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCT 841
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Qy        902 GCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTT 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTT 968

Qy        962 TGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGG 1028

Qy       1022 CTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCA 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCA 1088

Qy       1082 TTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATT 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 TTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATT 1148

Qy       1142 TTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGA 1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 TTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGA 1208

Qy       1202 CTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGT 1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 CTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGT 1268

Qy       1262 ATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTG 1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 ATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTG 1328

Qy       1322 TAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTT 1381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 TAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTT 1388

Qy       1382 CATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGT 1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 CATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGT 1448

Qy       1442 GCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGA 1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 GCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGA 1508

Qy       1502 AATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGG 1561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1509 AATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGG 1568

Qy       1562 AGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGG 1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 AGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGG 1628

Qy       1622 AGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGA 1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1629 AGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGA 1688

Qy       1682 AGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGT 1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1689 AGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGT 1748

Qy       1742 TGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGT 1801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1749 TGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGT 1808

Qy       1802 ATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATG 1861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1809 ATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATG 1868
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Qy      1862 TGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGC 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1869 TGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGC 1928

Qy      1922 TTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGAT 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1929 TTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGAT 1988

Qy      1982 TAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGAT 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1989 TAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGAT 2048

Qy      2042 CCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATT 2101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2049 CCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATT 2108

Qy      2102 TGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAG 2161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2109 TGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAG 2168

Qy      2162 AGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGA 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2169 AGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGA 2228

Qy      2222 GCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATG 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2229 GCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATG 2288

Qy      2282 AAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGA 2341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2289 AAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGA 2348

Qy      2342 AGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATT 2401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2349 AGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATT 2408

Qy      2402 CCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAG 2461
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2409 CCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAG 2468

Qy      2462 ACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATT 2521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2469 ACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATT 2528

Qy      2522 TGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTG 2581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2529 TGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTG 2588

Qy      2582 TCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCT 2641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2589 TCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCT 2648

Qy      2642 GTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTA 2701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2649 GTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTA 2708

Qy      2702 CCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACAC 2761
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2709 CCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACAC 2768

Qy      2762 TGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCC 2821
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2769 TGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCC 2828

Qy      2822 CTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGA 2881
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2829 CTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGA 2888

Qy      2882 TGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACA 2941
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2889 TGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACA 2948

Qy      2942 GTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGC 3001
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2949 GTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGC 3008

Qy      3002 CTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATC 3061
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3009 CTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATC 3068

Qy      3062 CTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAA 3121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3069 CTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAA 3128

Qy      3122 ACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTG 3181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3129 ACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTG 3188

Qy      3182 ACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGG 3241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3189 ACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGG 3248

Qy      3242 GCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCA 3301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3249 GCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCA 3308

Qy      3302 GCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACG 3361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3309 GCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACG 3368

Qy      3362 ACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGA 3421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3369 ACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGA 3428

Qy      3422 GGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCA 3481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3429 GGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCA 3488

Qy      3482 ATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCC 3541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3489 ATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCC 3548

Qy      3542 TCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3549 TCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3608

Qy      3602 CCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3661
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3609 CCTCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3668

Qy      3662 GGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAC 3721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3669 GGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAC 3728

Qy      3722 AGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCA 3781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3729 AGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCA 3788

Qy      3782 AGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCC 3841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3789 AGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCC 3848

Qy      3842 ATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTG 3901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3849 ATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTG 3908

Qy      3902 CATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTT 3961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3909 CATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTT 3968

Qy      3962 TTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCAT 4021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3969 TTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCAT 4028

Qy      4022 TTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTA 4081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       4029 TTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTA 4088
Qy       4082 TCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTA 4141
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4089 TCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTA 4148

Qy       4142 AAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAAC 4201
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4149 AAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAAC 4208

Qy       4202 ATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGA 4261
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4209 ATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGA 4268

Qy       4262 ACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCC 4321
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4269 ACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCC 4328

Qy       4322 CCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAA 4381
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4329 CCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAA 4388

Qy       4382 CAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAAC 4441
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4389 CAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAAC 4448

Qy       4442 TTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGA 4501
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4449 TTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGA 4508

Qy       4502 AGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTT 4561
             ||  ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       4509 AG-TTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTT 4567

Qy       4562 TTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4568 TTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4627

Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4628 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4687

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4688 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4747

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4748 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4807

Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4808 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4867

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTC 4921
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4868 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTC 4927

Qy       4922 AACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCA 4981
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4928 AACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCA 4987

Qy       4982 TCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCT 5041
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4988 TCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCT 5047

Qy       5042 AAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGA 5101
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5048 AAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGA 5107

Qy       5102 GATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGG 5161
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5108 GATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGG 5167

Qy       5162 CATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTT 5221
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5168 CATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTT 5227

Qy       5222 GGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGT 5281
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5228 GGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGT 5287

Qy       5282 CACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACT 5341
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5288 CACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACT 5347

Qy       5342 GCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCT 5401
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5348 GCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCT 5407

Qy       5402 ATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTG 5461
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5408 ATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTG 5467

Qy       5462 GTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGA 5521
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5468 GTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGA 5527

Qy       5522 CTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGA 5581
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5528 CTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGA 5587

Qy       5582 CTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCT 5641
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5588 CTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCT 5647

Qy       5642 CCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCAT 5701
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5648 CCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCAT 5707

Qy       5702 GACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTC 5761
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Db       5708 GACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTC 5767

Qy       5762 CCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAG 5821
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Db       5768 CCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAG 5827

Qy       5822 ATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTAC 5881
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Db       5828 ATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTAC 5887

Qy       5882 TTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAA 5941
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5888 TTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAA 5947

Qy       5942 ACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTG 6001
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5948 ACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTG 6007

Qy       6002 TGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATA 6061
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6008 TGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATA 6067

Qy       6062 TAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATA 6121
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Db       6068 TAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATA 6127

Qy       6122 TTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAA 6181
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Db       6128 TTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAA 6187

Qy       6182 ATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTG 6241
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6188 ATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTG 6247
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Qy       6242 GTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATG 6301
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Db       6248 GTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATG 6307

Qy       6302 CCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATG 6361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6308 CCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATG 6367

Qy       6362 ATATATAATTTAAAGTTAAAAAAAAAAAAA 6391
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Db       6368 ATATATAATTTAAAGTTAAAAAAAAAAAA 6397


RESULT 3
AR380649
LOCUS       AR380649               6378 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1194 from patent US 6607879.
ACCESSION   AR380649
VERSION     AR380649.1  GI:40088283
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6378)
  AUTHORS   Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
  TITLE     Compositions for the detection of blood cell and immunological
            response gene expression
  JOURNAL   Patent: US 6607879-A 1194 19-AUG-2003;
            Incyte Corporation; Palo Alto, CA
FEATURES             Location/Qualifiers
     source          1. .6378
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           99.2%;  Score 6364.4;  DB 6;  Length 6378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Db       1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Db       1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561

Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621
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Qy      1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
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Db      1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy      1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy      1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Db      1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801

Qy      1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Db      1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861

Qy      1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921

Qy      1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981

Qy      1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041

Qy      2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101

Qy      2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161

Qy      2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221

Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281

Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341

Qy      2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401

Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
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Db      2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461

Qy      2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Db      2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521

Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Db      2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581

Qy      2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
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Db      2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641

Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Db      2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701

Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761

Qy      2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821

Qy      2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881

Qy      2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
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Db      2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941

Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001

Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Db      3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061

Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121

Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181

Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241

Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301

Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361

Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db      3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Db      3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541

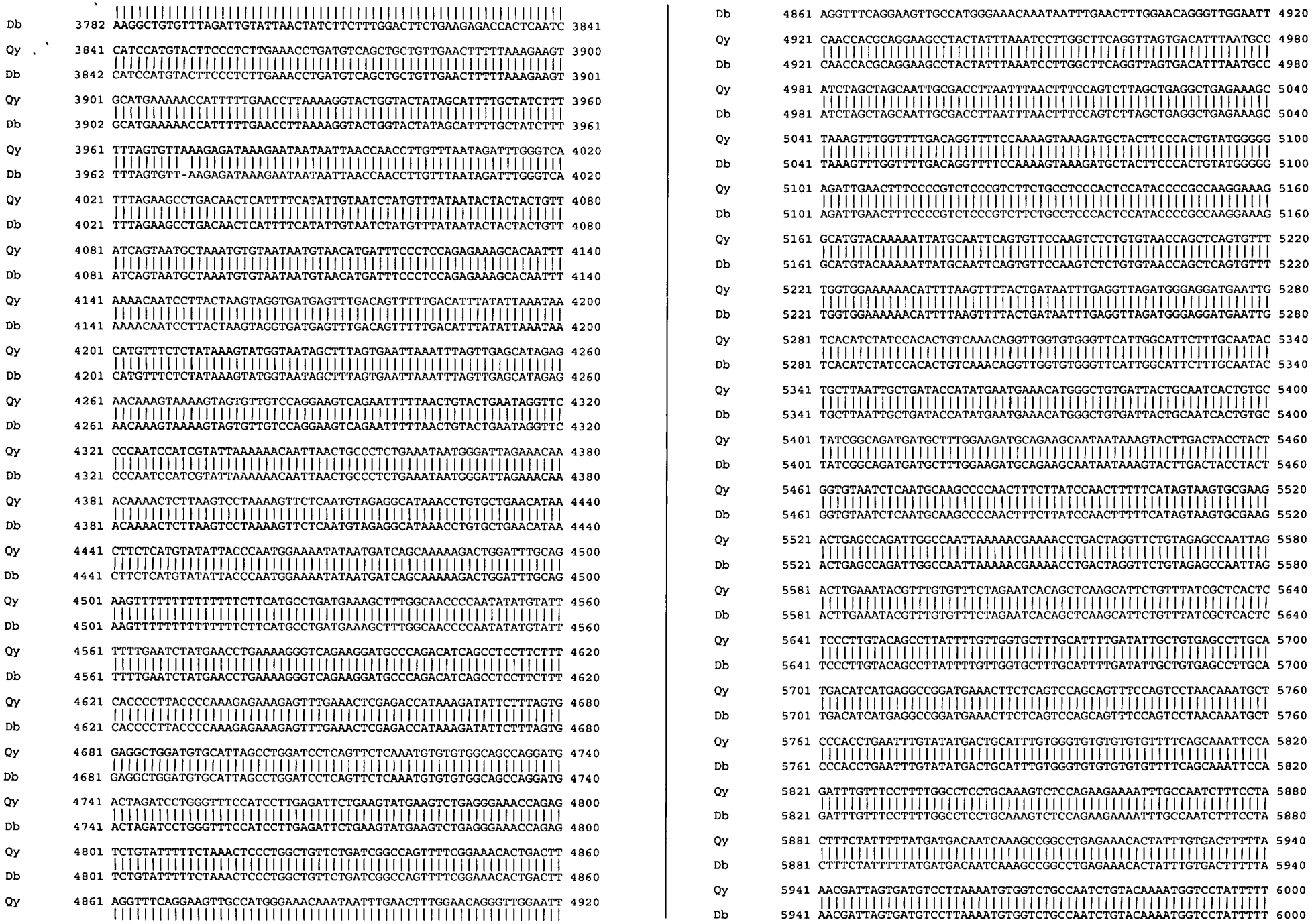
Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Db      3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661

Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721

Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
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Db      3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781

Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Db 3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
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Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Db 5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Qy 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 4
AR575515
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DEFINITION  Sequence 40 from patent US 6773883.
ACCESSION   AR575515
VERSION     AR575515.1  GI:56576609
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6378)
  AUTHORS   Mutter,G.L.
  TITLE     Prognostic classification of endometrial cancer
  JOURNAL   Patent: US 6773883-A 40 10-AUG-2004;
            The Brigham & Women's Hospital, Inc.; Boston, MA
FEATURES             Location/Qualifiers
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ORIGIN
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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
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Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
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Qy      1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Db      1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441

Qy      1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Qy      1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Db      1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561

Qy      1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
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Db      1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621

Qy      1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy      1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
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Qy      1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Qy      1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Qy      1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Qy      1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
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Qy      1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
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Qy      2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
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Db      2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101

Qy      2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
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Db      2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161

Qy      2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
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Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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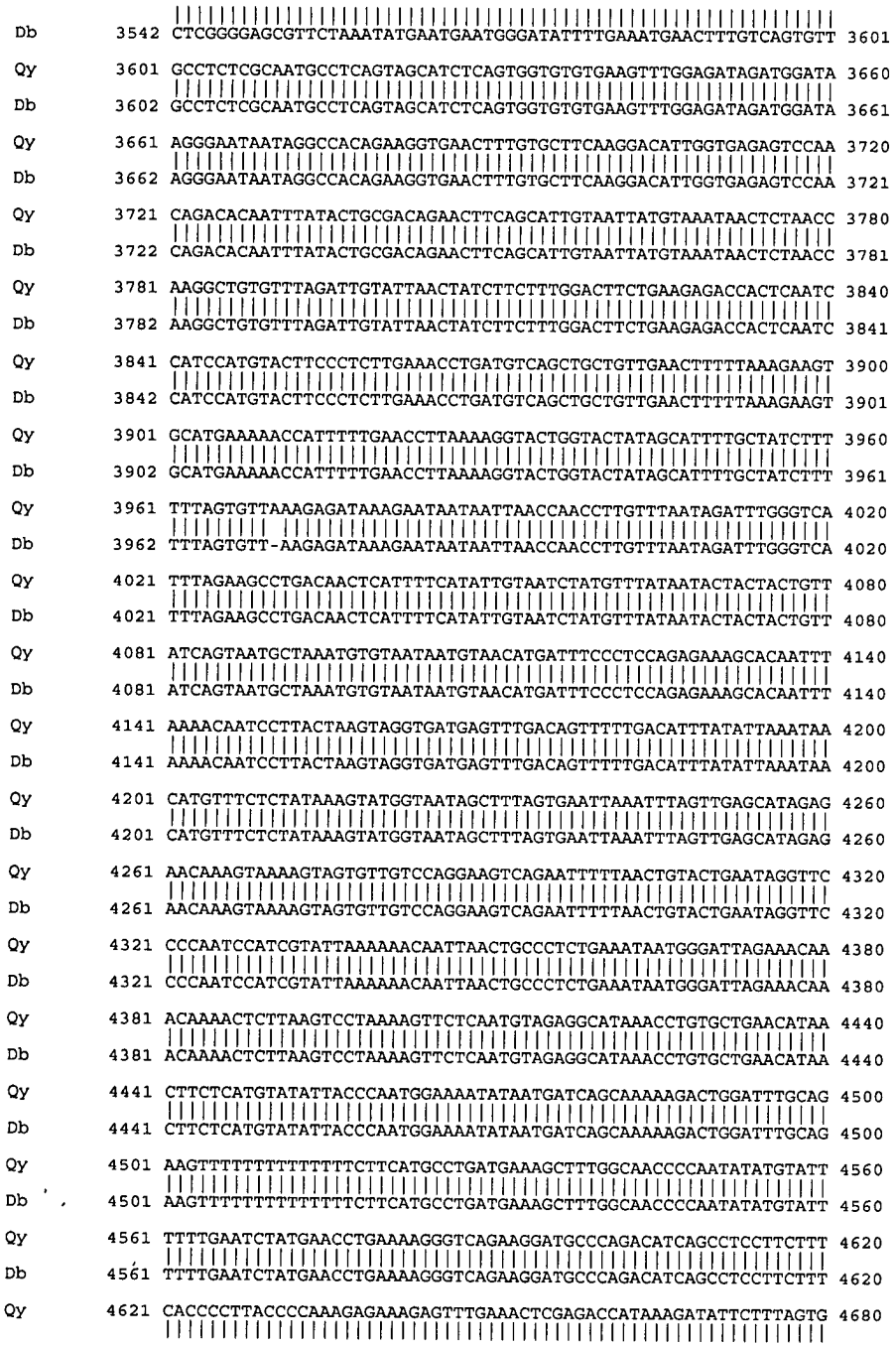
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RESULT 5
AX330200
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DEFINITION Sequence 709 from Patent WO0194629.
ACCESSION AX330200
VERSION AX330200.1 GI:18103178
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 709 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.2%; Score 6364.4; DB 6; Length 6378;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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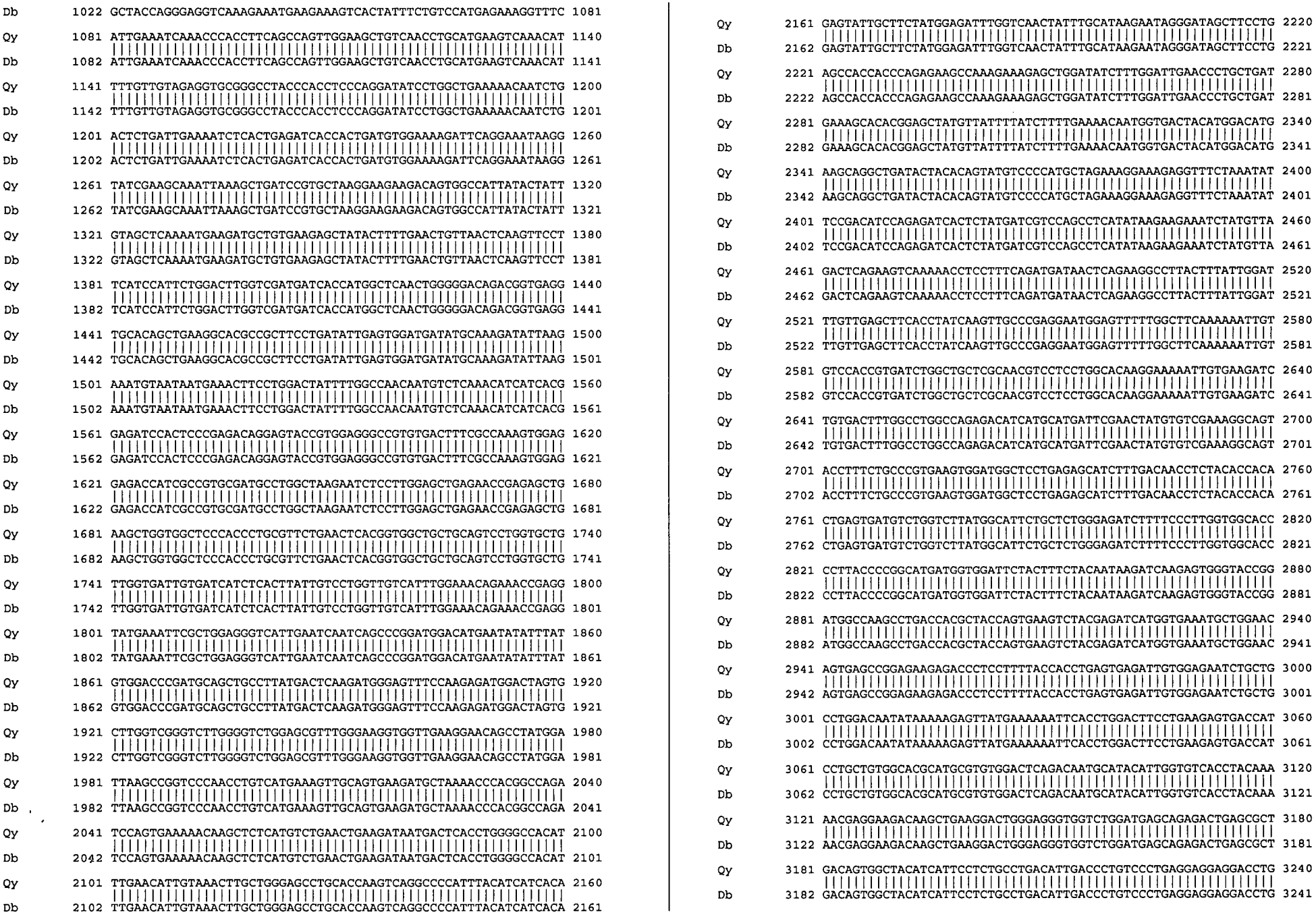
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081
Qy 1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
Db 1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141
Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
Db 1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201
Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db 1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261
Qy 1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db 1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db 1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db 1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441
Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db 1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501
Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db 1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561
Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db 1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621
Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db 1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681
Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db 1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db 2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db 2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db 2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db 2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db 2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db 2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001
Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241

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Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301

Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361

Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541

Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661

Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721

Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781

Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841

Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901

Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961

Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020

Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080

Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140

Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200

Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260

Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320

Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380

Qy      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440

Qy      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500

Qy      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560

Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620

Qy      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680

Qy      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

Qy      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860

Qy      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920

Qy      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160

Qy      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280

Qy      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340

Qy      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy      5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
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Db .     6361 GATATATAATTTAAAGTT 6378
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RESULT 6
AX336347
LOCUS       AX336347               6378 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 6856 from Patent WO0194629.
ACCESSION   AX336347
VERSION     AX336347.1  GI:18127066
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 6856 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .6378
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match 99.2%; Score 6364.4; DB 6; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Db      2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001

Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061

Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121

Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181

Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241

Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Db      3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301

Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
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Db      3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361

Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db      3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Db      3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
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Db      3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541

Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Db      3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661

Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
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Db      3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721

Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
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Db      3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781

Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Db      3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841

Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
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Db      3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901

Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
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Db      3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961

Qy      3961 TTTAGTGTTAAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020

Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
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Db      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080

Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Db      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140

Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Db      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200

Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
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Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320

Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Db      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380

Qy      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500

Qy      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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Qy      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
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Db      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Db      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

Qy      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Db      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860

Qy      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Db      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Db       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 7
HUMPDGFRAA
LOCUS HUMPDGFRAA 6378 bp mRNA linear PRI 11-APR-1996
DEFINITION Human platelet-derived growth factor receptor alpha (PDGFRA) mRNA, complete cds.
ACCESSION M21574
VERSION M21574.1 GI:189733
KEYWORDS platelet-derived growth factor receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6378)
AUTHORS Matsui,T., Heidaran,M., Miki,T., Popescu,N., La Rochelle,W., Kraus,M., Pierce,J. and Aaronson,S.
TITLE Isolation of a novel receptor cDNA establishes the existence of two PDGF receptor genes
JOURNAL Science 243 (4892), 800-804 (1989)
PUBMED 2536956
COMMENT Original source text: Homo sapiens cDNA to mRNA.
Draft entry and computer-readable sequence for [1] kindly submitted by S.Tronick, 29-NOV-1988.
FEATURES Location/Qualifiers
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ORIGIN

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Qy      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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RESULT 8
CS079378
LOCUS       CS079378                6633 bp    DNA     linear   PAT 06-MAY-2005
DEFINITION  Sequence 13 from Patent WO2005020972.
ACCESSION   CS079378
VERSION     CS079378.1  GI:63093782
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE   1
  AUTHORS   Shima,D., Calias,P. and Adamis,A.P.
  TITLE     Combination therapy for the treatment of ocular neovascular
            disorders
  JOURNAL   Patent: WO 2005020972-A 13 10-MAR-2005;
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ORIGIN

  Query Match             99.2%;  Score 6364.4;  DB 6;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db      3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db      3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
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Db      3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db      3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db      3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796
Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db      3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
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Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
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Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db      4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096
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Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
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Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
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Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
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Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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RESULT 9
AR206726
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DEFINITION  Sequence 1 from patent US 6372438.
ACCESSION   AR206726
VERSION     AR206726.1  GI:21505415
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6373)
  AUTHORS   Williams,L.Thomas. and Escobedo,J.A.
  TITLE     Human platelet-derived growth factor receptors
  JOURNAL   Patent: US 6372438-A 1 16-APR-2002;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             74.5%;  Score 4777;  DB 6;  Length 6373;
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  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   11;  Gaps    8;

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Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127

Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187

Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247

Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307

Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427

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Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487

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Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
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Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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RESULT 10
AR036472
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DEFINITION Sequence 5 from patent US 5872218.
ACCESSION AR036472
VERSION AR036472.1 GI:5953140
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6375)
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and Williams,L.Thomas.
TITLE Human platelet-derived growth factor receptor extracellular domain antibodies
JOURNAL Patent: US 5872218-A 5 16-FEB-1999;
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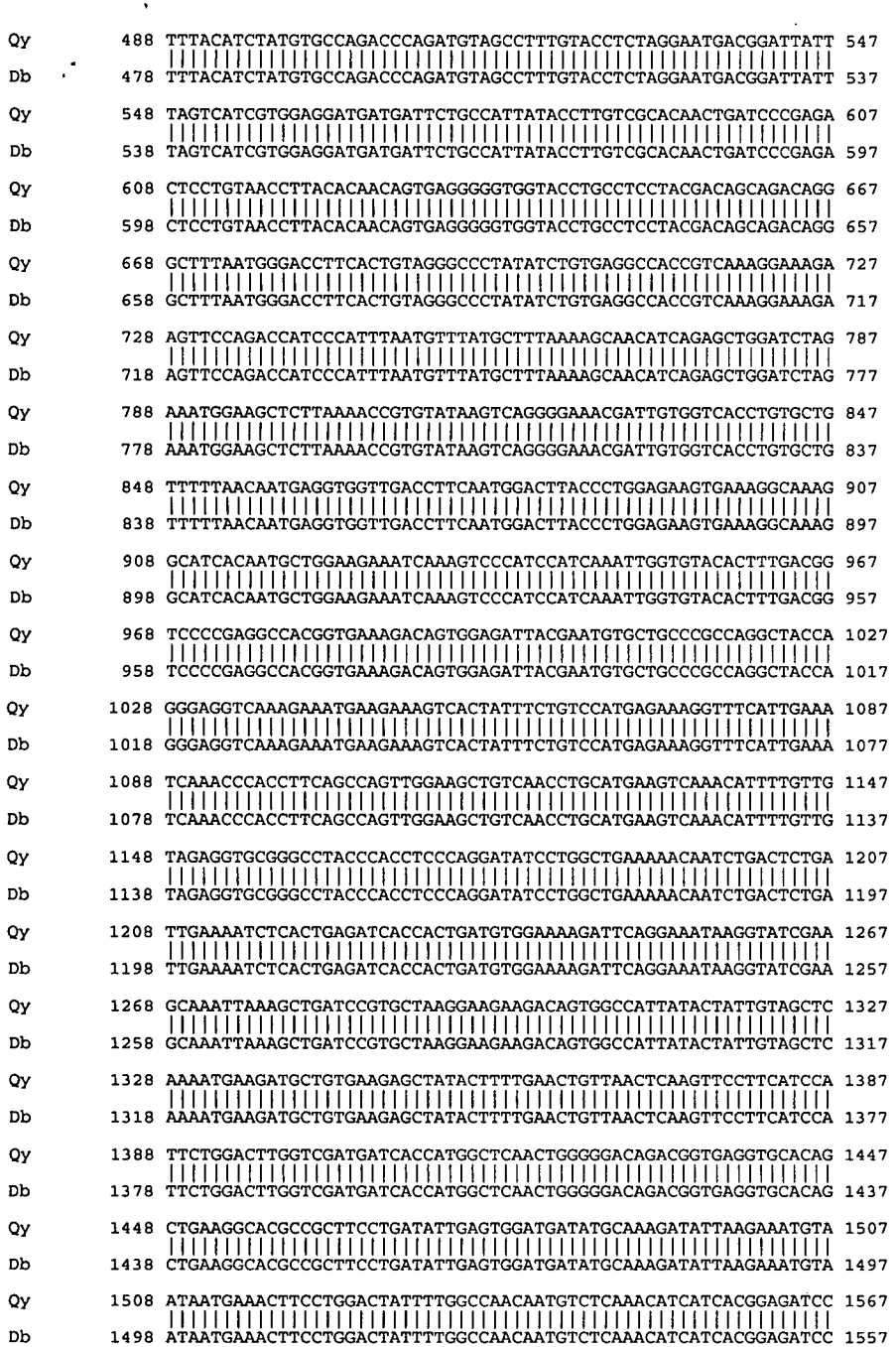
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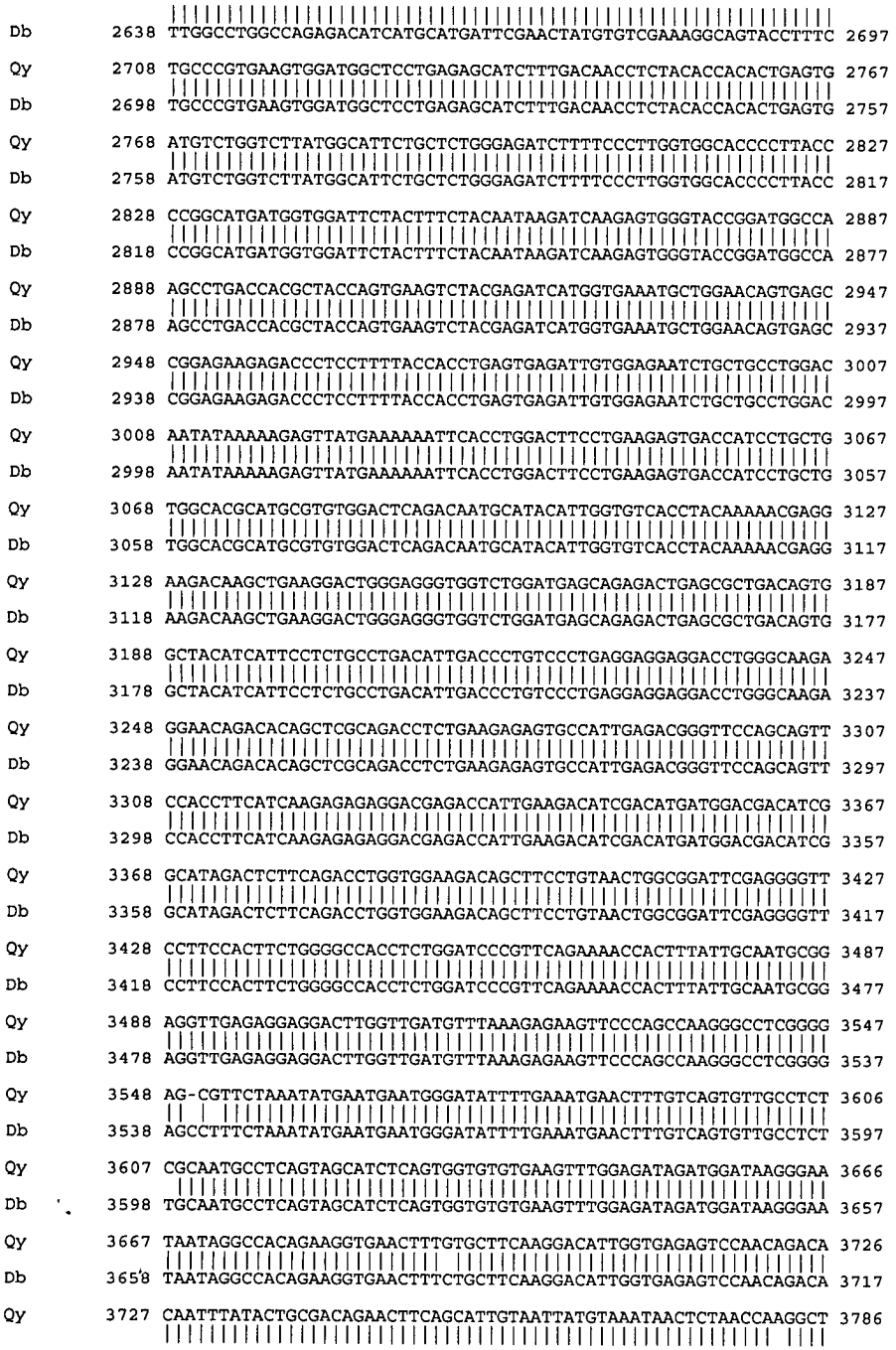
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Qy 2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
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RESULT 11
AR069431
LOCUS       AR069431               6375 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 5 from patent US 5891652.
ACCESSION   AR069431
VERSION     AR069431.1  GI:7220319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6375)
  AUTHORS   Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
            Williams,L.Thomas.
  TITLE     Methods of using domains of extracellular region of human
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                     /organism="unknown"
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ORIGIN

  Query Match             74.3%;  Score 4765.6;  DB 6;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

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Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
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Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy       1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
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Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
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Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
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Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
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Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
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Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
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Qy      3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
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Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
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Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
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Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
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Qy      3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy      3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db      3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy      3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Qy      3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
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Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
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Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

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Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
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Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

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             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908


RESULT 12
BD166138
LOCUS       BD166138               6375 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Platelet-derived growth factor receptors.
ACCESSION   BD166138
VERSION     BD166138.1  GI:27871950
KEYWORDS    JP 2002186490-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 6375)
  AUTHORS   Williams,L.T. and Escobedo,J.A.
  TITLE     Platelet-derived growth factor receptors
  JOURNAL   Patent: JP 2002186490-A 3 02-JUL-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186490-A/3
            PD   02-JUL-2002
            PF   27-SEP-2001 JP 2001298110
            PR   31-JAN-1991 US       650794
            PI   LEWIS T WILLIAMS,JAIME A ESCOBEDO
            PC   C12N15/09,A61K38/00,A61K38/55,A61K45/00,A61P9/00,A61P9/10, PC
             A61P17/02,
            PC   A61P35/00,C12N9/12,C12Q1/48,G01N33/15,G01N33/50,G01N33/566, PC
              C12N15/00,
            PC   A61K37/02,A61K37/64
            CC   N = A, C, G, or T
            CC   Note: Nucleotide number 1 of this sequence
            is identical to the
            CC              nucleotide
            CC   number 1 of the previous 4100 long sequence
            CC   Human PDGF receptor alpha
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(6375).
FEATURES              Location/Qualifiers
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                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             74.3%;  Score 4765.6;  DB 6;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  ||||||||| ||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

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Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
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Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
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Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db      1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
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Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
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Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
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Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

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Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627

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Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
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Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
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Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
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Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
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Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
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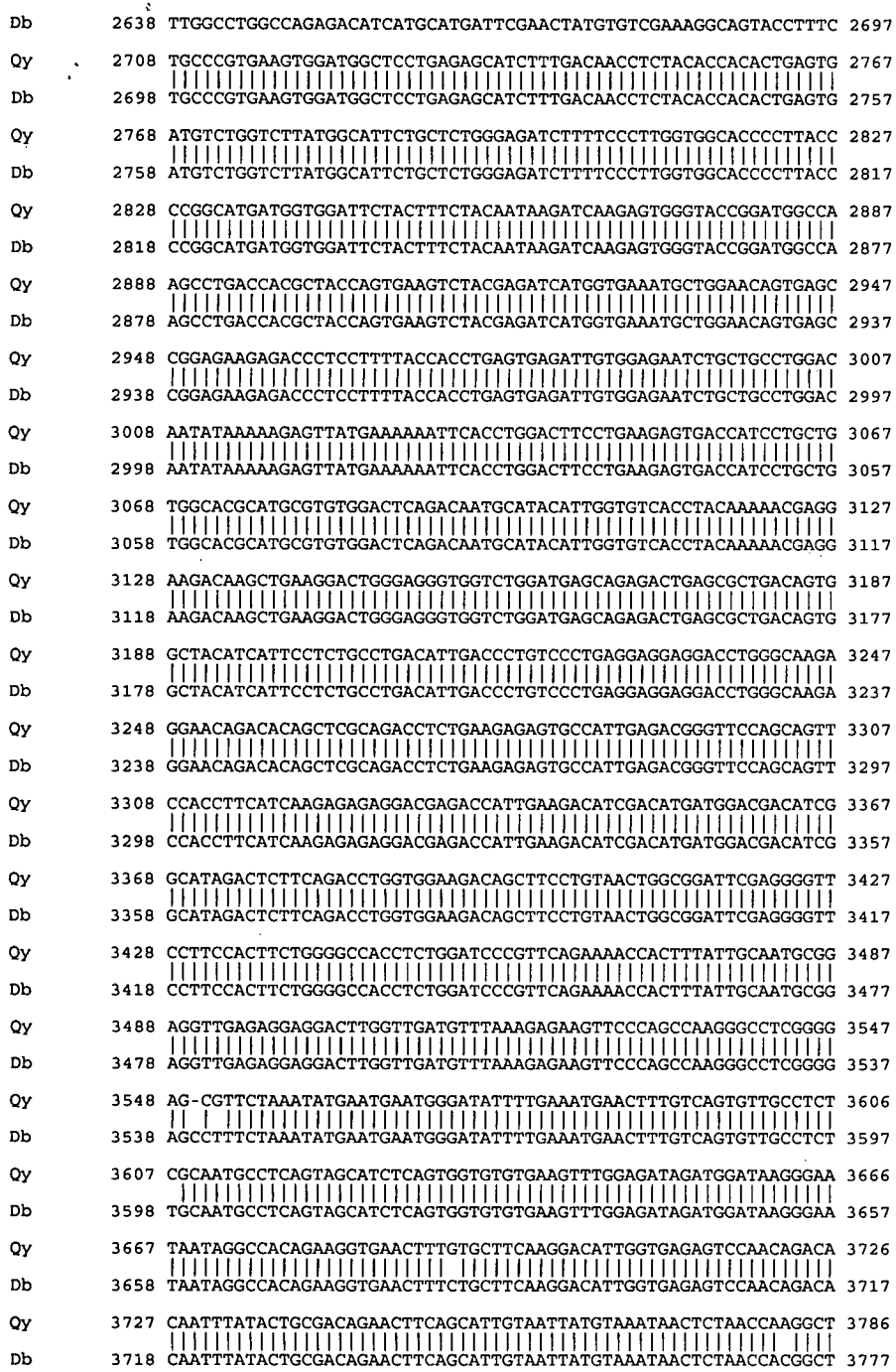
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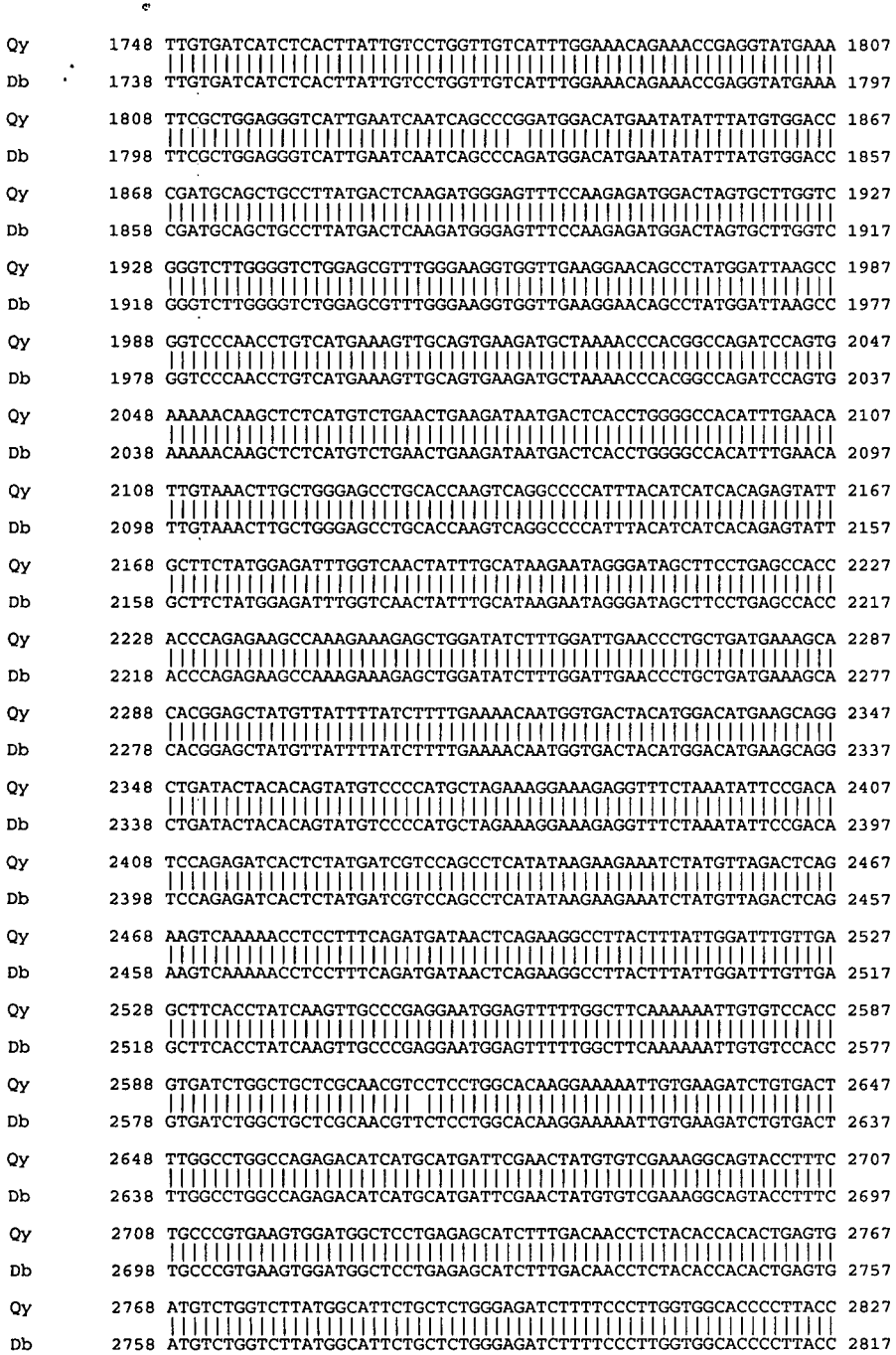
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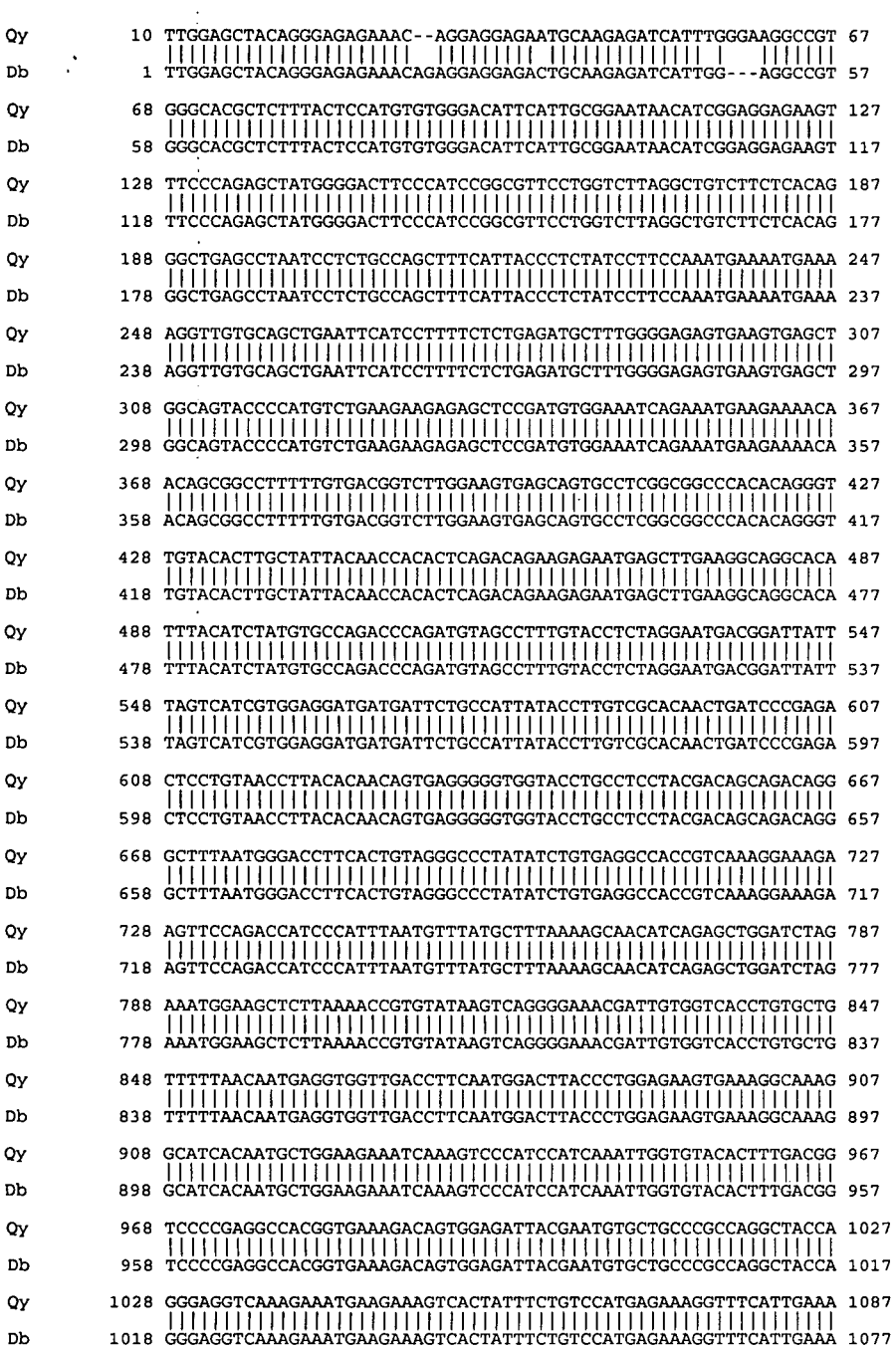
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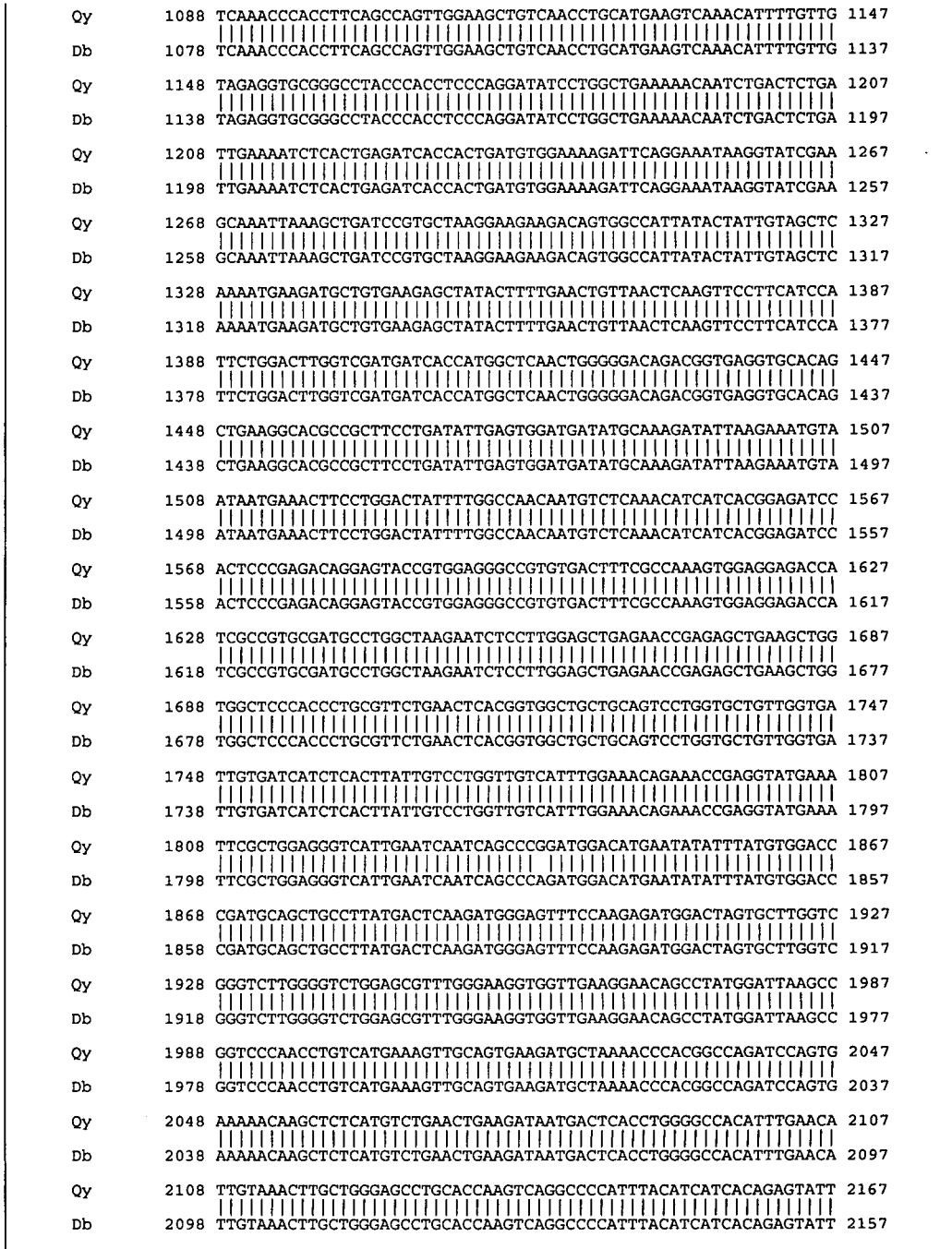
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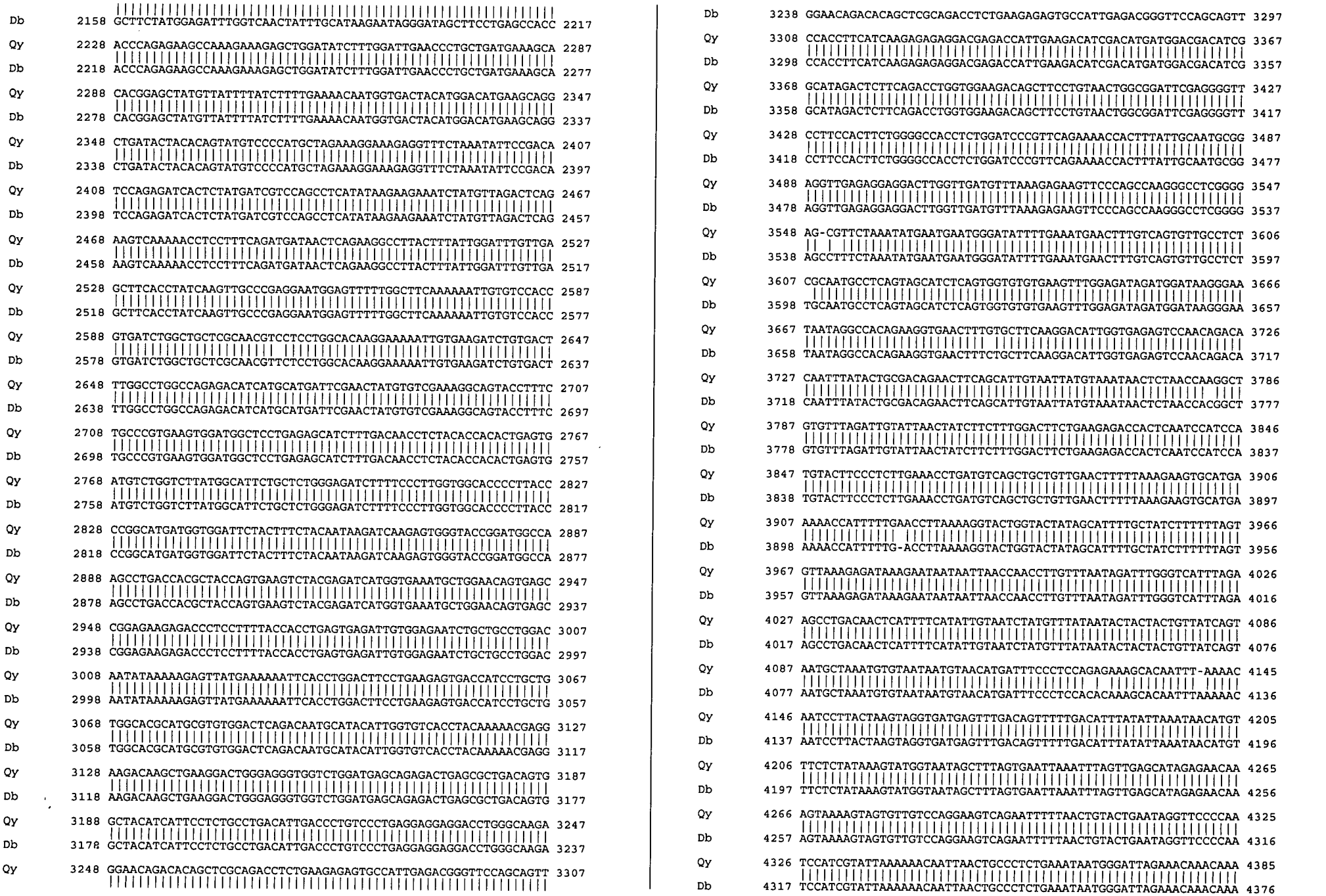
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RESULT 14
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DEFINITION  Human platelet-derived growth factor A type receptor mRNA, complete
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ACCESSION   M22734
VERSION     M22734.1  GI:189725
KEYWORDS    growth factor receptor; platelet-derived growth factor A type
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE   1  (bases 1 to 6375)
  AUTHORS   Claesson-Welsh,L., Eriksson,A., Westermark,B. and Heldin,C.H.
  TITLE     cDNA cloning and expression of the human A-type platelet-derived
            growth factor (PDGF) receptor establishes structural similarity to
            the B-type PDGF receptor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86 (13), 4917-4921 (1989)
  PUBMED    2544881
COMMENT     Original source text: Human foreskin fibroblast AG 1518 cell line,
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RESULT 15
AR036471
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VERSION     AR036471.1  GI:5953139
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SOURCE      Unknown.
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            Unclassified.
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  AUTHORS   Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
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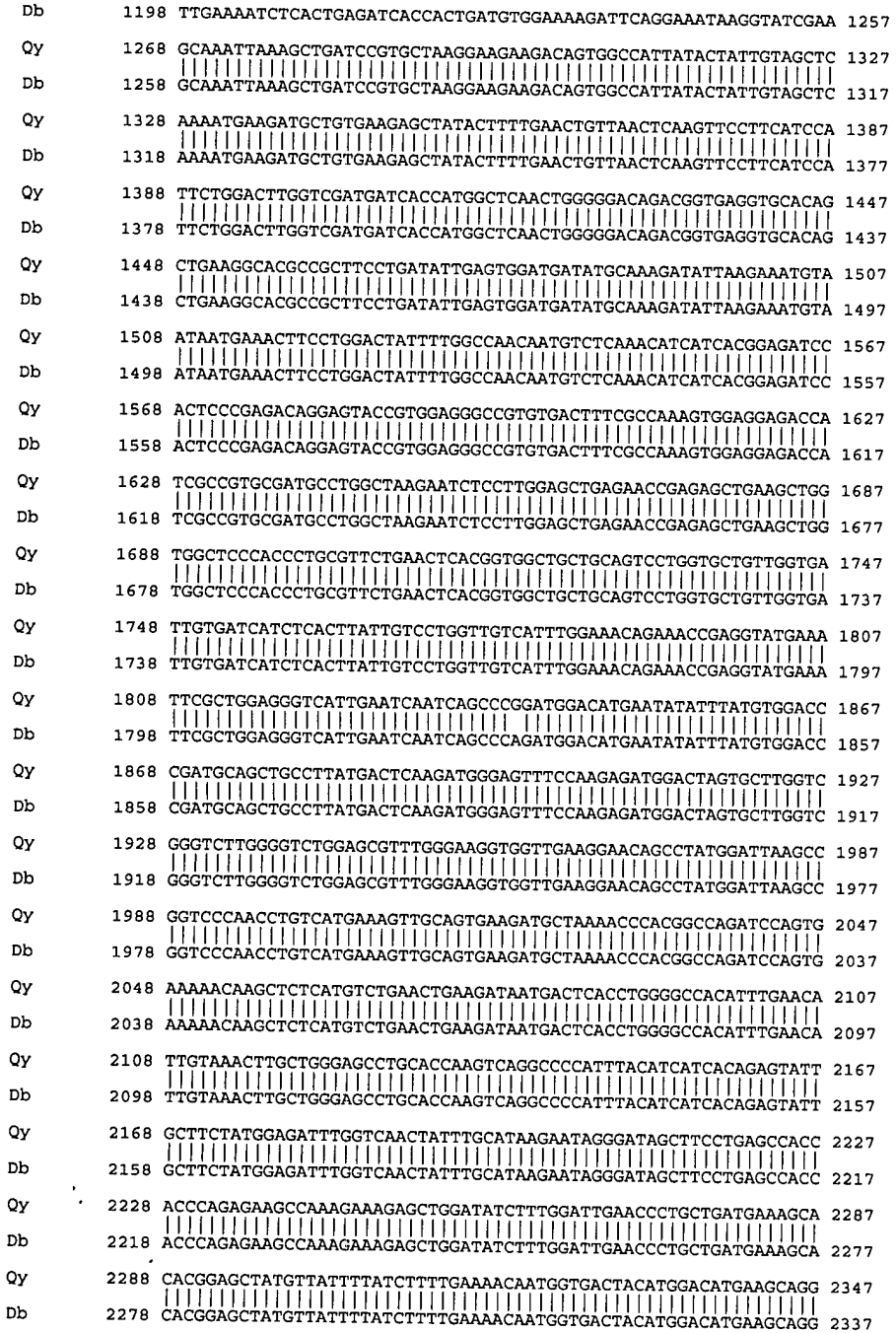
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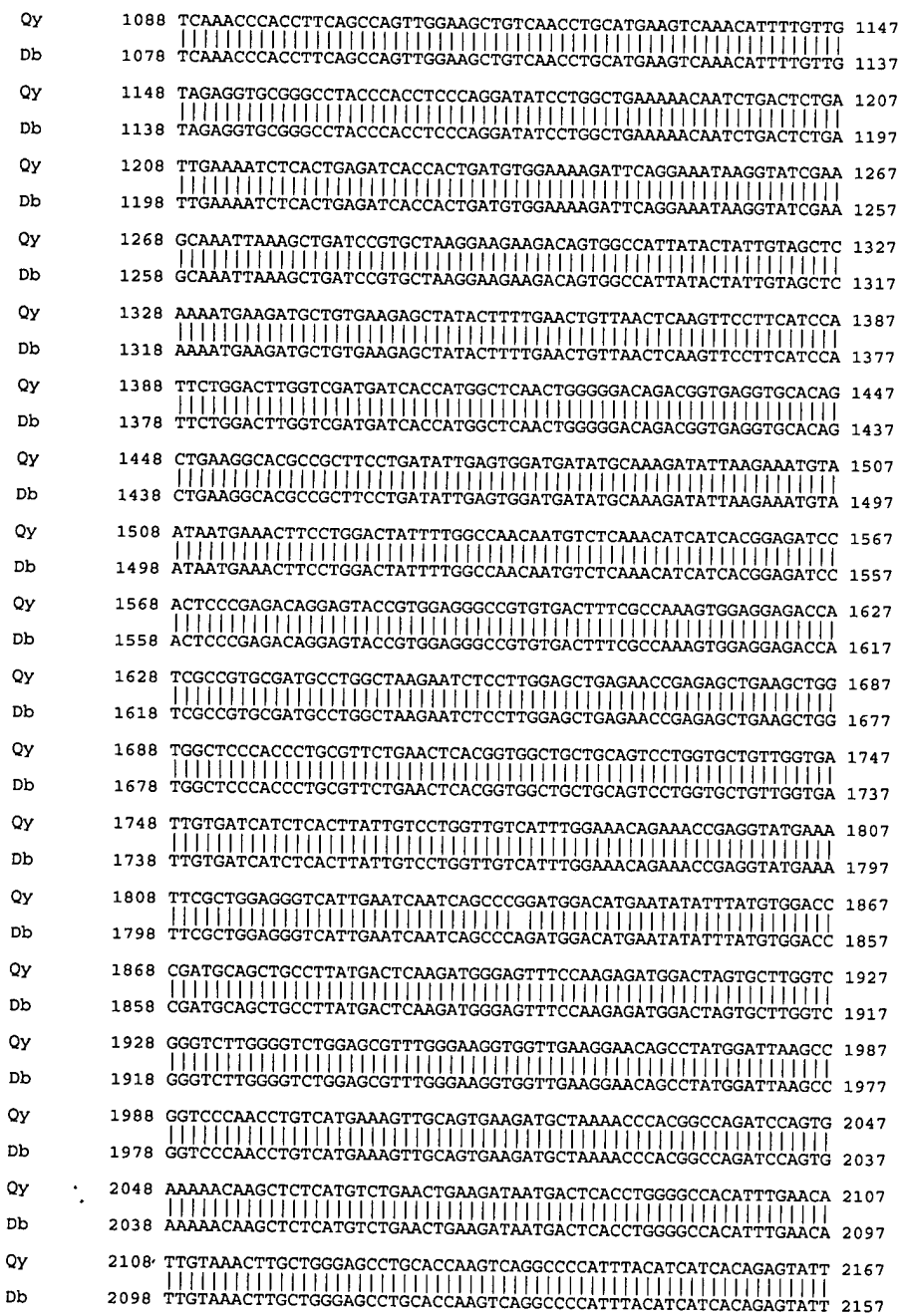
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RESULT 17
BD166137
LOCUS       BD166137               4100 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Platelet-derived growth factor receptors.
ACCESSION   BD166137
VERSION     BD166137.1  GI:27871949
KEYWORDS    JP 2002186490-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 4100)
  AUTHORS   Williams,L.T. and Escobedo,J.A.
  TITLE     Platelet-derived growth factor receptors
  JOURNAL   Patent: JP 2002186490-A 2 02-JUL-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186490-A/2
            PD   02-JUL-2002
            PF   27-SEP-2001 JP 2001298110
            PR   31-JAN-1991 US       650794
            PI   LEWIS T WILLIAMS,JAIME A ESCOBEDO
            PC   C12N15/09,A61K38/00,A61K38/55,A61K45/00,A61P9/00,A61P9/10, PC
             A61P17/02,
            PC   A61P35/00,C12N9/12,C12Q1/48,G01N33/15,G01N33/50,G01N33/566, PC
              C12N15/00,
            PC   A61K37/02,A61K37/64
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             63.0%;  Score 4037.2;  DB 6;  Length 4100;
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Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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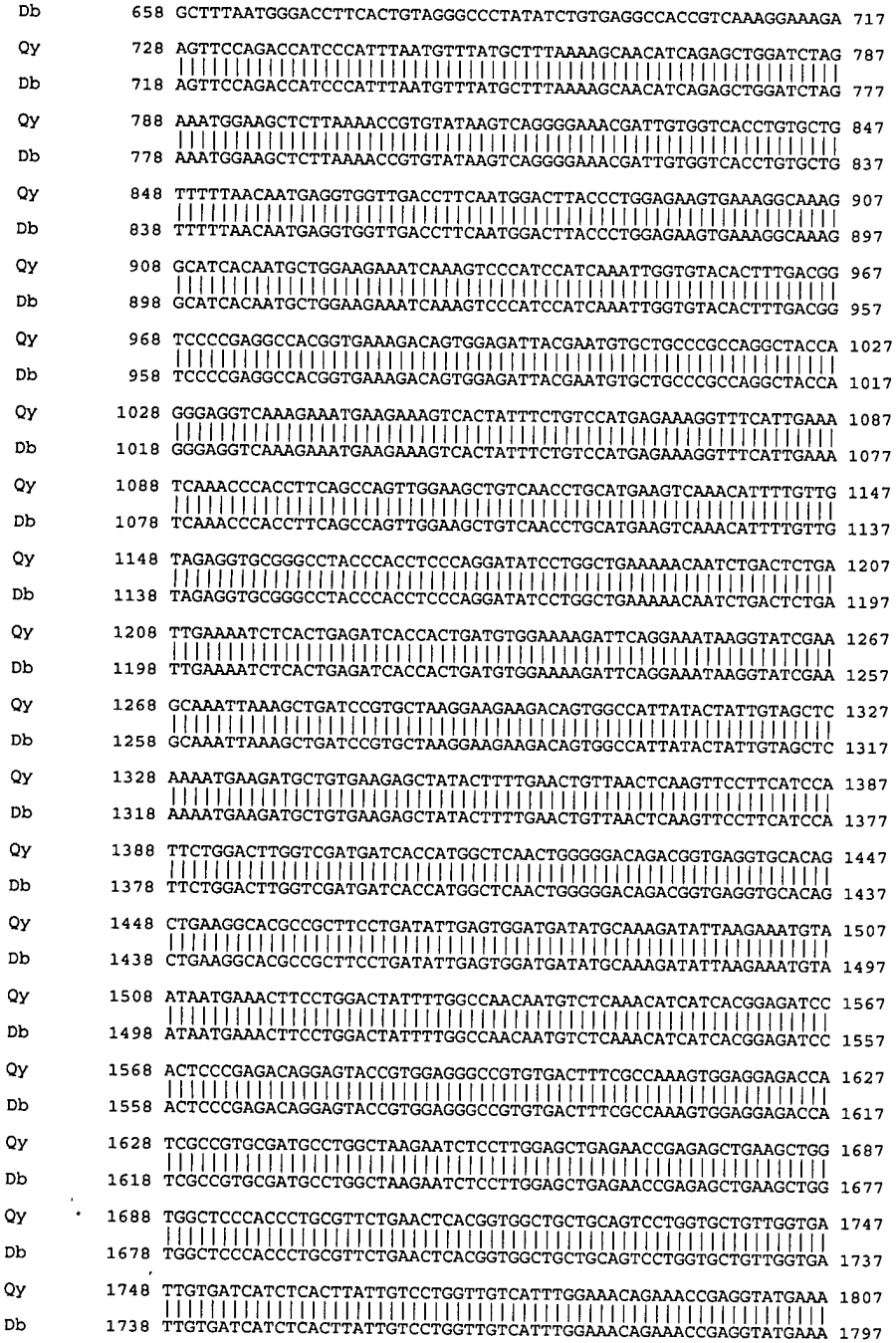
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Qy 728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy 848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db 838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897
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Db       2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

Qy       3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
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Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy       3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
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Db       3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
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Db       3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237

Qy       3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
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Db       3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297

Qy       3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357

Qy       3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
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Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

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Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
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Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657

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Db       3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717

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Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

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I73452
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DEFINITION Sequence 3 from patent US 5686572.
ACCESSION I73452
VERSION I73452.1 GI:3009593
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4100)
AUTHORS Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and Williams,L.Thomas.
TITLE Domains of extracellular region of human platelet derived growth factor receptor polypeptides
JOURNAL Patent: US 5686572-A 3 11-NOV-1997;
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/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 63.0%; Score 4037.2; DB 6; Length 4100;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 4089; Conservative 0; Mismatches 8; Indels 7; Gaps 4;

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Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
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Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537
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Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db       838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
Db       898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy       1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
Db       1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy       1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
Db       1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy       1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
Db       1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy       1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db       1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy       1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db       1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy       1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
Db       1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

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Qy       1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
Db       1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy       1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db       1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy       1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
Db       1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy       1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
Db       1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy       1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
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Qy       1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
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Qy       1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db       1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy       2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
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Qy       2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
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Qy       2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
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Qy       2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
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Qy       2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
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Db       2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757

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Qy       3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
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Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy       3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
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Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
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Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
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Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
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Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897

Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
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Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
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RESULT 19
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DEFINITION  Sequence 35 from patent US 5750375.
ACCESSION   AR007257
VERSION     AR007257.1  GI:3966741
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.Anne. and Kindsvogel,W.R.
  TITLE     Methods of producing secreted receptor analogs and biologically
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Query Match 59.9%; Score 3838.8; DB 6; Length 4054;
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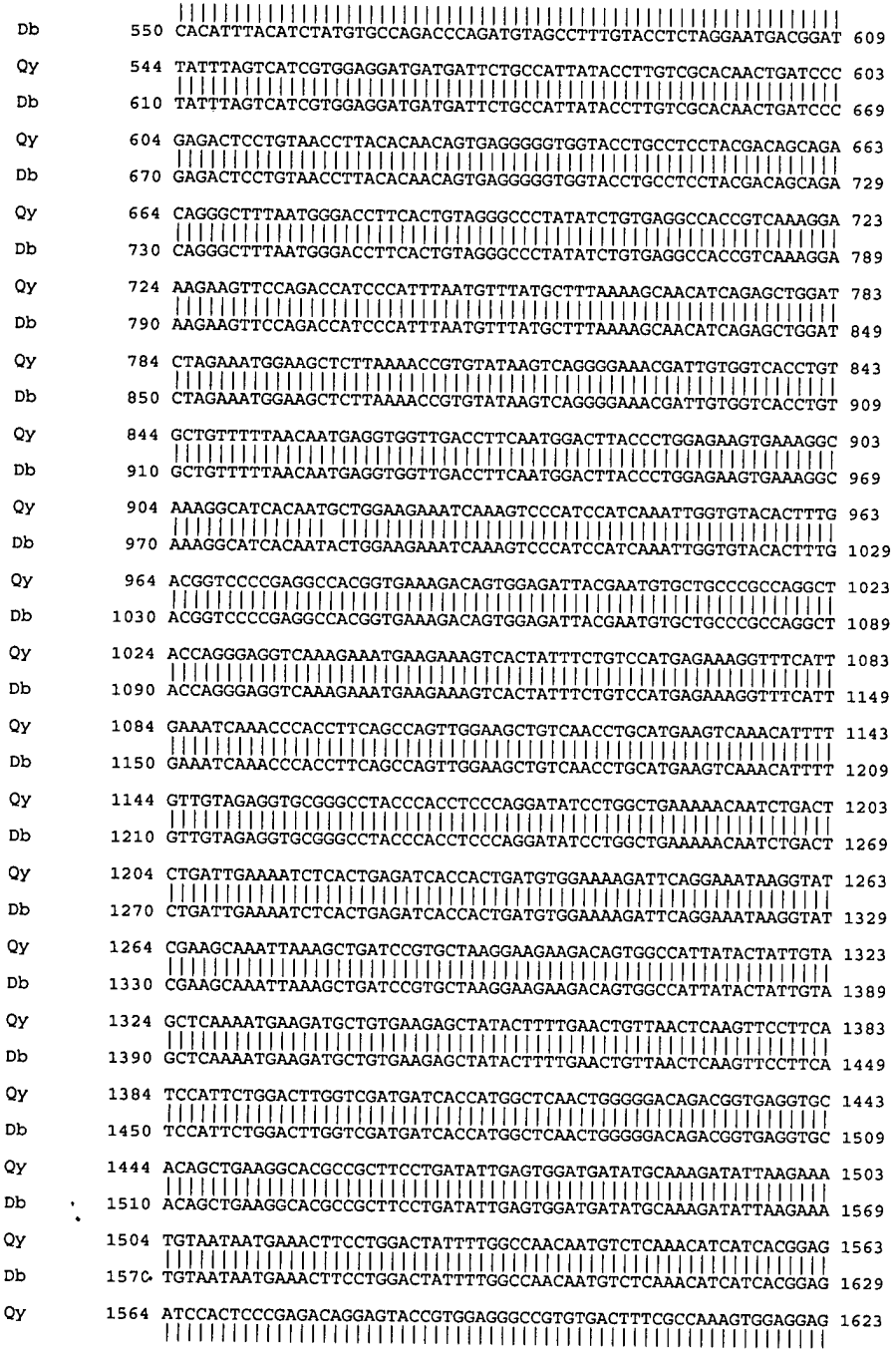
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Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Db 550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609
Qy 544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
Db 610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669
Qy 604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
Db 670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729
Qy 664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
Db 730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789
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RESULT 20
AR062461

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DEFINITION  Sequence 35 from patent US 5843725.
ACCESSION   AR062461
VERSION     AR062461.1  GI:5990152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.Anne. and Kindsvogel,W.R.
  TITLE     Methods of producing secreted receptor analogs and biologically
            active dimerized polypeptide fusions
  JOURNAL   Patent: US 5843725-A 35 01-DEC-1998;
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 59.9%; Score 3838.8; DB 6; Length 4054;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3862; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
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Db      2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349

Qy      2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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Qy      2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
Db      2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529

Qy      2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
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Qy      2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Qy      2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
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Qy      2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
Db      2770 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2829

Qy      2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
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Qy       2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
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RESULT 21
AR170043
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DEFINITION  Sequence 35 from patent US 6291212.
ACCESSION   AR170043
VERSION     AR170043.1  GI:17908002
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.Anne. and Kindsvogel,W.R.
  TITLE     DNA constructs encoding ligand-binding fusion proteins
  JOURNAL   Patent: US 6291212-A 35 18-SEP-2001;
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            59.9%;  Score 3838.8;  DB 6;  Length 4054;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

Qy        244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Db        370 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 429

Qy        364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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Db        430 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489

Qy        424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
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Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Db        550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

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Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Db        730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789
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Qy        844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
Db        910 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969
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Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
Db       1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089
Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db       1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149
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Db       1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209
Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db       1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269
Qy       1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
Db       1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329
Qy       1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db       1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389
Qy       1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
Db       1390 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1449
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Db       1510 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1569
Qy       1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
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Qy       1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
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Qy       1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
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Qy       1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
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Qy       2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
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Qy       2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
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Qy       3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
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Db       3130 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3189

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Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
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Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053
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RESULT 22
AR170470
LOCUS       AR170470               4054 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 35 from patent US 6291646.
ACCESSION   AR170470
VERSION     AR170470.1  GI:17908429
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.Anne. and Kindsvogel,W.R.
  TITLE     Dimerized polypeptide fusions
  JOURNAL   Patent: US 6291646-A 35 18-SEP-2001;
FEATURES             Location/Qualifiers
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  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

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Qy        364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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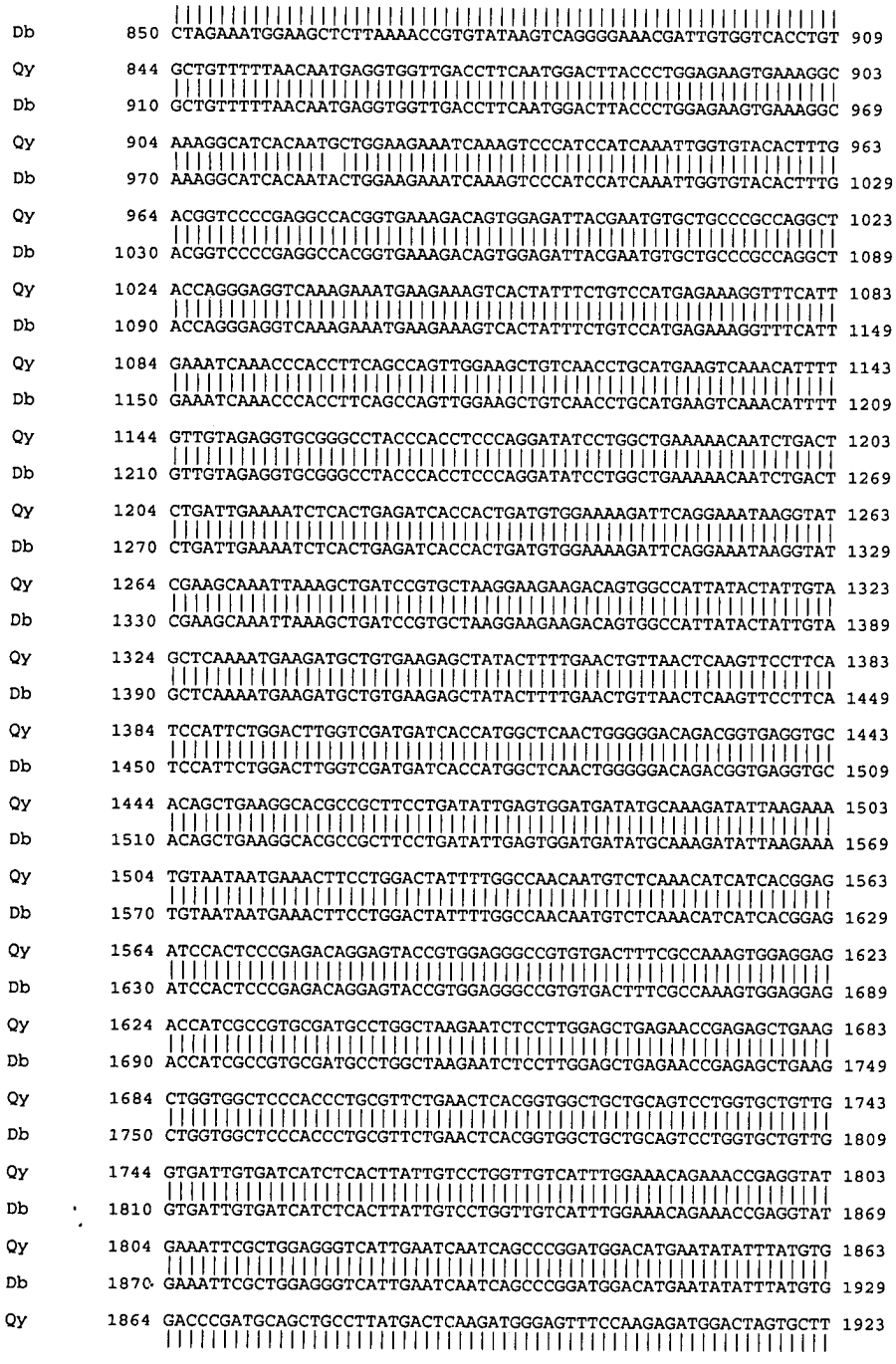
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Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Qy        724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
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Db        790 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 849

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Qy 1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
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Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
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Qy 2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
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Qy 2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
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Qy 2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
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Qy 2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
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Qy       3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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RESULT 23
I27747
LOCUS       I27747                 4054 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 35 from patent US 5567584.
ACCESSION   I27747
VERSION     I27747.1  GI:1818523
KEYWORDS    .
SOURCE      Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.A. and Kindsvogel,W.R.
  TITLE     Methods of using biologically active dimerized polypeptide fusions
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  JOURNAL   Patent: US 5567584-A 35 22-OCT-1996;
FEATURES             Location/Qualifiers
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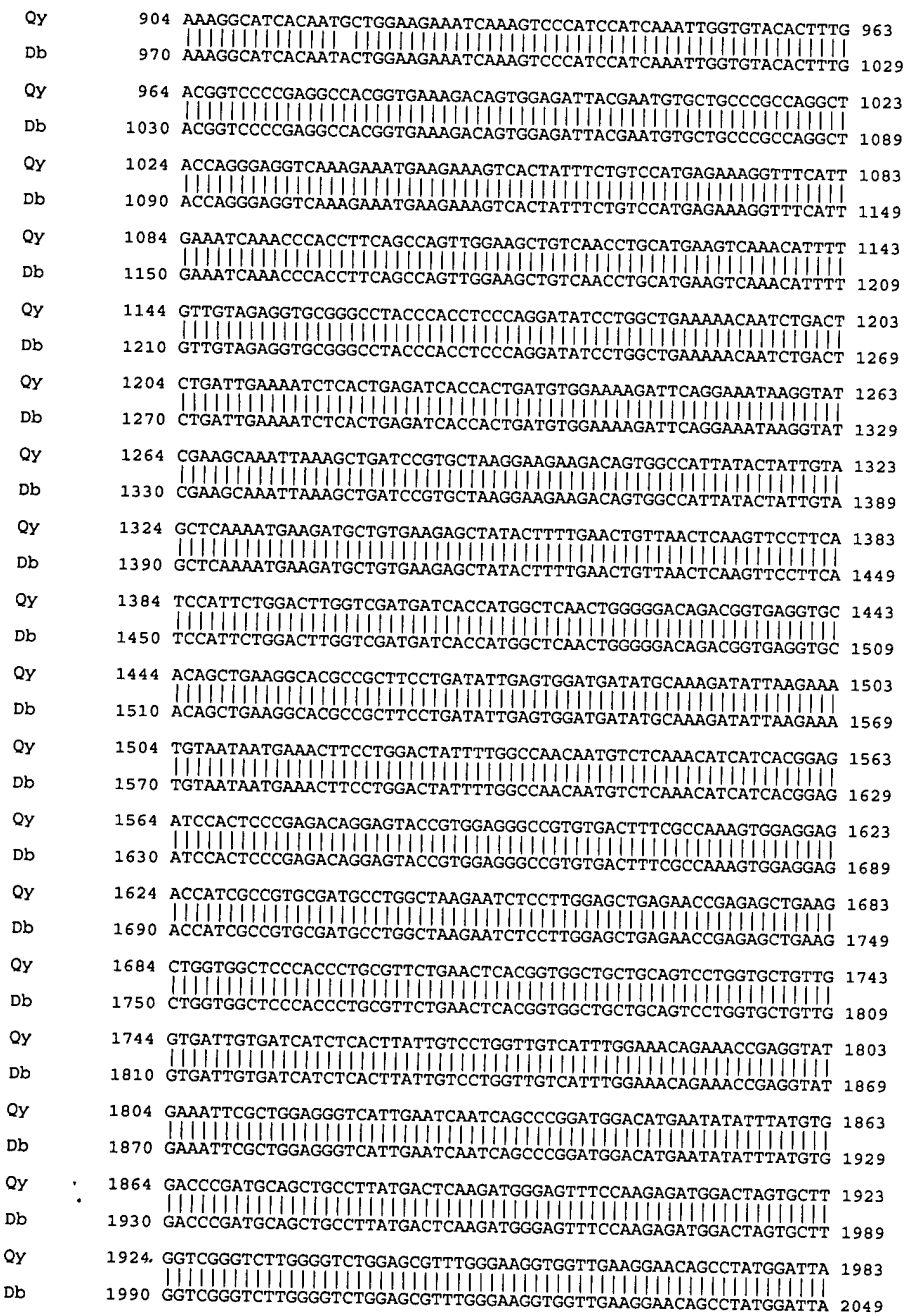
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Db 1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089
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Qy      3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Qy      3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
Db      3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

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Db      3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

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VERSION     AR262570.1  GI:28074081
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.A. and Kindsvogel,W.R.
  TITLE     Ligand-binding, dimerized polypeptide fusions
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Qy       364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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Qy       424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
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Qy       544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
Db       610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy       604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
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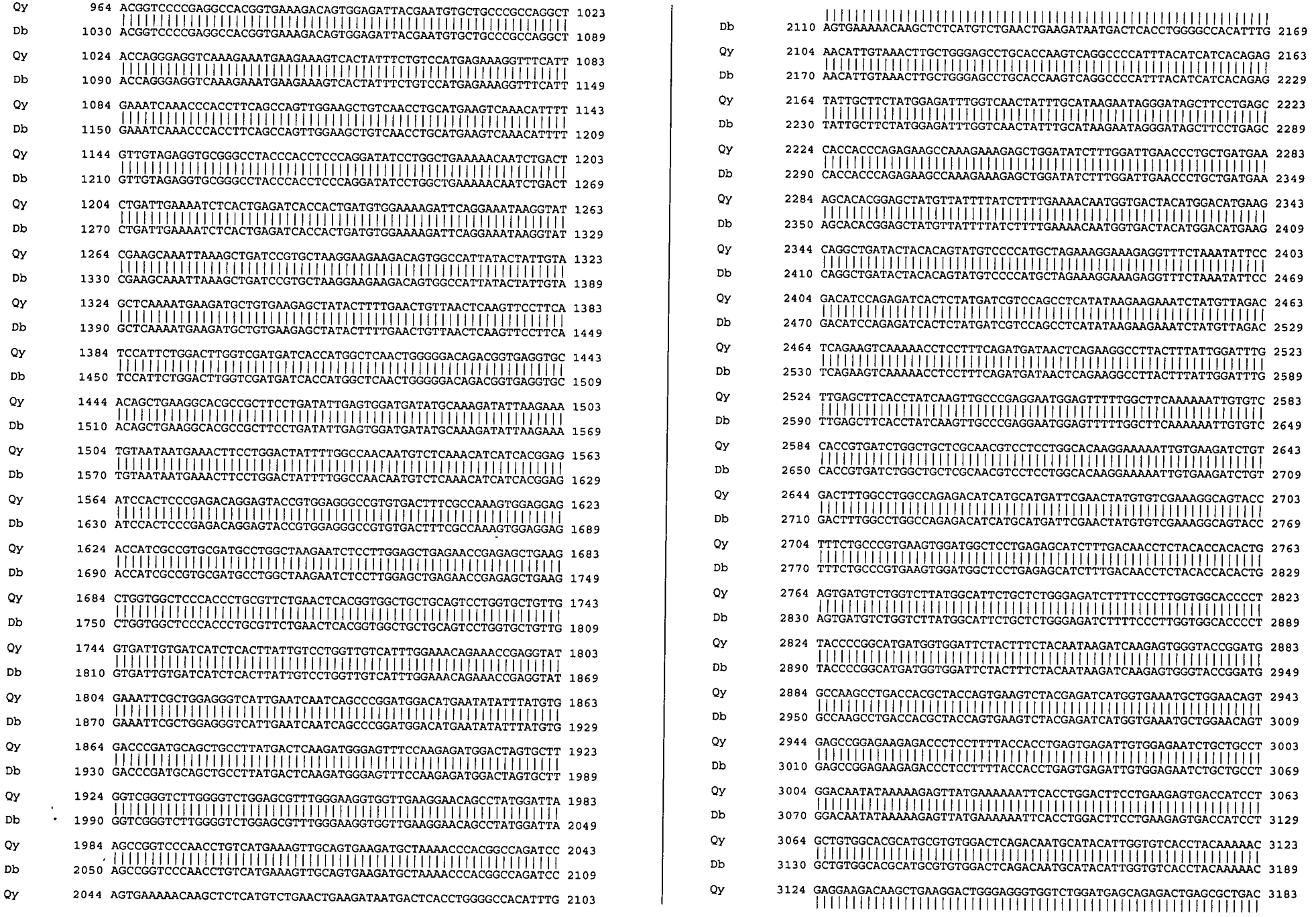
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Qy       904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
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Qy 964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Qy 1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db 1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149
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Qy 1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
Db 1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629
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Db 1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689
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Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
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Db       3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Db       3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

Qy       3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903
             || |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       3910 CC-TGTACTTCCCTCTTGAAACCTGATGT-AGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3967

Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053


RESULT 25
AR369685
LOCUS       AR369685               4054 bp    mRNA    linear   PAT 12-SEP-2003
DEFINITION  Sequence 35 from patent US 6300099.
ACCESSION   AR369685
VERSION     AR369685.1  GI:34605955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4054)
  AUTHORS   Sledziewski,A.Z., Bell,L.A. and Kindsvogel,W.R.
  TITLE     Methods for producing secreted ligand-binding fusion proteins
  JOURNAL   Patent: US 6300099-A 35 09-OCT-2001;
            ZymoGenetics, Inc.; Seattle, WA;
            EPX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             59.9%;  Score 3838.8;  DB 6;  Length 4054;
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Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

Qy        244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
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Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Db        370 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 429

Qy        364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489

Qy        424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

Qy        544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy        604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729

Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789

Qy        724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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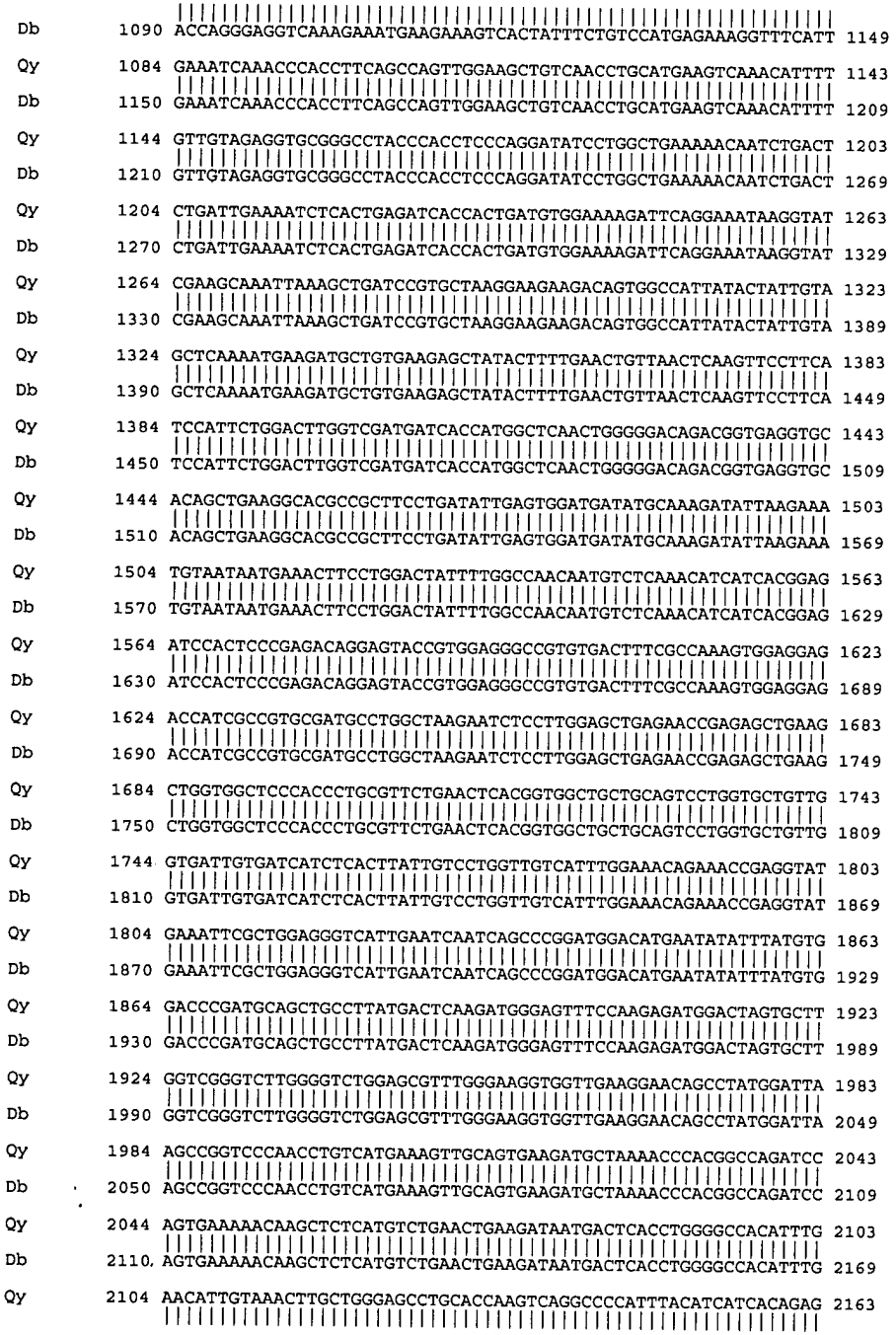
Qy        784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 909

Qy        844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAAGGCATCACAATACTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 1029

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
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Db 1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149
Qy 1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db 1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209
Qy 1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db 1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269
Qy 1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
Db 1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329
Qy 1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db 1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389
Qy 1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
Db 1390 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1449
Qy 1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
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Qy 1444 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1503
Db 1510 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1569
Qy 1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
Db 1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629
Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
Db 1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689
Qy 1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
Db 1690 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1749
Qy 1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
Db 1750 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1809
Qy 1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
Db 1810 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1869
Qy 1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
Db 1870 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1929
Qy 1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
Db 1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989
Qy 1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
Db 1990 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 2049
Qy 1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
Db 2050 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2109
Qy 2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
Db 2110 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2169
Qy 2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
Db 2170 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2229
Qy 2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
Db 2230 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2289
Qy 2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
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Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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Db 2410 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2469
Qy 2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
Db 2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529
Qy 2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
Db 2530 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2589
Qy 2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
Db 2590 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2649
Qy 2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
Db 2650 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2709
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Qy 2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
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Qy 2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
Db 2950 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 3009
Qy 2944 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3003
Db 3010 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3069
Qy 3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
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Qy 3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
Db 3130 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3189
Qy 3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
Db 3190 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3249
Qy 3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Qy       3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
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Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
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Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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RESULT 26
MUSPDGFAR
LOCUS       MUSPDGFAR               6576 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Mus musculus PDGF-alpha-receptor (PDGF-alpha-R) mRNA, complete cds.
ACCESSION   M84607
VERSION     M84607.1  GI:200274
KEYWORDS    platelet-derived growth factor alpha-receptor.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Wang,C., Kelly,J., Bowen-Pope,D.F. and Stiles,C.D.
  TITLE     Retinoic acid promotes transcription of the platelet-derived growth
            factor alpha-receptor gene
  JOURNAL   Mol. Cell. Biol. 10 (12), 6781-6784 (1990)
   PUBMED   2174116
REFERENCE   2  (bases 1 to 6576)
  AUTHORS   Do,M.S., Fitzer-Attas,C., Gubbay,J., Greenfeld,L., Feldman,M. and
            Eisenbach,L.
  TITLE     Mouse platelet-derived growth factor alpha receptor: sequence,
            tissue-specific expression and correlation with metastatic
            phenotype
  JOURNAL   Oncogene 7 (8), 1567-1575 (1992)
   PUBMED   1321404
COMMENT     Original source text: Mus musculus (strain C57/black) cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .6576
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                     /mol_type="mRNA"
                     /strain="C57/black"
                     /db_xref="taxon:10090"
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                     /codon_start=1
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                     /db_xref="GI:200275"
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                     NHTQTDESEIEGRHIYIYVPDPDMAFVPLGMTDSLVIVEEDDSAIIPCRTTDPETQVT
                     LHNNGRLVPASYDSRQGFNGTFSVGPYICEATVKGRTFKTSEFNVYALKATSELNLEM
                     DARQTVYKAGETIVVTCAVFNNEVVDLQWTYPGEVRNKGITMLEEIKLPSIKLVYTLT
                     VPKATVKDSGEYECAARQATKEVKEMKRVTISVHEKGFVEIEPTFGQLEAVNLHEVRE
                     FVVEVQAYPTPRISWLKDNLTLIENLTEITTDVQKSQETRYQSKLKLIRAKEEDSGHY
                     TIIVQNEDDVKSYTFELSTLVPASILDLVDDHHGSGGGQTVRCTAEGTPLPEIDWMIC
                     KHIKKCNNDTSWTVLASNVSNIITELPRRGRSTVEGRVSFAKVEETIAVRCLAKNNLS
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ORIGIN

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Qy          4 TTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAAGG 63
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Qy         64 CCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAG 123
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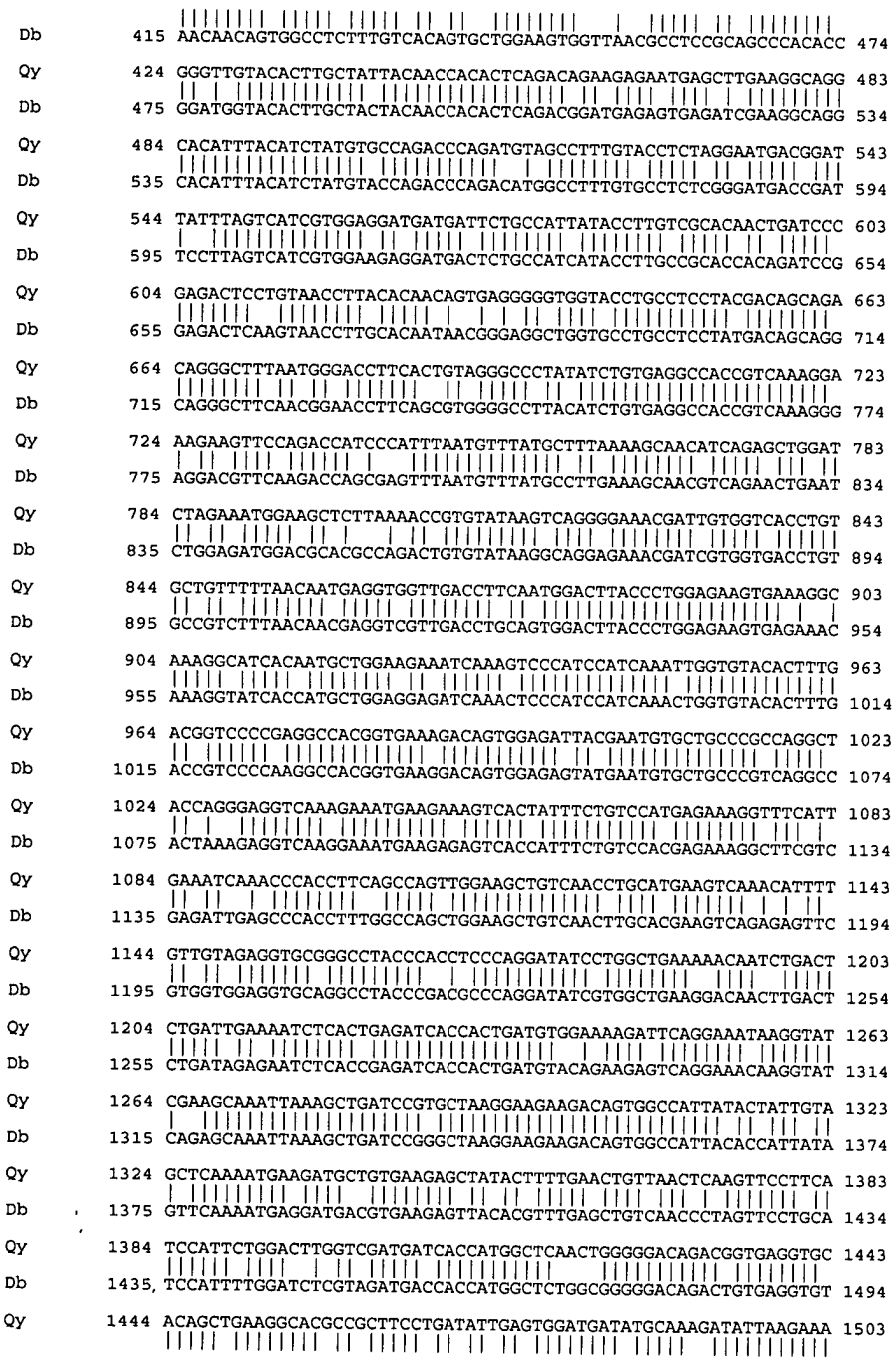
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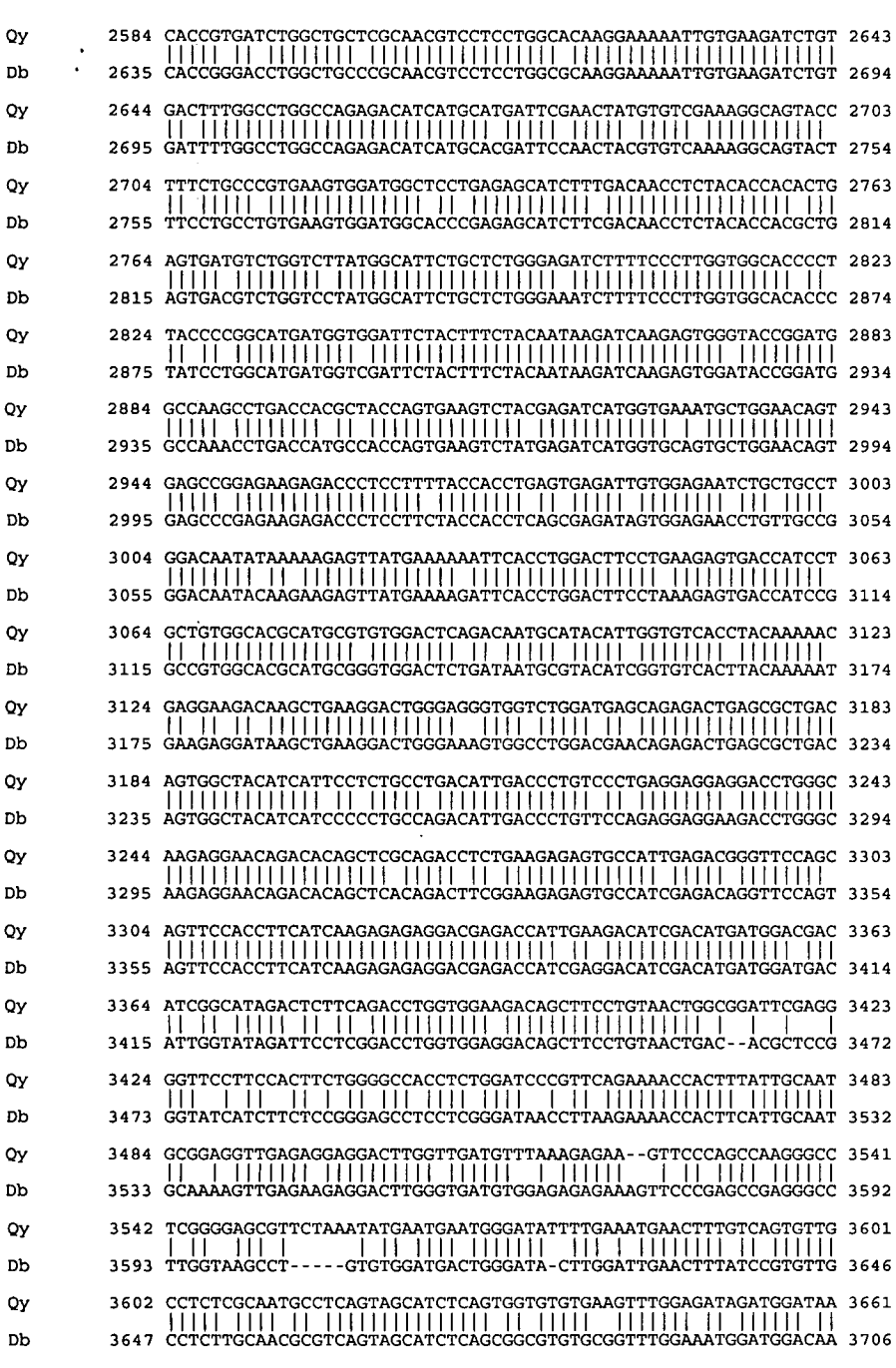
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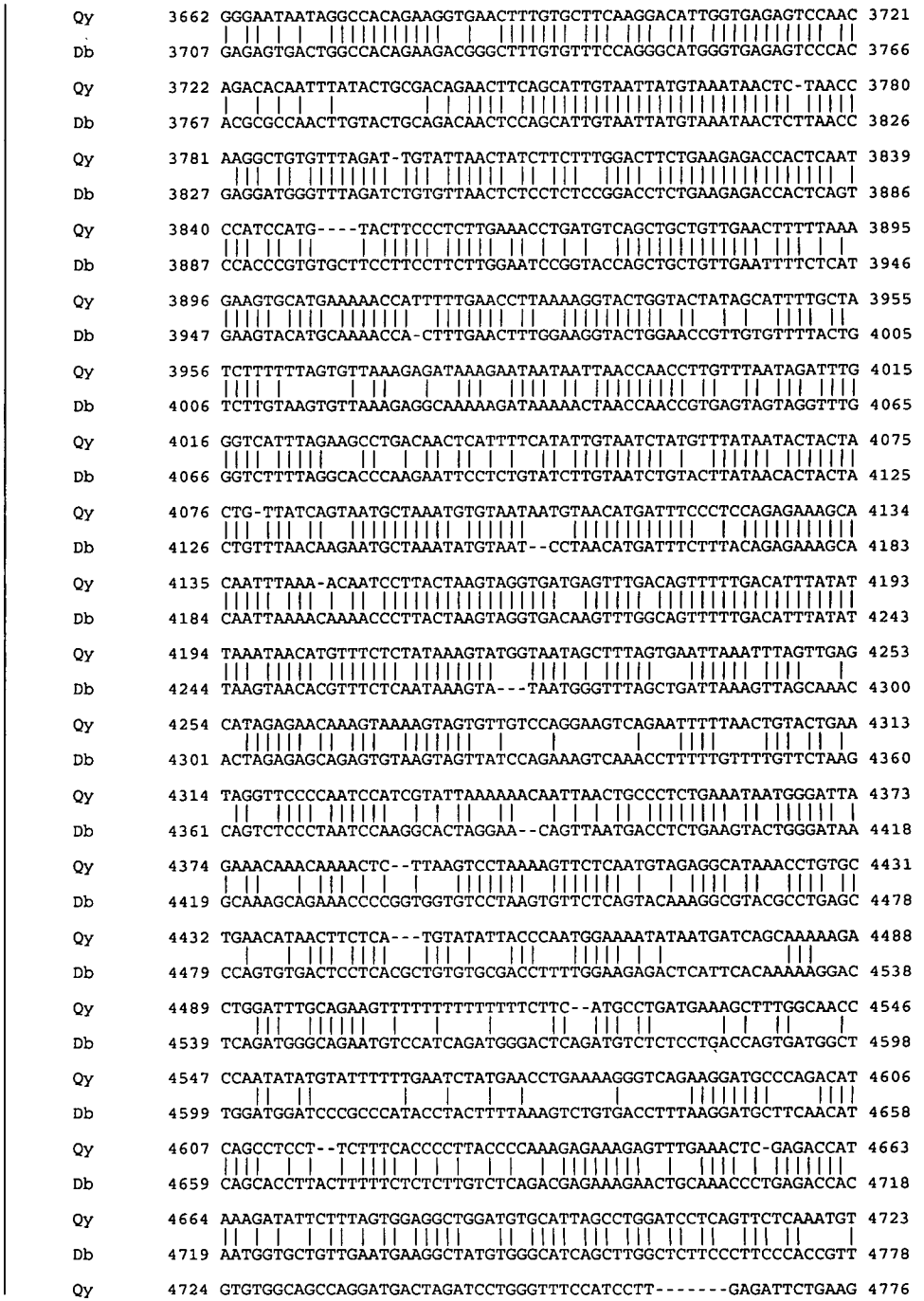
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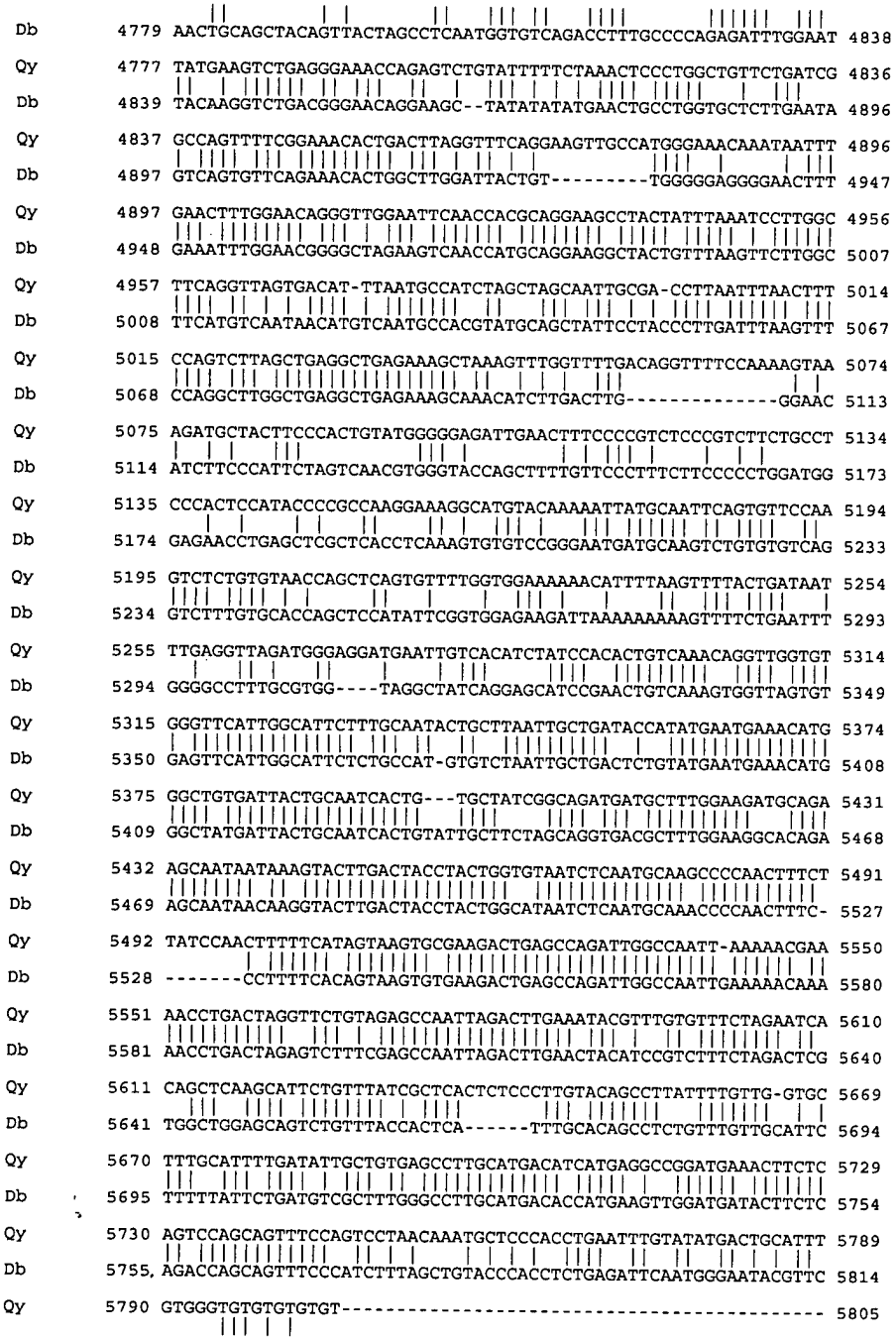
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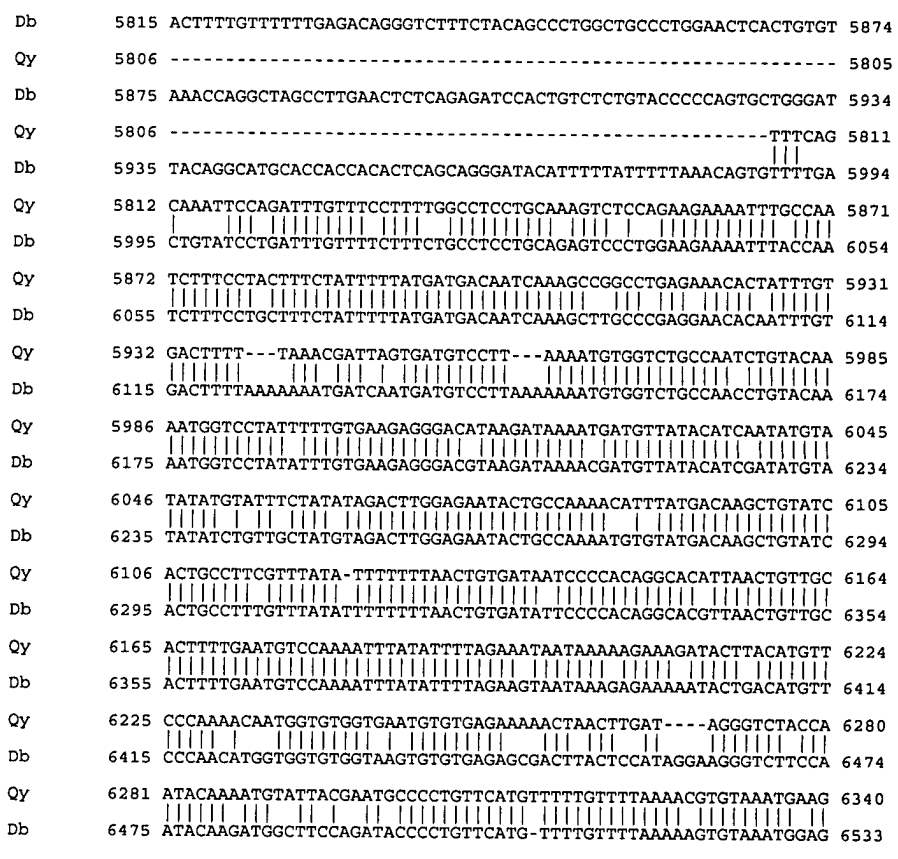
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Qy 484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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  TITLE     Nucleic acids encoding platelet derived growth factor-alpha
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ORIGIN
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Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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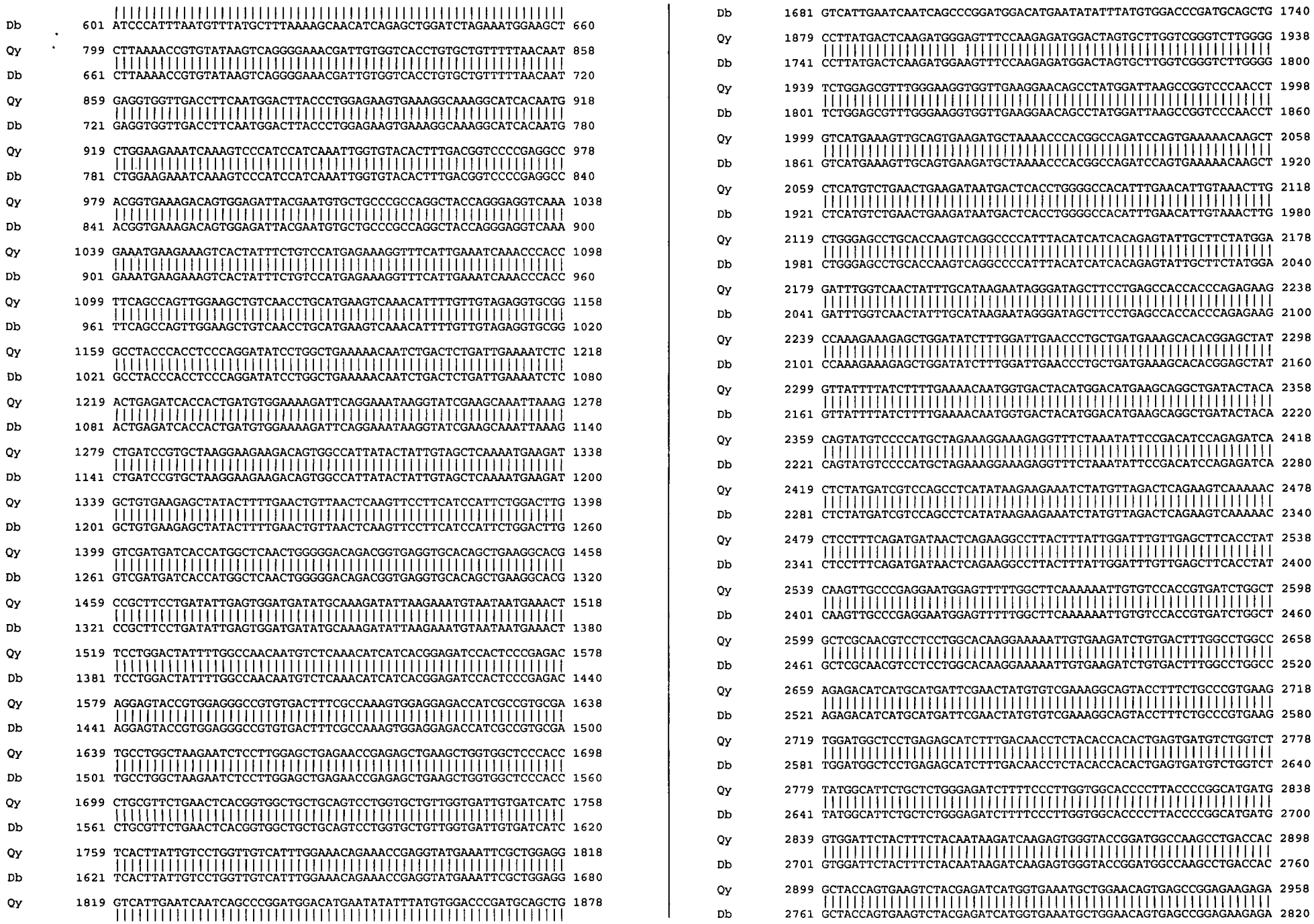
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DEFINITION Sequence 3 from patent US 6667173.
ACCESSION AR441855
VERSION AR441855.1 GI:42668123
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3270)
AUTHORS Kazlauskas,A. and Ikuno,Y.
TITLE Nucleic acids encoding platelet derived growth factor-alpha receptors
JOURNAL Patent: US 6667173-A 3 23-DEC-2003;
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REFERENCE   1  (bases 1 to 3270)
  AUTHORS   Kazlauskas,A. and Ikuno,Y.
  TITLE     Nucleic acids encoding platelet derived growth factor-alpha
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Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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ACCESSION   AR441858
VERSION     AR441858.1  GI:42668126
KEYWORDS    .
SOURCE      Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 3270)
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  JOURNAL   Patent: US 6667173-A 9 23-DEC-2003;
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ORIGIN

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Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
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Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
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Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
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Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
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Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
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RESULT 31
AR441856
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DEFINITION Sequence 5 from patent US 6667173.
ACCESSION AR441856
VERSION AR441856.1 GI:42668124
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3270)
AUTHORS Kazlauskas,A. and Ikuno,Y.
TITLE Nucleic acids encoding platelet derived growth factor-alpha receptors
JOURNAL Patent: US 6667173-A 5 23-DEC-2003;
The Schepens Eye Research Institute; Boston, MA
FEATURES Location/Qualifiers
source 1. .3270
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ORIGIN

Query Match 50.9%; Score 3266.8; DB 6; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3268; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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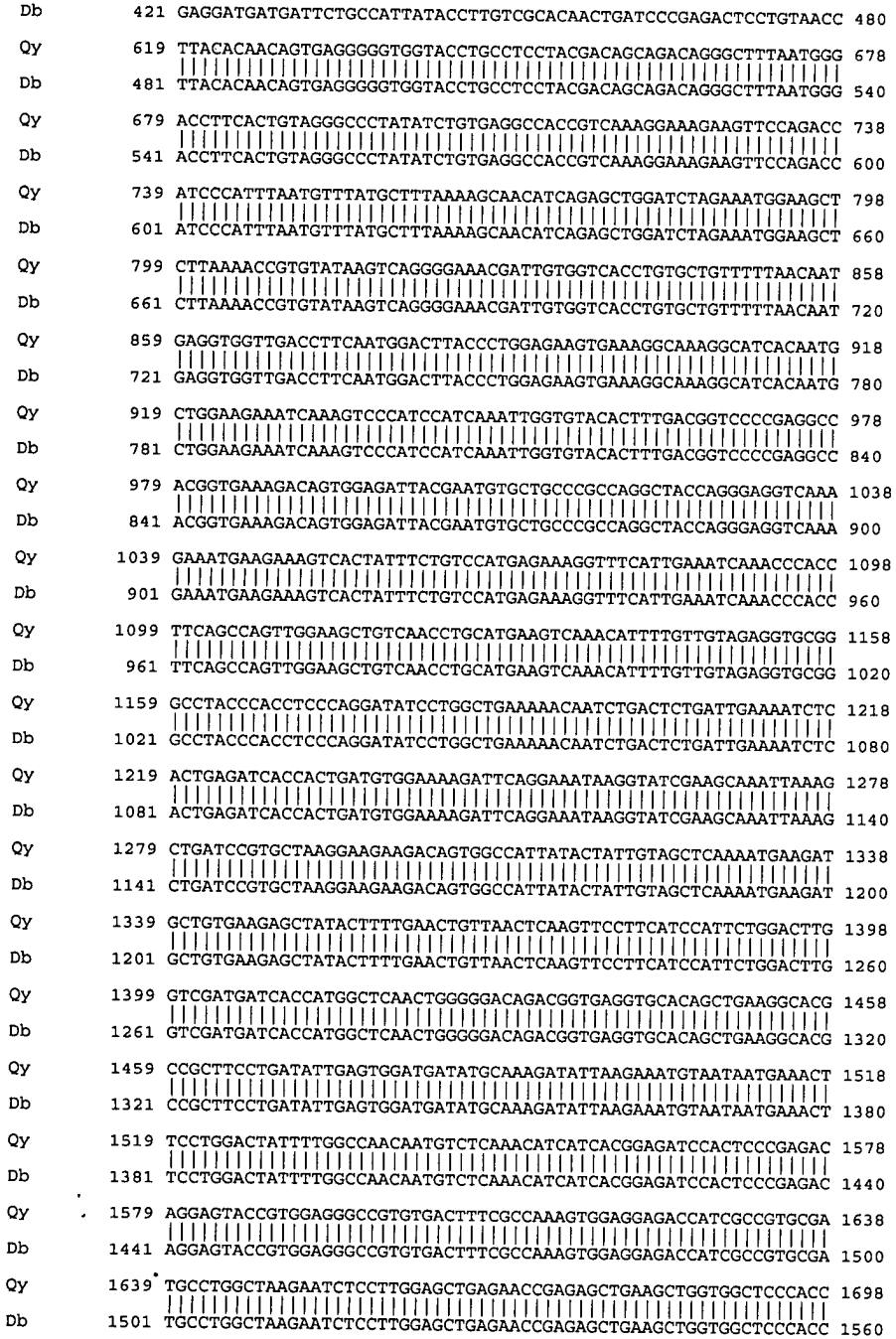
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Qy 1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
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Db 1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
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Qy 1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
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Db 2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
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Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
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RESULT 32
RATAPDGFR
LOCUS       RATAPDGFR               6264 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Rat alpha-platelet-derived growth factor receptor mRNA.
ACCESSION   M63837
VERSION     M63837.1  GI:202929
KEYWORDS    alpha-platelet-derived growth factor receptor.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 6264)
  AUTHORS   Lee,K.H., Bowen-Pope,D.F. and Reed,R.R.
  TITLE     Isolation and characterization of the alpha platelet-derived growth
            factor receptor from rat olfactory epithelium
  JOURNAL   Mol. Cell. Biol. 10 (5), 2237-2246 (1990)
   PUBMED   2157969
COMMENT     Original source text: Rat (strain Sprague-Dawley) olfactory
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ORIGIN

  Query Match           50.8%;  Score 3260.6;  DB 9;  Length 6264;
  Best Local Similarity  74.9%;  Pred. No. 0;
  Matches 4766;  Conservative    0;  Mismatches 1269;  Indels  324;  Gaps   42;

Qy          6 ACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAAGGCC 65
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Qy        126 GTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCAC 185
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Qy        186 AGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGA 245
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Qy        246 AAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAG 305
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Db        243 GAAGATTGTGCCGCTGAGTTCGTCCTTCTCTCTGAGATGCTTCGGGGAGAGCGAAGTGAG 302

Qy        306 CTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAA 365
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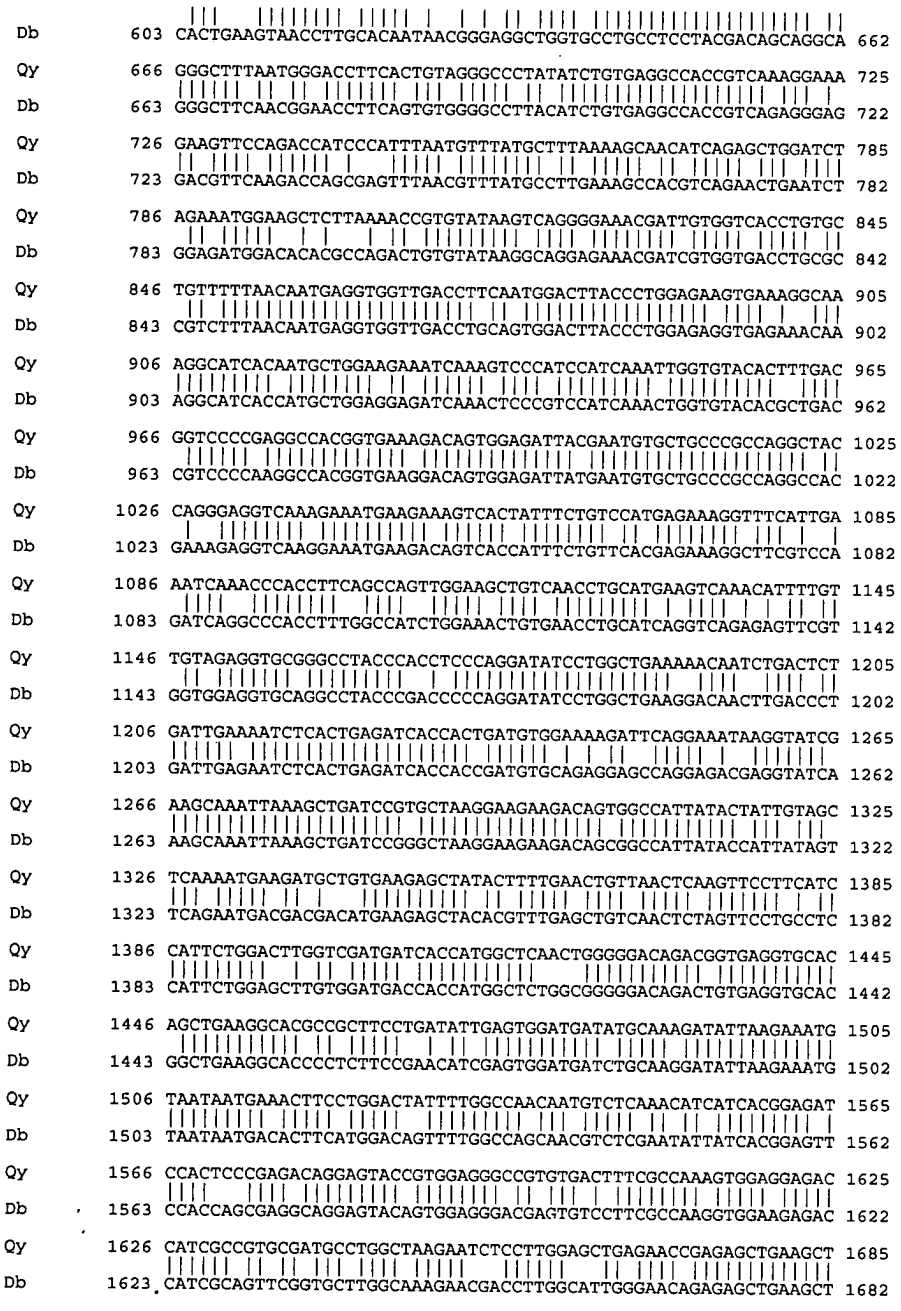
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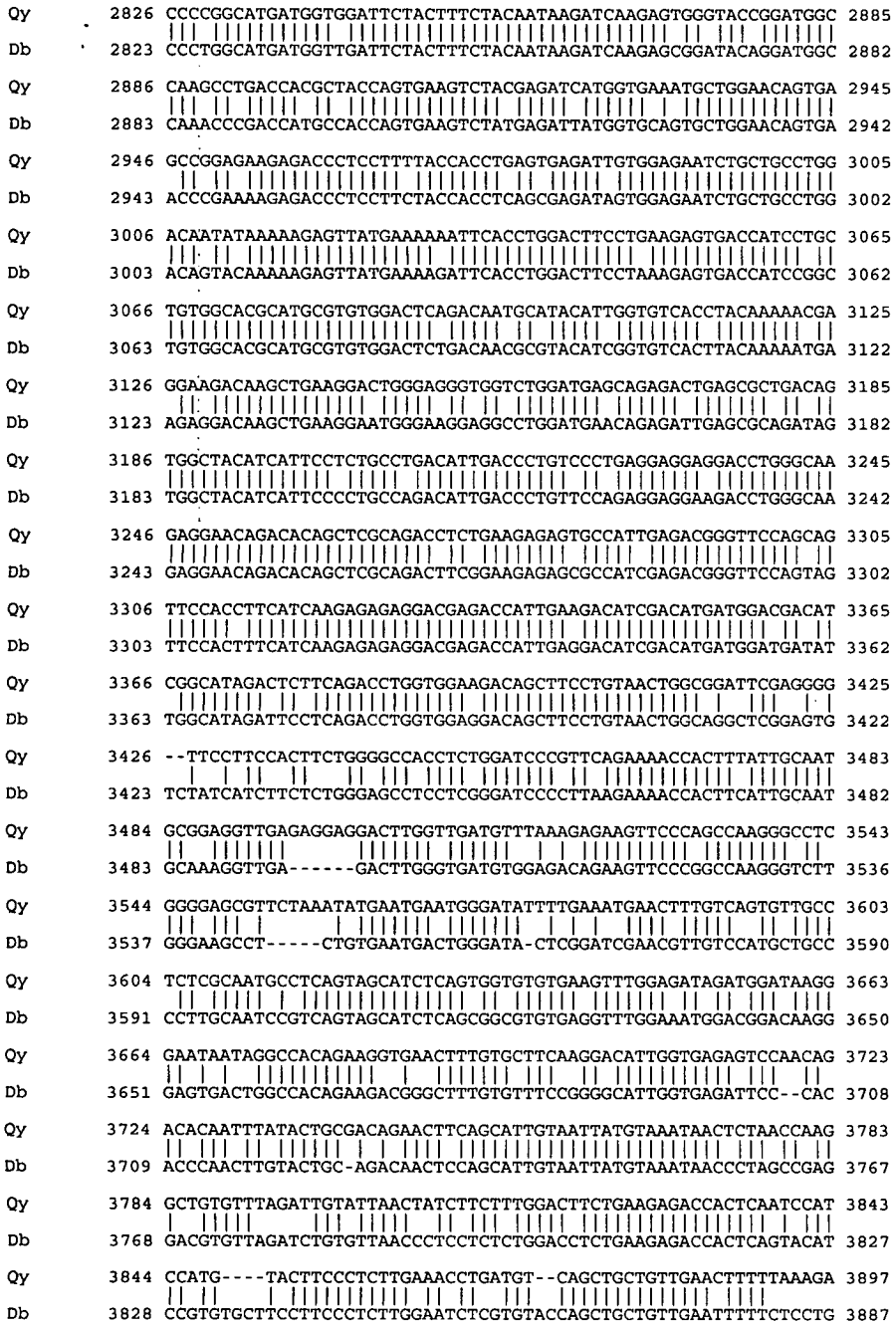
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              |||||||||||||||||||||||||||||||||||||||||||||||  ||||  |  ||||||||||
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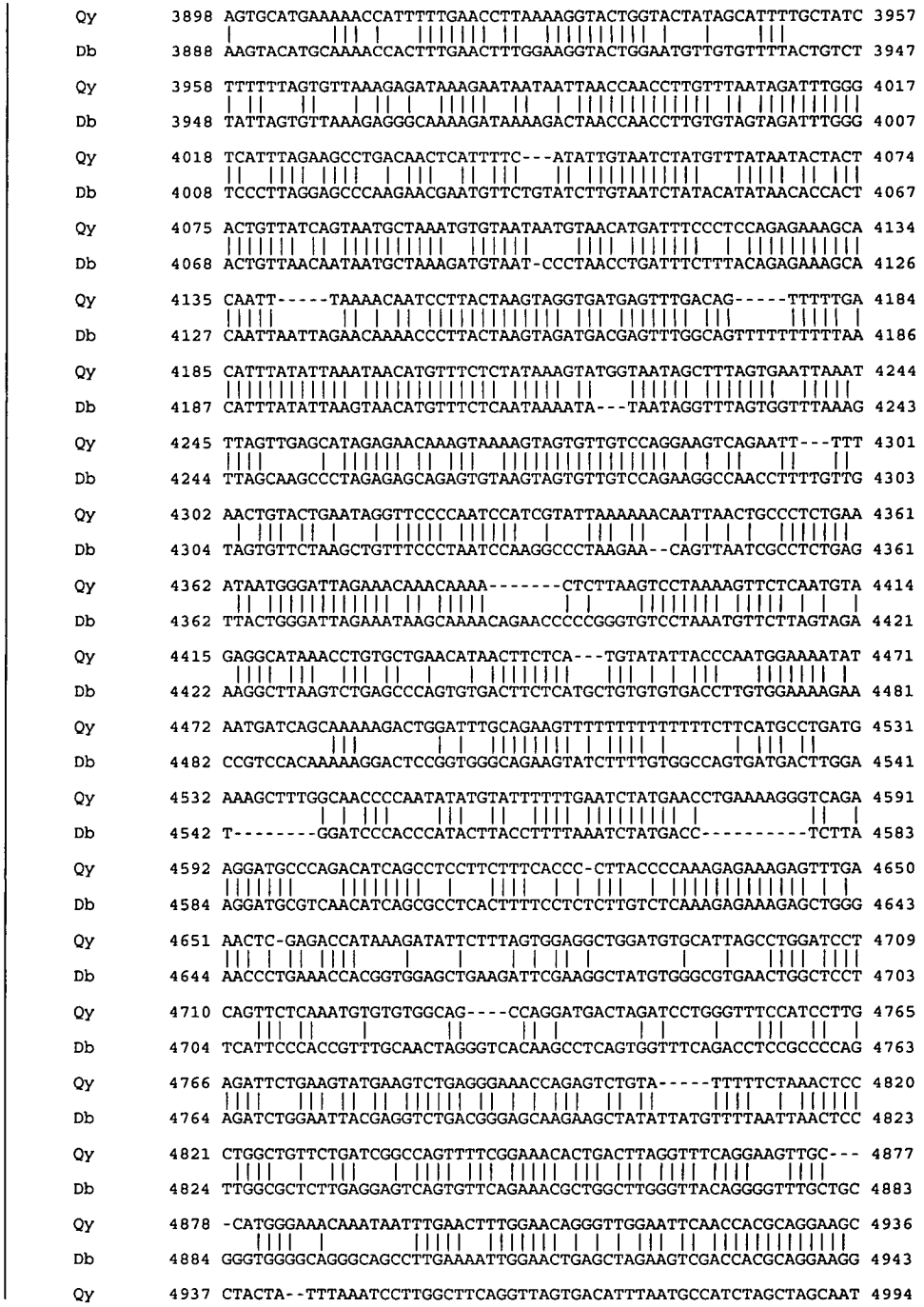
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VERSION AR322283.1 GI:33707867
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3199)
AUTHORS Escobedo,J.A. and Williams,L.T.
TITLE Methods for detecting human platelet-derived growth factor receptor agonists and antagonists
JOURNAL Patent: US 6566075-A 2 20-MAY-2003;
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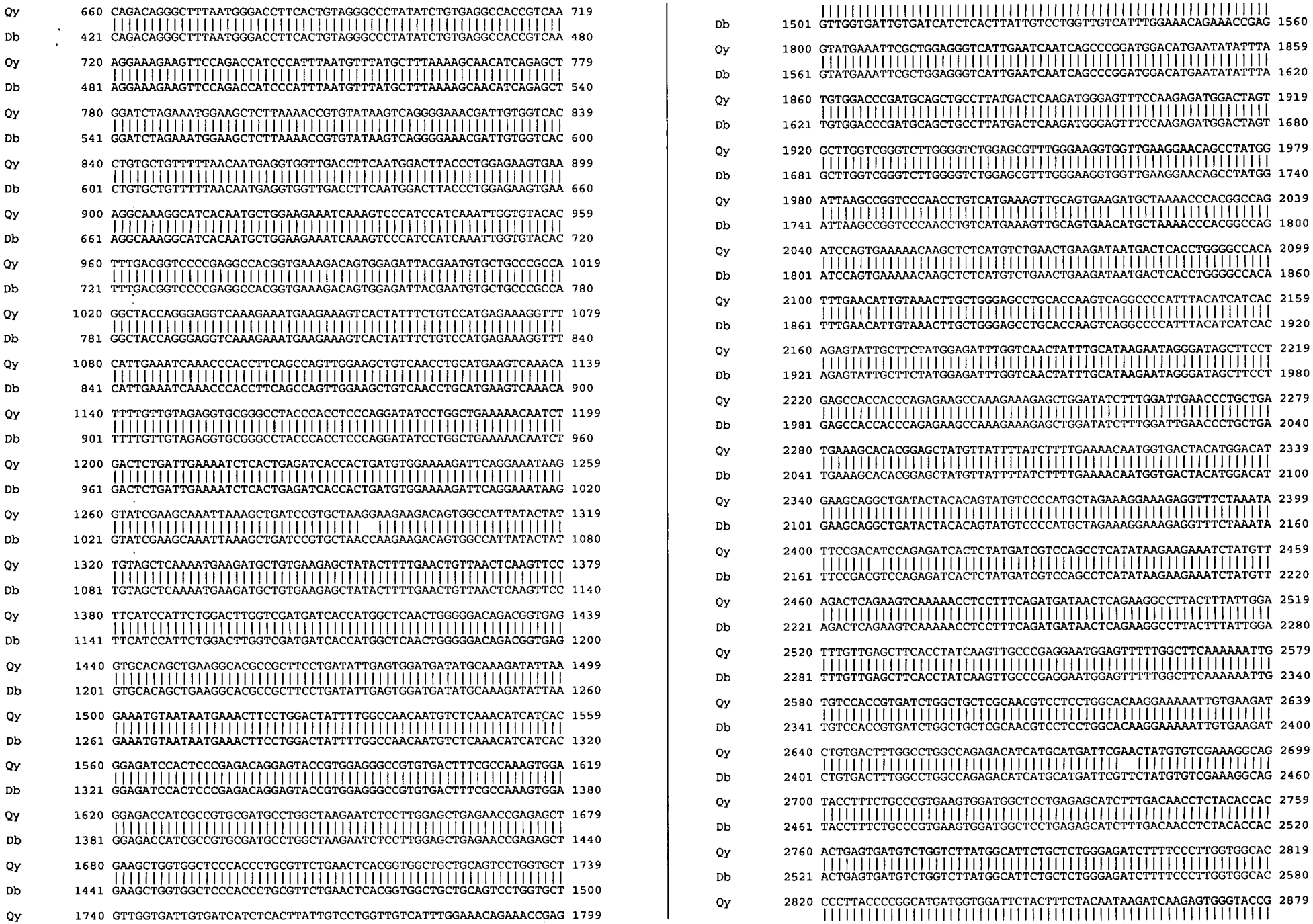
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Qy       3120 AAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGC 3179
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Qy       3180 TGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCT 3239
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Qy       3240 GGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTC 3299
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Db       3001 GGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTC 3060

Qy       3300 CAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGA 3359
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Db       3121 CGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTC 3180

Qy       3420 GAGGGGTTCCTTCCACTTCT 3439
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Db       3181 GA-GGGTTCCTTCCACTTCT 3199
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RESULT 34
AC098587
LOCUS       AC098587               132164 bp    DNA     linear   PRI 15-OCT-2002
DEFINITION  Homo sapiens BAC clone RP11-231C18 from 4, complete sequence.
ACCESSION   AC098587 AC025013
VERSION     AC098587.5  GI:23463020
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 132164)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  PUBMED    9847074
REFERENCE   2  (bases 1 to 132164)
  AUTHORS   Holmes,A., Cotton,M. and Doebber,A.
  TITLE     The sequence of Homo sapiens BAC clone RP11-231C18
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 132164)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 132164)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 132164)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 132164)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-OCT-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   7  (bases 1 to 132164)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-OCT-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Oct 2, 2002 this sequence version replaced gi:22138722.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0231C18
                Drafting Center: WIBR
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            This sequence is not the entire insert of the clone. This clone is
            overlapped by AC098868.

            A transposon was identified in the finished region of this clone
            and removed prior to submission. The transposon would insert after
            base pair 8353 of this sequence.

            There is an unresolved homopolymeric repeat from base 45105 to
            45144.

            Data from AC016089 was used to finish this clone.

            The sequence of AC025013 has been incorporated into AC098587.
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FEATURES             Location/Qualifiers
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                     /clone_lib="RPCI-11"
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  Query Match             48.4%;  Score 3101.6;  DB 8;  Length 132164;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 3134;  Conservative    0;  Mismatches   34;  Indels    2;  Gaps    1;

Qy       3218 CTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAG 3277
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Db      33915 CTGTGCAGGAGTTGTAATATTTGCTCTTCTCTCCCTCCTCCAGCTCGCAGACCTCTGAAG 33974

Qy       3278 AGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCA 3337
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Db      33975 AGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCA 34034

Qy       3338 TTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACA 3397
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Qy       3398 GCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCC 3457
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Db      34095 GCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCC 34154

Qy       3458 CGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTA 3517
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Qy       3518 AAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAATGAATGGGATATT 3577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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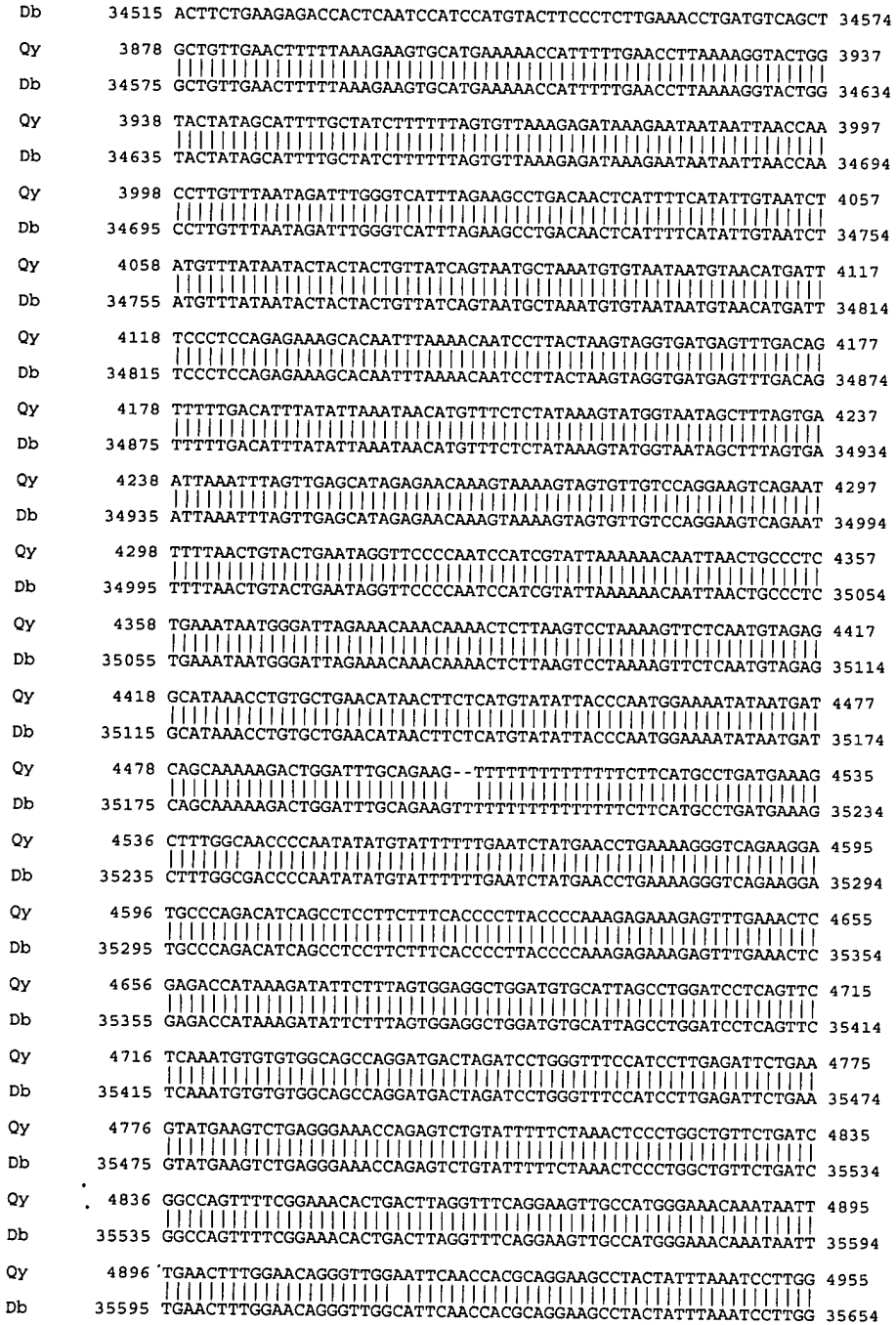
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Qy       3698 CAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAGAACTTCAGCATTG 3757
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Qy       3818 ACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCT 3877
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Db 34515 ACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCT 34574
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Qy       6156 AACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATAC 6215
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RESULT 35
BC053036

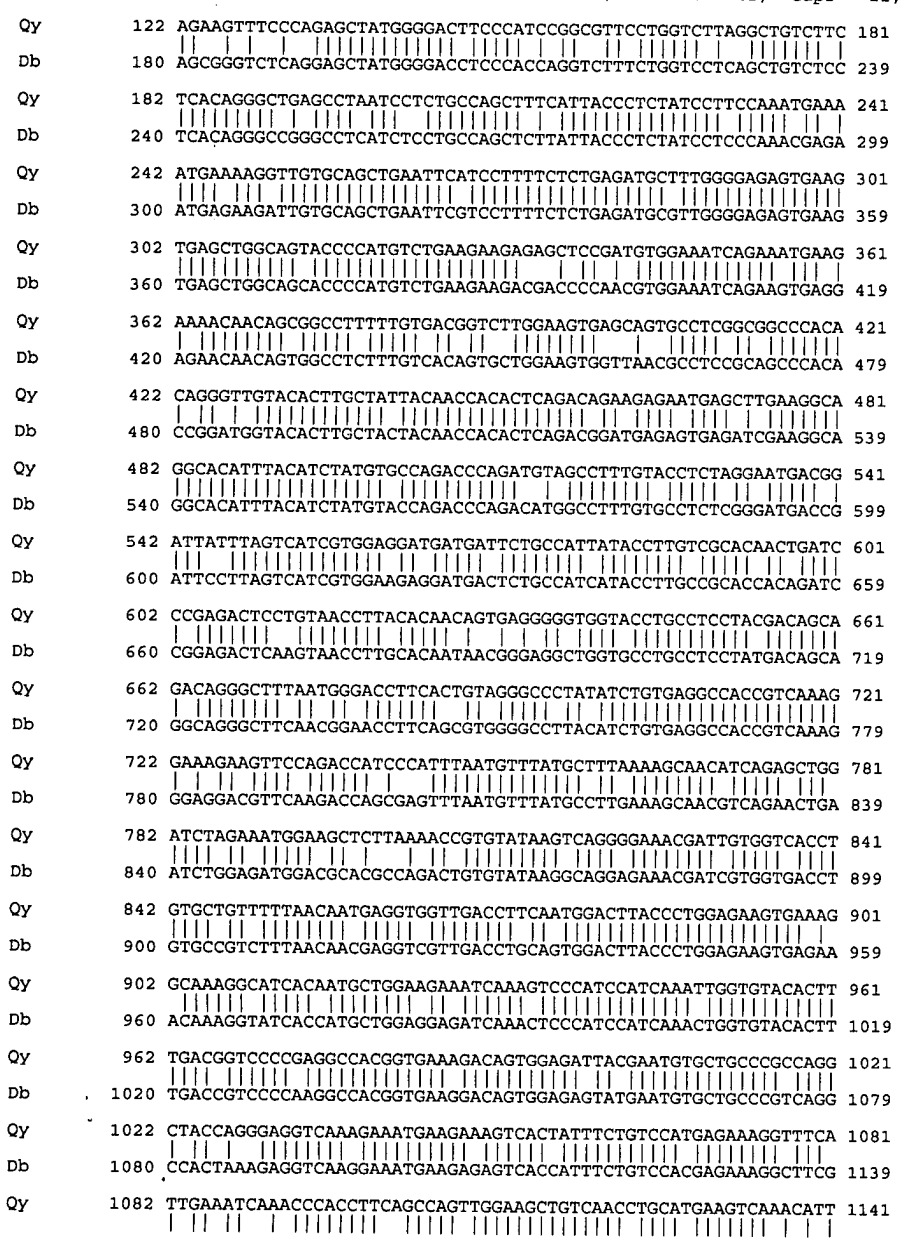
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DEFINITION  Mus musculus platelet derived growth factor receptor, alpha
            polypeptide, mRNA (cDNA clone MGC:62279 IMAGE:5704645), complete
            cds.
ACCESSION   BC053036
VERSION     BC053036.1  GI:31419835
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4238)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4238)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
   REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

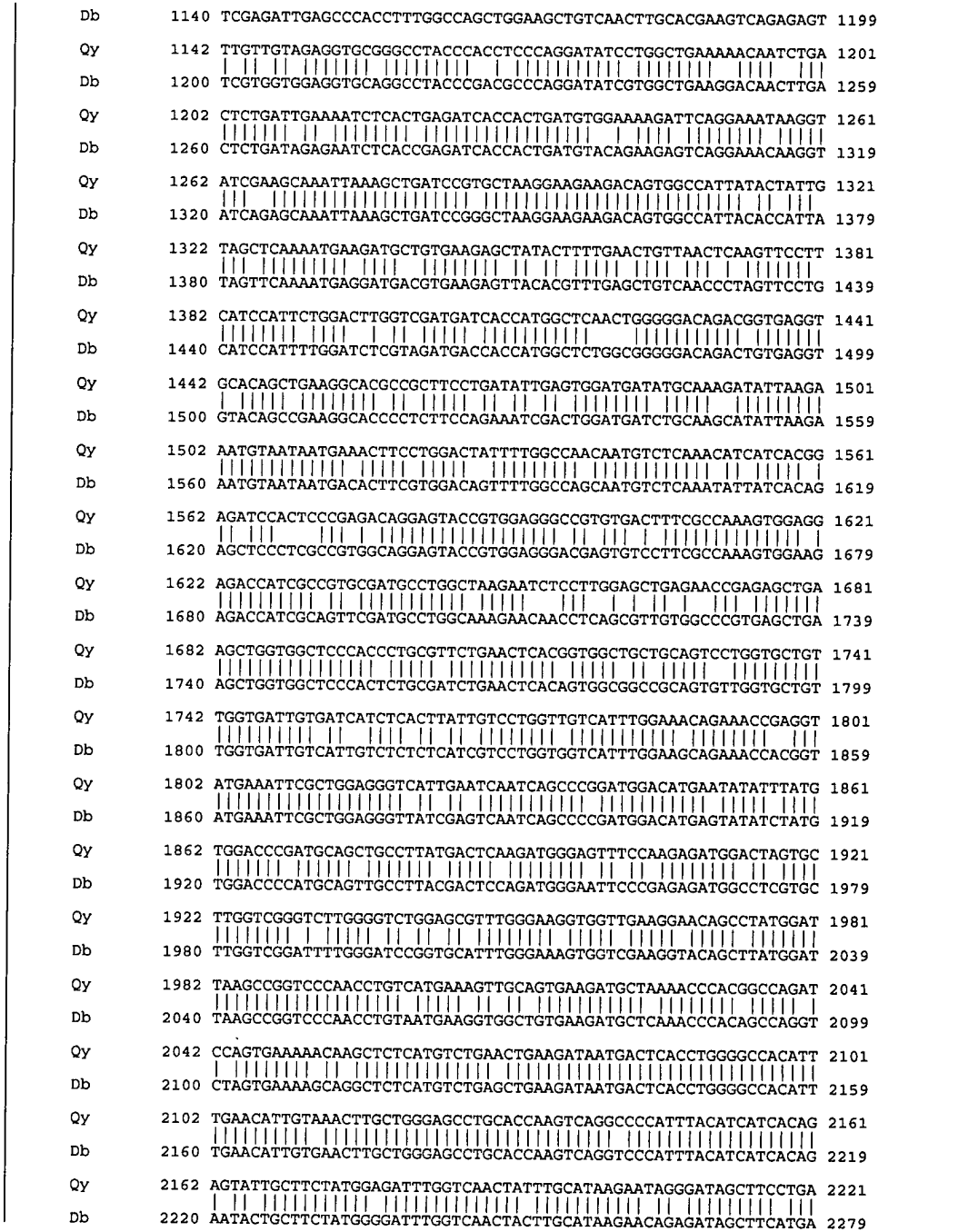
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ORIGIN

Query Match 45.0%; Score 2883.6; DB 9; Length 4238;
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Matches 3392; Conservative 0; Mismatches 629; Indels 21; Gaps 11;





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VERSION AY525124.2 GI:51594357
KEYWORDS .
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
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REFERENCE   1  (bases 1 to 3240)
  AUTHORS   Dickinson,P.J., Roberts,B.N., Mallen-St. Clair,J. and
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  TITLE     Evaluation of Receptor Tyrosine Kinase Expression in Canine Brain
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  JOURNAL   Unpublished
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  AUTHORS   Mallen-St. Clair,J. and London,C.A.
  TITLE     The Role of PDGFRA in Canine Cancer
  JOURNAL   Unpublished
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  AUTHORS   Mallen-St. Clair,J., Roberts,B.N., London,C.A., Dickinson,P.J. and
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            Davis, One Shields Avenue, Davis, CA 95616, USA
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  TITLE     Direct Submission
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ORIGIN
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Qy      529 CTAGGAATGACGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGT 588
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Db      361 CTAGGAATGACAGATTATTTAGTCATCGTGGAGGATGATGACTCTGCCATCATACCTTGT 420

Qy      589 CGCACAACTGATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCC 648
            || |||||||||| |||||||| || ||||||| || || ||| |||||||||| |||
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Qy      769 ACATCAGAGCTGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACG 828
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Db      601 ACGTCAGAACTTGATCTAGAAATGGAAGCTCTTAAAACTGTGTATAAGTCAGGGGAGACG 660

Qy      829 ATTGTGGTCACCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCT 888
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Db      781 TTGGTGTACACTCTGAGGGTCCCCGAGGCCACGGTGAAAGATAGTGGAGATTATGAATGT 840

Qy      1009 GCTGCCCGCCAGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCAT 1068
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Qy      1069 GAGAAAGGTTTCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCAT 1128
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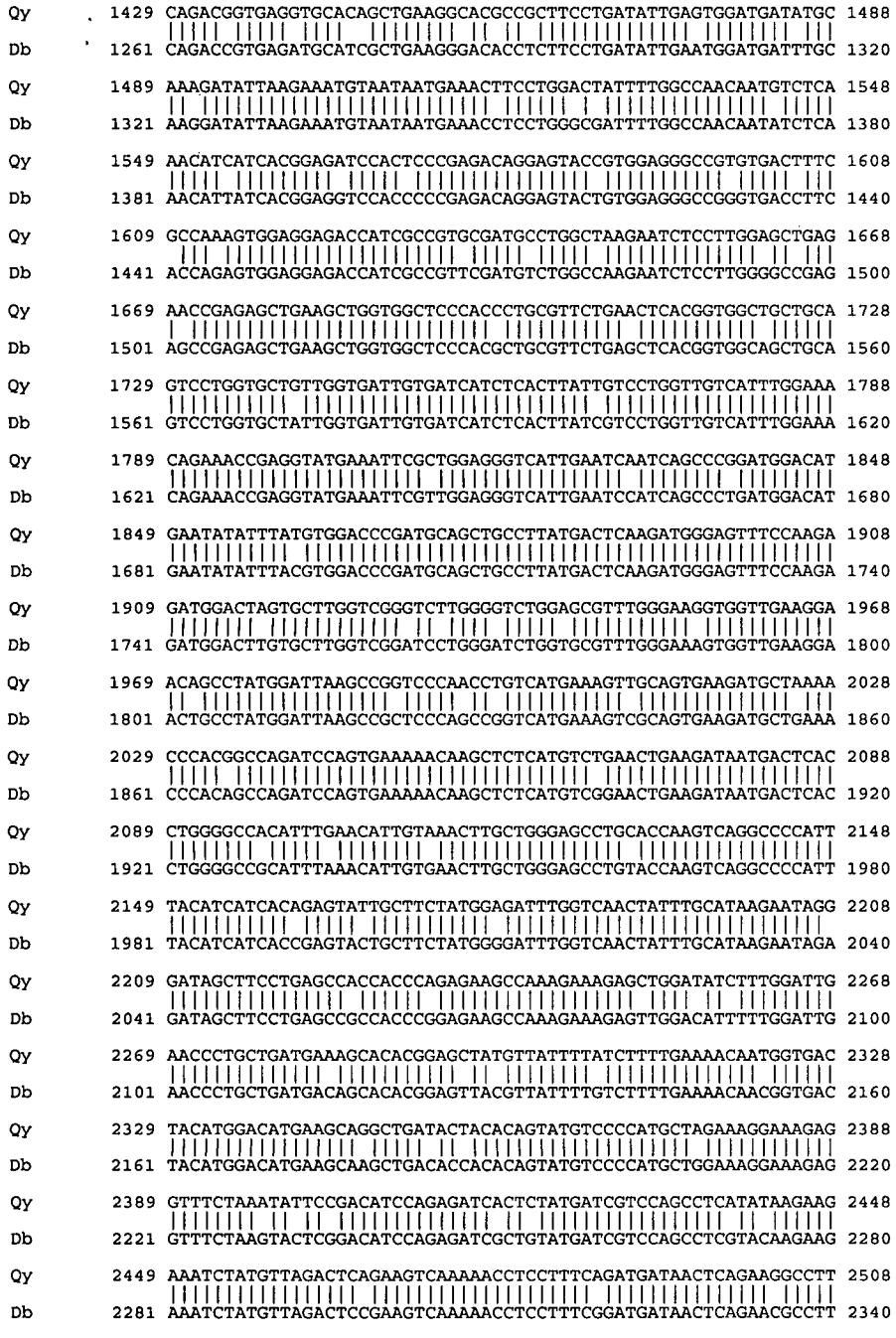
Qy      1129 GAAGTCAAACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTG 1188
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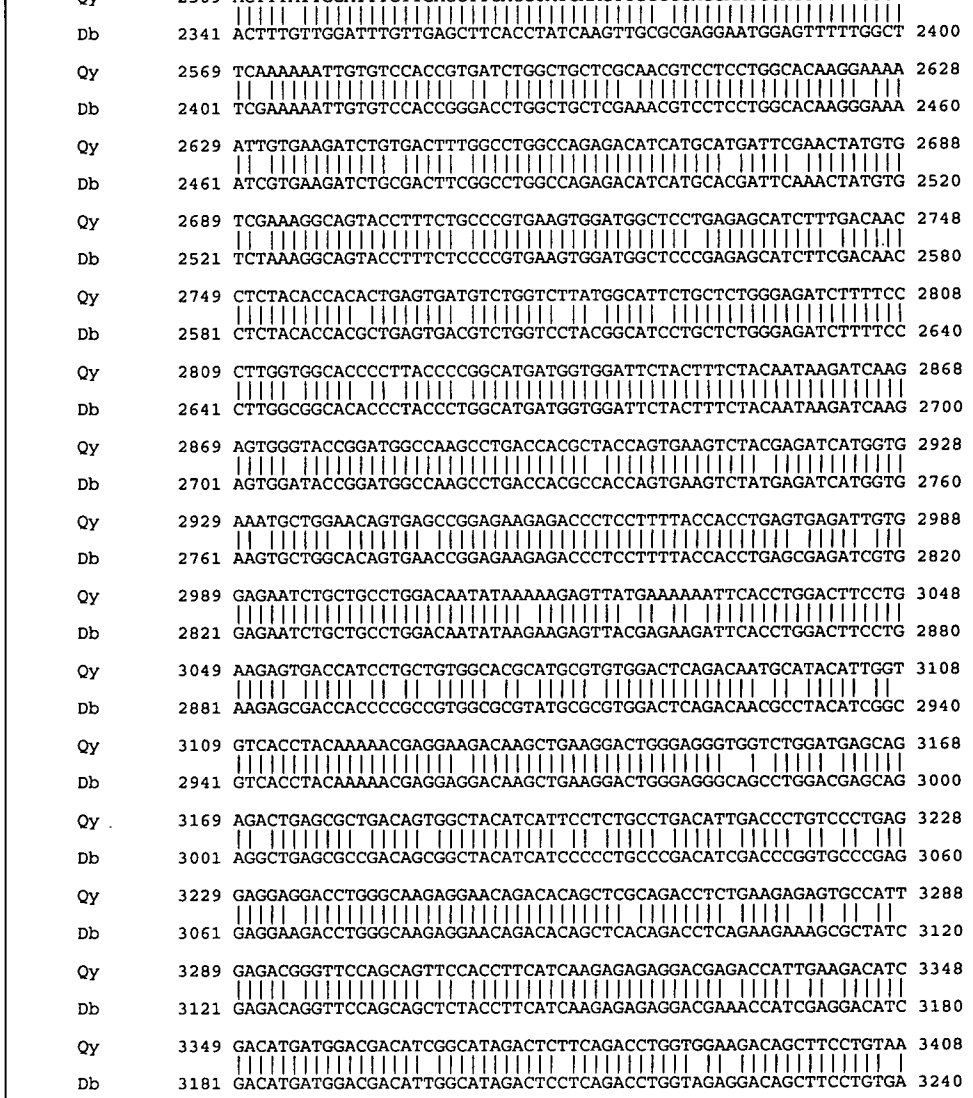
Qy      1189 AAAAACAATCTGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATT 1248
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Qy      1249 CAGGAAATAAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGC 1308
             |||||||||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db      1081 CAGGAAATAAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAGGAGGACAGTGGC 1140

Qy      1309 CATTATACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTA 1368
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Qy      1369 ACTCAAGTTCCTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGA 1428
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Db      1201 ACTCAAGTTCCCTCGTCTATTCTGGACTTGGTCGATGACCACCACGGCTCTACTGGGGGA 1260
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RESULT 37
MUSMPDGAA
LOCUS MUSMPDGAA 3564 bp mRNA linear ROD 27-APR-1993
DEFINITION M.musculus PDGF alpha receptor (mPDGF-alpha-R) mRNA, complete cds.
ACCESSION M57683
VERSION M57683.1 GI:199783
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

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REFERENCE   1  (bases 1 to 3564)
  AUTHORS   Wang,C., Kelly,J., Bowen-Pope,D.F. and Stiles,C.D.
  TITLE     Retinoic acid promotes transcription of the platelet-derived growth
            factor alpha-receptor gene
  JOURNAL   Mol. Cell. Biol. 10 (12), 6781-6784 (1990)
   PUBMED   2174116
COMMENT     Original source text: M.musculus (strain 129) F9-teratocarcinoma,
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                     LHNNGRLVPASYDSRQGFNGTFSVGPYICEAAVKGRTFKTSAFNVYALKATSELNLEM
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                     VPKATVKDSGEYECAARQATKEVKEMKRVTISVHEKGFVEIEPTFSQLEPVNLHEVRE
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     mat_peptide     148. .3345
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                     /product="unnamed"
ORIGIN

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  Best Local Similarity   84.6%;  Pred. No. 0;
  Matches 3019;  Conservative    0;  Mismatches  544;  Indels    7;  Gaps    3;

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
Db          1 AAGCTTGGGGCTTACTTTTCACTCCGGGTATCGGATTTTCTTTGCAAATTGACATAGAAG 60

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
Db         61 GAGAAGGTCTCAGGAGCTATGGGGACCTCCCACCAGGTCTTTCTGGTCCTCAGCTGTCTC 120

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
Db        121 CTCACAGGGCCGGGCCTCATCTCCTGCCAGCTCTTATTACCCTCTATCCTCCCAAACGAG 180

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
Db        181 AATGAGAAGATTGTGCAGCTGAATTCGTCCTTTTCTCTGAGATGCGTTGGGGAGAGTGAA 240

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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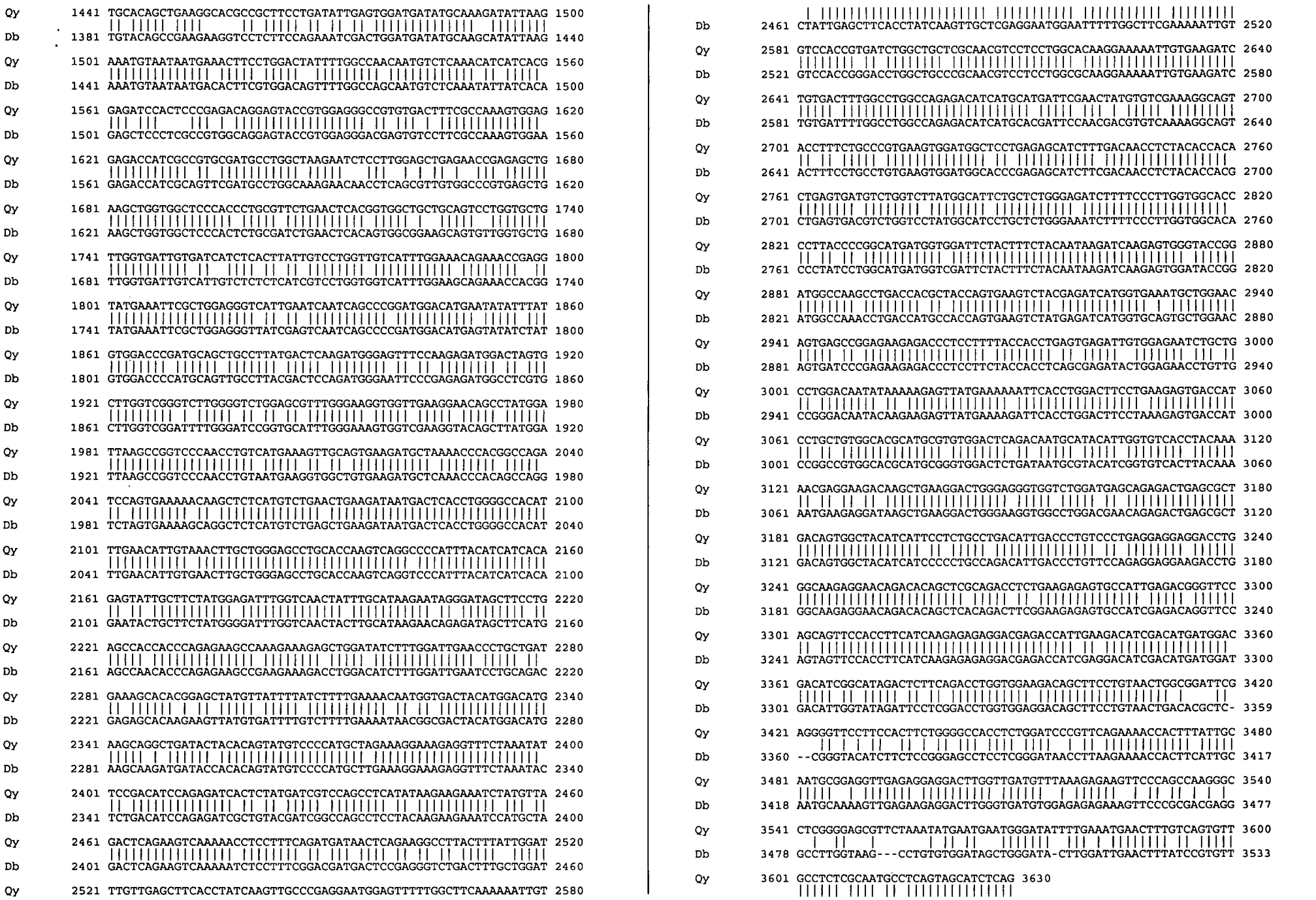
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Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db       1321 GCATCCATTTTGGATCTCGTAGATGACCACCATGGCTCTGGCGGGGGACAGACTGTGAGG 1380
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Db       3534 GCCTCTTGCAACGCGTCAGTAGCATCTCAG 3563


RESULT 38
BC063414
LOCUS       BC063414               3032 bp    mRNA    linear   PRI 24-JAN-2005
DEFINITION  Homo sapiens platelet-derived growth factor receptor, alpha
            polypeptide, mRNA (cDNA clone MGC:74795 IMAGE:5205969), complete
            cds.
ACCESSION   BC063414
VERSION     BC063414.1  GI:39645304
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3032)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 3032)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 135 Row: h Column: 23
            THis clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 15451787.
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ORIGIN

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Qy         81 ACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTAT 140
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Db        298 GTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTTTT 357

Qy        381 TGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGCTA 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        441 TTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 477
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Qy       501 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 560
Db       478 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 537

Qy       561 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 620
Db       538 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 597

Qy       621 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 680
Db       598 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 657

Qy       681 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACCAT 740
Db       658 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACCAT 717

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Db       718 CCCATTTAACGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCTCT 777

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Db       778 TAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAATGA 837

Qy       861 GGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATGCT 920
Db       838 GGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATGCT 897

Qy       921 GGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCCAC 980
Db       898 GGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCCAC 957

Qy       981 GGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAAGA 1040
Db       958 GGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAAGA 1017

Qy      1041 AATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACCTT 1100
Db      1018 AATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGGTTCATTGAAATCAAACCCACCTT 1077

Qy      1101 CAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGGGC 1160
Db      1078 CAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGGGC 1137

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Db      1138 CTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTCAC 1197

Qy      1221 TGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAGCT 1280
Db      1198 TGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAGCT 1257

Qy      1281 GATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGATGC 1340
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Qy      1401 CGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACGCC 1460
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Qy      1581 GAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATG 1640
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Db      1678 GCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTC 1737

Qy      1761 ACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGT 1820
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Db      1798 CATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCC 1857

Qy      1881 TTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTC 1940
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Qy      1941 TGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGT 2000
Db      1918 TGGAGCATTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGT 1977

Qy      2001 CATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCT 2060
Db      1978 CATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCT 2037

Qy      2061 CATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCT 2120
Db      2038 CATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCT 2097

Qy      2121 GGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGA 2180
Db      2098 GGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGA 2157

Qy      2181 TTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCC 2240
Db      2158 TTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCC 2217

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Qy      2388 GGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAA 2447
Db      2518 GGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAA 2577

Qy      2448 GAAATCTATGTTAGACT 2464
Db      2578 GAAATCTATGTTAGGCT 2594
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RESULT 39
CQ719900
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DEFINITION Sequence 5834 from Patent WO02068579.
ACCESSION CQ719900
VERSION CQ719900.1 GI:42280757
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 5834 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 31.6%; Score 2024; DB 6; Length 2717;
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Matches 2631; Conservative 0; Mismatches 85; Indels 506; Gaps 5;

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Db     1 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 60

Qy   248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
Db    61 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 120

Qy   308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
Db   121 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 180

Qy   368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
Db   181 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 240

Qy   428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
Db   241 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 300

Qy   488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Qy   548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
Db   361 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 420

Qy   608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
Db   421 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 480

Qy   668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
Db   481 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 540

Qy   728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy   788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
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Qy   848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
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Qy   908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Qy  1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
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Qy  1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
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Qy  1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
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Qy  1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
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Qy  1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
Db  1081 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1140

Qy  1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db  1141 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1200

Qy  1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db  1201 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGCCCTTTTTCTCT 1260

Qy  1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
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Qy  1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
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Qy  1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db  1390 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1449

Qy  1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
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Qy  1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
Db  1510 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1569

Qy  1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
Db  1570 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1629

Qy  1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
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Qy       1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
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Db       1690 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1749

Qy       1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
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Db       1750 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAAC---------------------- 1791

Qy       2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107

Db       1792 ------------------------------------------------------------ 1791

Qy       2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167

Db       1792 ------------------------------------------------------------ 1791

Qy       2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227

Db       1792 ------------------------------------------------------------ 1791

Qy       2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287

Db       1792 ------------------------------------------------------------ 1791

Qy       2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347

Db       1792 ------------------------------------------------------------ 1791

Qy       2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
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Db       1792 ------------------------------AAAGGAAAGAGGTTTCTAAATATTCCGACA 1821

Qy       2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db       1822 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGGTAAAA 1881

Qy       2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
                ||| | |  | |
Db       1882 GTGTCTATACTCAC---------------------------------------------- 1895

Qy       2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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Db       1896 -------------------------------------TCTGGGTGTTGGTGTGTCCACC 1917

Qy       2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
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Qy       2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
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Qy       2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
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Qy       2768 ATGTCTGGTCTTATGGCATT-CTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826
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Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886
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Qy       2887 AAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAG 2946
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Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGA 3006
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Qy       3007 CAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCT 3066
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Qy       3067 GTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAG 3126
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Qy       3187 GGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAG 3246
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Qy       3247 AGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGT 3306
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Qy       3307 TCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATC 3366
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Qy       3367 GGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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RESULT 40
AF188842
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DEFINITION  Gallus gallus platelet-derived growth factor receptor alpha
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ACCESSION   AF188842
VERSION     AF188842.1  GI:6014686
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
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REFERENCE   1  (bases 1 to 3614)
  AUTHORS   Ataliotis,P.
  TITLE     Platelet-derived growth factor A modulates limb chondrogenesis both
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  JOURNAL   Mech. Dev. 94 (1-2), 13-24 (2000)
   PUBMED   10842055
REFERENCE   2  (bases 1 to 3614)
  AUTHORS   Ataliotis,P. and Mercola,M.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1999) MRC-LMCB, University College London, Gower
            Street, London WC1E 6BT, UK
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ORIGIN

Query Match 31.1%; Score 1995.4; DB 5; Length 3614;
Best Local Similarity 73.4%; Pred. No. 0;
Matches 2655; Conservative 0; Mismatches 931; Indels 31; Gaps 7;

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Qy   197 TAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGC 256
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Qy  1874 AGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCT 1933
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Qy  1994 AACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAAC 2053
Db  1871 AACCTGTGATGAAAGTAGCCGTGAAAATGCTGAAACCTACAGCTAGATCCAGCGAAAAAC 1930
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Qy       2054 AAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAA 2113
Db       1931 AGGCGCTCATGTCTGAACTGAAGATAATGACACATCTTGGGCCCCACCTGAATATTGTGA 1990

Qy       2114 ACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCT 2173
Db       1991 ACCTGCTTGGAGCTTGTACGAAATCAGGTCCTATTTACATAATCACTGAATACTGCTTTT 2050

Qy       2174 ATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAG 2233
Db       2051 ACGGTGATTTGGTGAACTATCTGCACAAGAACAGGGACAACTTCCTCAGCCGACATCCAG 2110

Qy       2234 AGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGA 2293
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Qy       2294 GCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATA 2353
Db       2171 GCTATGTGATTTTATCATTTGAAAACACCGGAGAATATATGGATATGAAACAAGCTGATA 2230

Qy       2354 CTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGA 2413
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Db       2291 GATCTGTATATGATCGACCTGCTTCATATAAGAAGAAATCTTTGTCAGAATCAGAAGTAA 2350

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Db       3305 GGGGAAGCTTACCGTGCTGTATACAGACTTCTGCTACACAGAGAAAACCACTTCGTTGCA 3364

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Db       3422 AAGGAATCAGCCTGAGAATGAAAGGGAGAGAACTGTCAAAGATGGATTTTTTTAGTGTTG 3481

Qy       3602 CCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3661
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Qy       3722 AGACACAATTTATACTG 3738
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RESULT 41
AC160350/c
LOCUS       AC160350              202012 bp    DNA     linear   HTG 01-JUL-2005
DEFINITION  Bos taurus clone CH240-91E18, WORKING DRAFT SEQUENCE, 8 unordered
            pieces.
ACCESSION   AC160350
VERSION     AC160350.2  GI:68302746
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 202012)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 202012)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 202012)
  AUTHORS   Cow Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jun 29, 2005 this sequence version replaced gi:62860298.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: FFVF
                Center clone name: CH240-91E18
            -------------- Summary Statistics
              Assembly program: Atlas 3.0;
                Consensus quality: 199154 bases at least Q40
                Consensus quality: 200661 bases at least Q30
                Consensus quality: 201199 bases at least Q20
                Estimated insert size: 203634; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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ORIGIN

  Query Match             27.6%;  Score 1767.2;  DB 14;  Length 202012;
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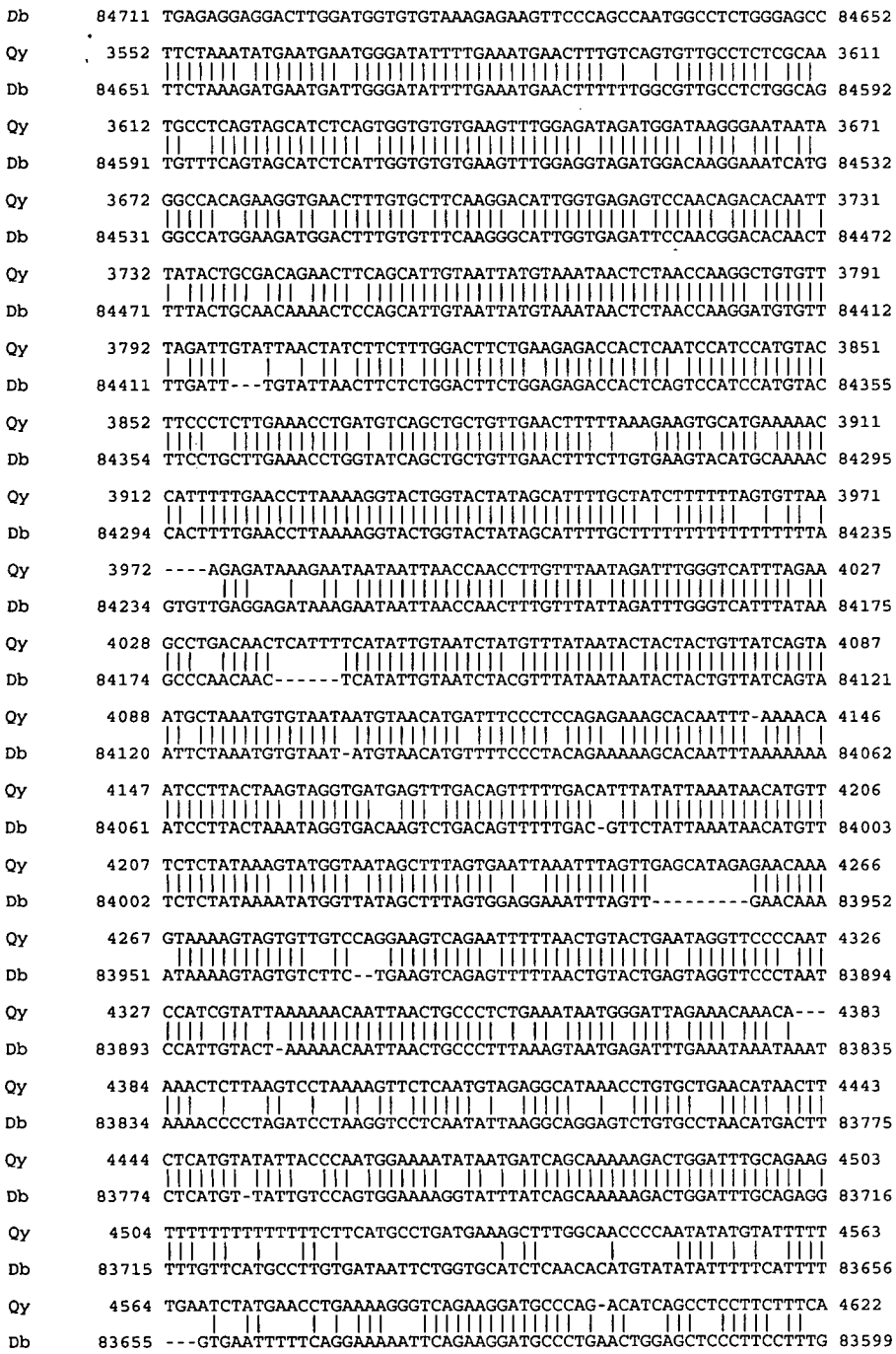
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Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
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Qy       3432 CCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGT 3491
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Qy 3612 TGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATA 3671
Db 84591 TGTTTCAGTAGCATCTCATTGGTGTGTGAAGTTTGGAGGTAGATGGACAAGGAAATCATG 84532
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Qy 3732 TATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTT 3791
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Db 84294 CACTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTTTTTTTTTTTTTTTTA 84235
Qy 3972 ----AGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAA 4027
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Qy 4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTA 4087
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Qy 4982 TCTAGCTAGCAATTGCGA-CCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Qy 5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Qy 5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Qy 5516 CGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCA 5575
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Qy 5636 C-----ACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGT 5690
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Qy       5751 AACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGT--GTGTGTGTTTT 5808
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Qy       5809 CAGCAAATTCCAGATTTGTTTCC-TTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTG 5867
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Qy       5868 CCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTAT 5927
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Qy       5928 TTGTGACTTTT----TAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTAC 5983
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Qy       6164 CACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGT 6223
Db      82099 CACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAGAGAAAAATACCTAAACGT 82040

Qy       6224 TCCCAAAACAATGGTGTGGTGAATGTGTGAGAA-AAACTAACTTGATAGGGTCTACCAAT 6282
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Qy       6283 ACAAAATGTATTACGAATGCCCCTGTTCA-TGTTTTTGTTTTAAAACGTGTAAATGAAGA 6341
Db      81979 AC-AATTGTATTACAAATGCCCCTGTTCATTGTTTTTGTTTTAAAACATGTAAATGAAGA 81921

Qy       6342 TCTTTATATTTCAATAAATGATATATAATTTA 6373
Db      81920 TCTTTATATTTCAATAAATGAGATATATATAA 81889
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RESULT 42
AR441859
LOCUS AR441859 1767 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 11 from patent US 6667173.
ACCESSION AR441859
VERSION AR441859.1 GI:42668127
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Kazlauskas,A. and Ikuno,Y.
TITLE Nucleic acids encoding platelet derived growth factor-alpha receptors
JOURNAL Patent: US 6667173-A 11 23-DEC-2003;
The Schepens Eye Research Institute; Boston, MA
FEATURES Location/Qualifiers
source 1. .1767
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 27.6%; Score 1767; DB 6; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
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Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
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Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
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Db      1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
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Db      1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
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Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
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Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
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Db      1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
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Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
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Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
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Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCA 1905
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RESULT 43
XELPDGFAR
LOCUS       XELPDGFAR                4049 bp    mRNA    linear   VRT 09-AUG-1993
DEFINITION  Xenopus laevis PDGF alpha receptor mRNA, complete cds.
ACCESSION   M80798
VERSION     M80798.1  GI:214652
KEYWORDS    PDGF alpha receptor; growth factor receptor; tyrosine kinase
            receptor.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 4049)
  AUTHORS   Jones,S.D., Ho,L., Smith,J.C., Yordan,C., Stiles,C.D. and
            Mercola,M.
  TITLE     The Xenopus platelet-derived growth factor alpha receptor: cDNA
            cloning and demonstration that mesoderm induction establishes the
            lineage-specific pattern of ligand and receptor gene expression
  JOURNAL   Dev. Genet. 14 (3), 185-193 (1993)
   PUBMED   8358864
COMMENT     Original source text: Xenopus laevis (library: lambda gt10) oocyte
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ORIGIN
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  Matches 2333;  Conservative    0;  Mismatches  936;  Indels   24;  Gaps    6;

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Db       402 AGTTGTTACGGTCCATGATGCCTGCCATGAGGGCATCTCTTATTTTGGGATGTCTCCTGA 461

Qy       182 TCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAA 241
             | | ||| | | |   ||| ||     |   | | || ||| | ||  ||||  | |
Db       462 TTATAGGTCCGTGGGCAATTCTTGCTGAAAATCCTTTGCCCACCATATTTCCTGACAAGG 521

Qy       242 ATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAG 301
             ||||   ||||  |  | || | || |||||| | || | ||||  ||| || ||||| |
Db       522 ATGAGTTGGTTCAGGCGTTGCACTCCTCCTTTACACTAAAATGCACTGGCGAAAGTGAGG 581

Qy       302 TGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAG 361
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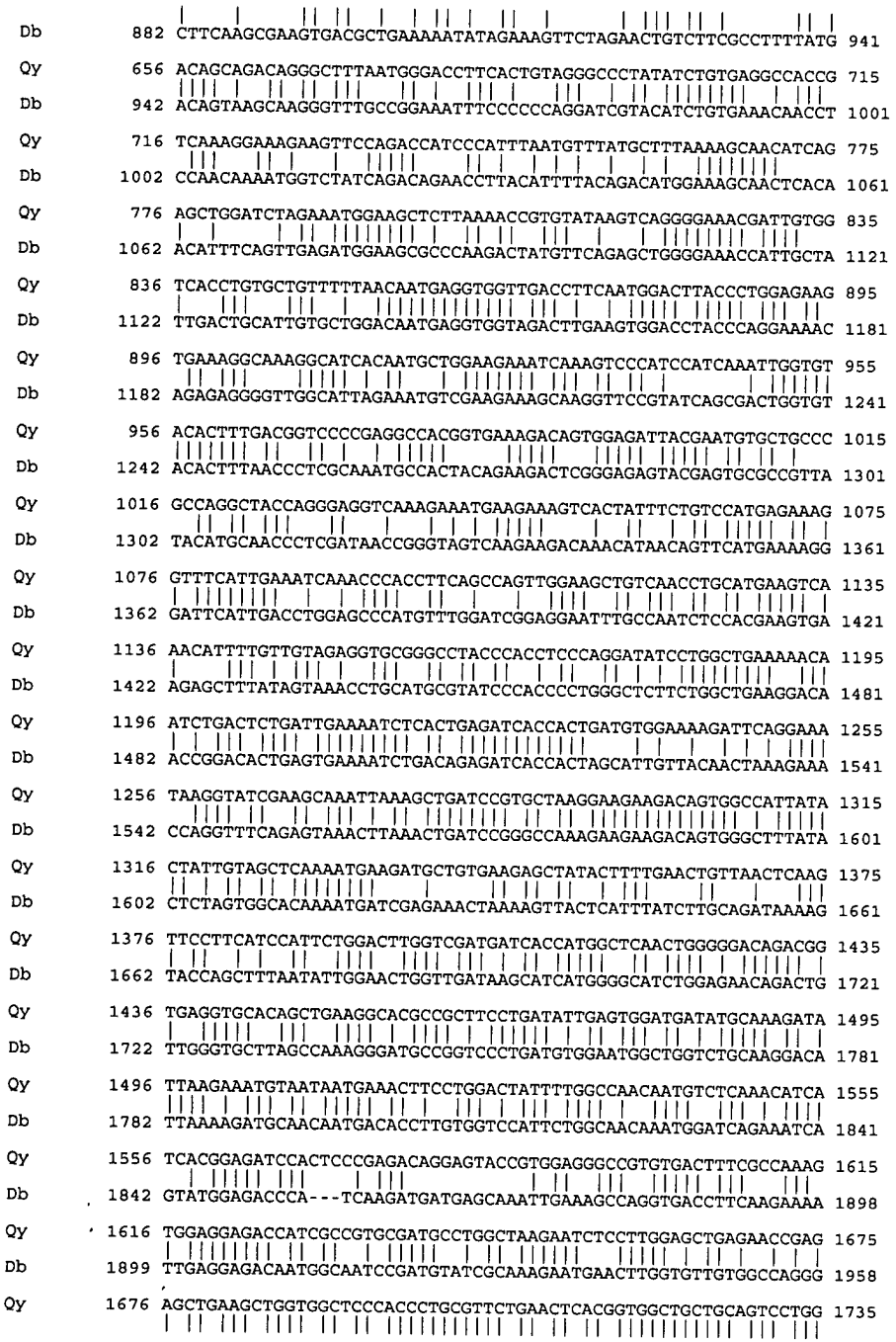
Qy       362 AAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACA 421
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Db       642 AAAACAACAGCGGCCTCTTTGTGTCCATTCTGGAAGTGAGCGATGCGTCTGCCTTTGATA 701

Qy       422 CAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCA 481
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Qy       482 GGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGG 541
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RESULT 44
BC043948

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LOCUS       BC043948               6114 bp    mRNA    linear   VRT 04-NOV-2003
DEFINITION  Xenopus laevis platelet derived growth factor receptor, alpha
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ACCESSION   BC043948
VERSION     BC043948.1  GI:27695221
KEYWORDS    MGC.
SOURCE      Xenopus laevis (African clawed frog)
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            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1  (bases 1 to 6114)
  AUTHORS   Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.
            and Richardson,P.
  TITLE     Genetic and genomic tools for Xenopus research: The NIH Xenopus
            initiative
  JOURNAL   Dev. Dyn. 225 (4), 384-391 (2002)
   PUBMED   12454917
REFERENCE   2  (bases 1 to 6114)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   3  (bases 1 to 6114)
  AUTHORS   Klein,S. and Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2003) National Institutes of Health, Xenopus Gene
            Collection (XGC), National Institute of Child Health and Human
            Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
            20892-7510, USA
  REMARK    NIH-MGC Project
COMMENT     Contact: XGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Igor Dawid
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 97 Row: c Column: 8
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 214652.
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ORIGIN

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Qy      1245 GATTCAGGAAATAAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAG 1304
Db      1317 AACTAAAGAAACCAGGTTTCAGAGTAAACTTAAACTGATCCGGGCCAAAGAAGAAGACAG 1376

Qy      1305 TGGCCATTATACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACT 1364
Db      1377 TGGGCTATATACTCTGGTGGCACAAAATGATGCAGAAACTAAAAGTTACTCATTTATGTT 1436

Qy      1365 GTTAACTCAAGTTCCTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGG 1424
Db      1437 GCAGATAAAAGTACCAGCTTTGATATTGGAACTGGTTGATAAGCATCATGGGGCATCTGG 1496

Qy      1425 GGGACAGACGGTGAGGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGAT 1484
Db      1497 TGAACAGACTGTTGGGTGCTTAGCCAAAGGGATGCCGGTCCCTGATGTGGAATGGCTGGT 1556

Qy      1485 ATGCAAAGATATTAAGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGT 1544
Db      1557 CTGCAAGGACATTAAAAGATGCAACAATGACACCTTGTGGTCCATTCTGGCAACAAATGG 1616

Qy      1545 CTCAAACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGAC 1604
Db      1617 ATCAGAAATCAGTATGGAGACCCA---TCAAGATGATGAGCAAATTGAAAGCCAGGTGAC 1673

Qy      1605 TTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGC 1664
Db      1674 CTTCAAGAAAATTGAGGAGACAATGGCAATCCGATGTATCGCAAAGAATGAACTTGGTGT 1733

Qy      1665 TGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGC 1724
Db      1734 TGTGGCCAGGGAACTAAAGTTGGTTGCACCTACCCTGCGTTCGGAGCTAACTGTGGCTGC 1793

Qy      1725 TGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTG 1784
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Db       1794 TGCTGTCTTGGTCCTTCTGGTGATTGTCATCATATCCCTCATTGTACTTGTCATCATATG 1853

Qy       1785 GAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGG 1844

Db       1854 GAAACAGAAACCAAGGTATGAAATAAGATGGCGAGTAATCGAGTCCATCAGCCCAGATGG 1913

Qy       1845 ACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCC 1904

Db       1914 CCATGAATATATCTATGTGGATCCAATGCAGCTTCCTTATGACTCTCGGTGGGAGTTCCC 1973

Qy       1905 AAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGA 1964

Db       1974 AAGAGATGGACTTGTTCTTGGTCGCATCCTTGGCTCTGGAGCTTTTGGGAAAGTGGTTGA 2033

Qy       1965 AGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCT 2024

Db       2034 AGGCGCCGCATATGGATTAAGTCGTTCTCAGCCAGTTATGAAAGTTGCTGTTAAAATGTT 2093

Qy       2025 AAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGAC 2084

Db       2094 GAAACCTACTGCCCGGTCAAGTGAAAAGCAGGCACTGATGTCCGAACTGAAGATTATGAC 2153

Qy       2085 TCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCC 2144

Db       2154 GCACCTTGGCGCACATCTCAATATAGTAAATTTACTAGGAGCCTGTACCAAGTCGGGTCC 2213

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Db       2214 AATTTATATCATTACTGAATACTGCTTCTACGGTGACCTCGTGAATTACCTGCATAAGAA 2273

Qy       2205 TAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGG 2264

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Db       2334 GCTGAACCCAGCTGATGAAAGCACAAGAAGCTACGTTATTTTATCATTTGAAAACAATGG 2393

Qy       2325 TGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAA 2384

Db       2394 CGACTACATGGACATGAAACAGGCTGACACCATGCAGTATGTACCTATGCTGGAAATGAA 2453

Qy       2385 AGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAA 2444

Db       2454 AGAACCCTCCAAGTATTCAGATATCCAGAGATCCTTGTATGACCGTCCTGCATCGTACAA 2513

Qy       2445 GAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGG 2504

Db       2514 GAAGAAGCCTTT------ATCAGAAGTGAAAAATATCTTGTCTGATGATGGATTCGAGGG 2567

Qy       2505 CCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTT 2564

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Qy       2565 GGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGG 2624

Db       2628 AGCCTCTAAAAATTGTGTACATCGGGATTTGGCAGCTCGAAATGTCCTATTAGCACATGG 2687

Qy       2625 AAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTA 2684

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Db       2748 CGTATCCAAAGGCAGCACTTTCCTTCCTGTGAAGTGGATGGCACCTGAAAGCATCTTCGA 2807

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Qy       2805 TTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGAT 2864

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Qy       2865 CAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCAT 2924

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Qy       2925 GGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGAT 2984

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Qy       2985 TGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTT 3044

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Qy       3105 TGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGA 3164

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Qy       3165 GCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCC 3224

Db       3225 GCAGAGGCTGAGTGCTGACAGCGGTTACATTATTCCCCTTCCCGATATTGACCCCGTCTC 3284

Qy       3225 TGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGC 3284

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Qy       3285 CATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGA 3344

Db       3342 AATCGAGACTGGTTCCAGCAGTTCCACTTTTATAAAGAGGGAGGATGAGACCATTGAAGA 3401

Qy       3345 CATCGACATGATGGACGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCT 3404

Db       3402 CATTGAGATGATGGACGACATTGGGATTGATCCCTCGGATCTAGTGGAGGACAGTTTCCT 3461

Qy       3405 GTAA 3408

Db       3462 GTGA 3465
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RESULT 45
AY229892
LOCUS       AY229892               2550 bp    mRNA    linear   PRI 25-JUN-2003
DEFINITION  Homo sapiens FIP1L1/PDGFRA fusion protein (FIP1L1/PDGFRA fusion)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AY229892
VERSION     AY229892.1  GI:32140871
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2550)
  AUTHORS   Griffin,J.H., Leung,J., Bruner,R.J., Caligiuri,M.A. and
            Briesewitz,R.
  TITLE     Discovery of a fusion kinase in EOL-1 cells and idiopathic
            hypereosinophilic syndrome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7830-7835 (2003)
   PUBMED   12808148
REFERENCE   2  (bases 1 to 2550)
  AUTHORS   Briesewitz,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-FEB-2003) Biochemistry, Theravance, Inc., 901
            Gateway, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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                     apparent molecular weight of 110 kDa; amino terminal
                     FIP1L1 sequence is similar to NM_030917; alternatively
                     spliced; rearranged-in-hypereosinophilia-platelet derived
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                     EVTPGAEIQDGRFNLFKVQQGRTGNSEKETALPSTKAEFTSPPSLFKTGLPPSRNSTS
                     SQSQTSTASRKANSSVGKWQDRYGRAESPDLRRLPGAIDVIGQTITISRVEGRRRANE
                     NSNIQLPYDSRWEFPRDGLVLGRVLGSGAFGKVVEGTAYGLSRSQPVMKVAVKMLKPT
                     ARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDLVNYLHKNR
                     DSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLER
                     KEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGM
                     EFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLPVKWMAP
                     ESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKPDHAT
                     SEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARM
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                     /note="fusion junction resulting from an 800 kb deletion
                     associated with hypereosinophilic syndrome"
ORIGIN

  Query Match             23.9%;  Score 1535.8;  DB 8;  Length 2550;
  Best Local Similarity   99.9%;  Pred. No. 5.5e-304;
  Matches 1537;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1870 ATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGG 1929
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Db       1012 ATACAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGG 1071

Qy       1930 GTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGG 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGG 1131

Qy       1990 TCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAA 2049
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Db       1132 TCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAA 1191

Qy       2050 AAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATT 2109
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Db       1192 AAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATT 1251

Qy       2110 GTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGC 2169
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Qy       2170 TTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCAC 2229
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Db       1312 TTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCAC 1371

Qy       2230 CCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACA 2289
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Db       1372 CCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACA 1431

Qy       2290 CGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCT 2349
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Db       1432 CGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCT 1491

Qy       2350 GATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATC 2409
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Qy       2410 CAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAA 2469
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Qy       2470 GTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGC 2529
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Db       1612 GTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGC 1671

Qy       2530 TTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGT 2589
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Db       1672 TTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGT 1731

Qy       2590 GATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTT 2649
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Db       1732 GATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTT 1791

Qy       2650 GGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTG 2709
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Db       1792 GGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTG 1851

Qy       2710 CCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGAT 2769
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Db       1852 CCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGAT 1911

Qy       2770 GTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCC 2829
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Db       1912 GTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCC 1971

Qy       2830 GGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAG 2889
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Qy       2890 CCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCG 2949
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Qy       2950 GAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAA 3009
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Qy       3010 TATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTG 3069
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Db       2152 TATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTG 2211

Qy       3070 GCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAA 3129
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Db       2212 GCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAA 2271

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Qy       3190 TACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGG 3249
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Qy       3310 ACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGC 3369
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RESULT 46
AF200951
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DEFINITION  Danio rerio platelet-derived growth factor receptor alpha mRNA,
            complete cds.
ACCESSION   AF200951
VERSION     AF200951.1  GI:12003180
KEYWORDS    .
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 3788)
  AUTHORS   Liu,L., Balasubramaniyan,N.V. and Ge,R.
  TITLE     The zebrafish PDGF-A/PDGFR-alpha signalling system in early
            embryogenesis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3788)
  AUTHORS   Liu,L., Balasubramaniyan,N.V. and Ge,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1999) Department of Biological Sciences, National
            University of Singapore, Lower Kent Ridge Road, Singapore 119260,
            Republic of Singapore
FEATURES             Location/Qualifiers
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     CDS             126. .3305
                     /note="PDGFR-alpha; tyrosine kinase"
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ORIGIN

  Query Match           19.3%;  Score 1239.6;  DB 5;  Length 3788;
  Best Local Similarity   65.7%;  Pred. No. 2.9e-243;
  Matches 1940;  Conservative    0;  Mismatches  979;  Indels   33;  Gaps    8;

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Db        392 CATCTACATTTATGTGCCAGATCCACAAACCCCATTTGTGCCGTCCATGACCCCGTTTGA 451

Qy        546 TTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGA 605
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Qy        900 AGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACAC 959
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RESULT 47
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LOCUS	AC120348 244565 bp DNA linear ROD 20-NOV-2004
DEFINITION	Mus musculus chromosome 5, clone RP23-55P22, complete sequence.
ACCESSION	AC120348
VERSION	AC120348.9 GI:55908981
KEYWORDS	HTG.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 244565)
AUTHORS	Birren,B., Nusbaum,C. and Lander,E.
TITLE	Mus musculus chromosome 5, clone RP23-55P22
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 244565)
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,

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            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
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            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 244565)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
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            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 244565)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
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            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Nov 20, 2004 this sequence version replaced gi:54291898.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
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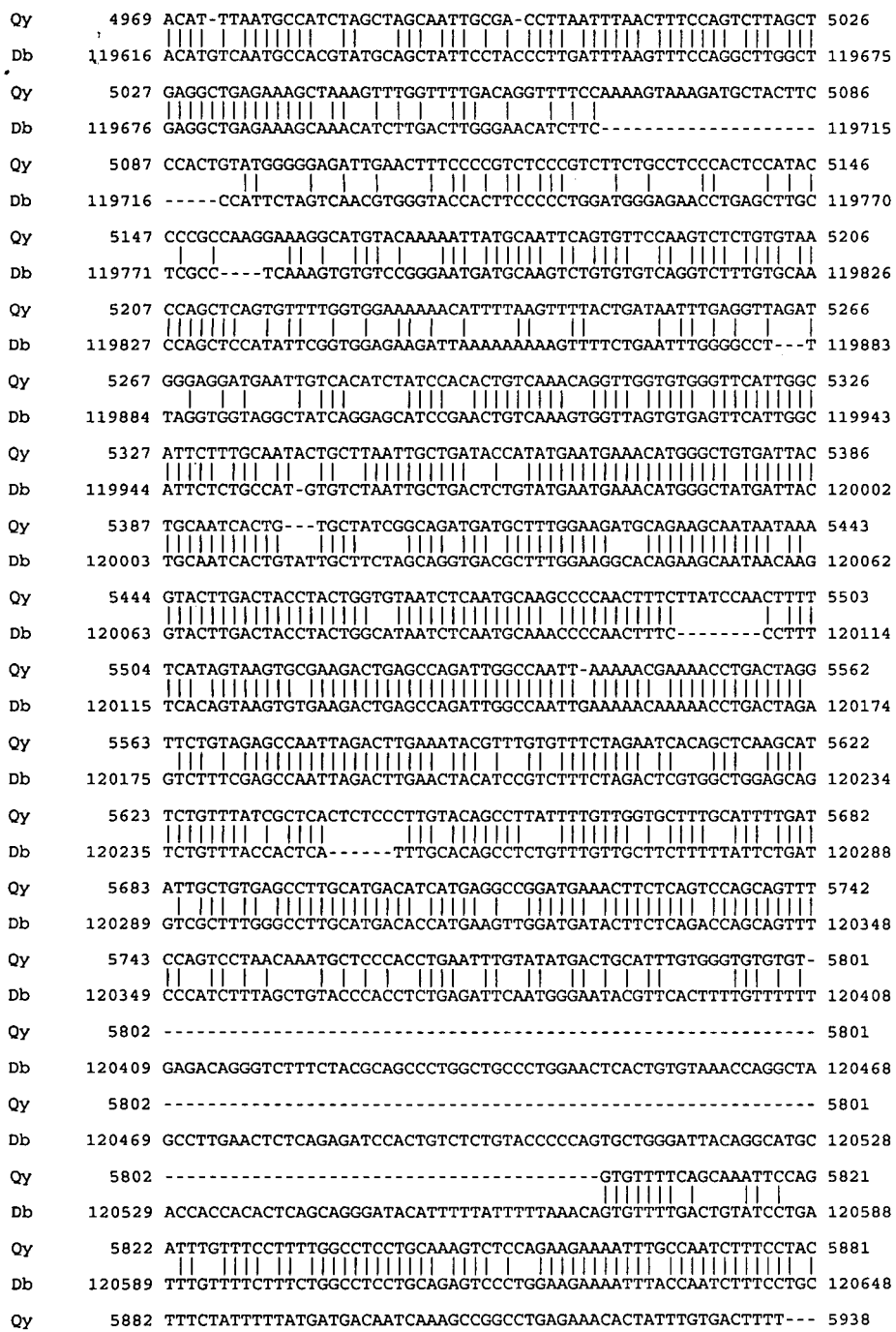
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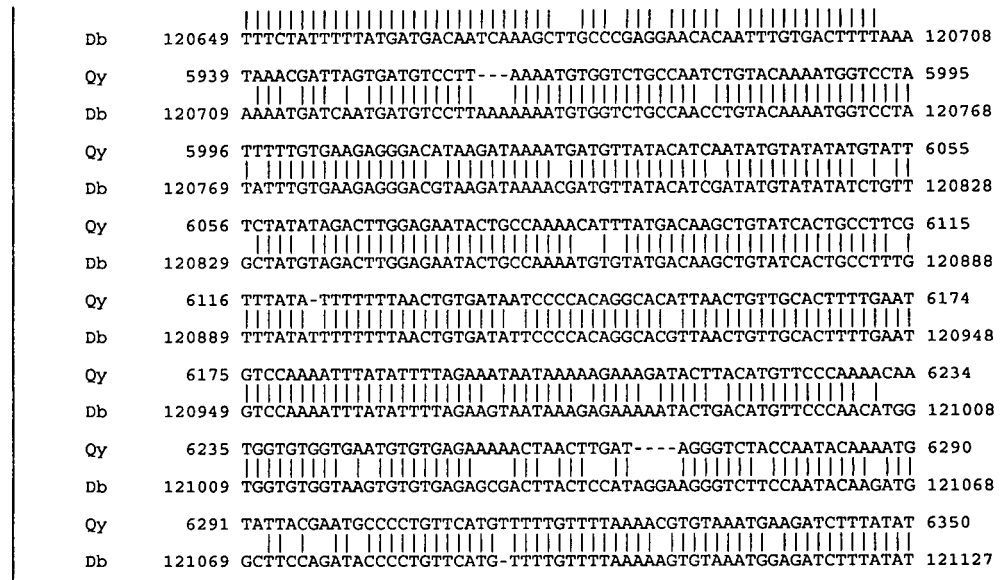
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RESULT 48
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LOCUS       AC019028              264425 bp    DNA     linear   ROD 30-SEP-2003
DEFINITION  Mus musculus chromosome 5, clone RP23-88A22, complete sequence.
ACCESSION   AC019028
VERSION     AC019028.13  GI:18643683
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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REFERENCE   1  (bases 1 to 264425)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 5, clone RP23-88A22
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 264425)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
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            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
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REFERENCE   3  (bases 1 to 264425)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 264425)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Feb 10, 2002 this sequence version replaced gi:18482277.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
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              | ||||| ||||| || | | |  |||||||||||||| ||| | | ||||| |||| ||
Db     234388 TCCTTCCTTCTTGGAATCCGGTACCAGCTGCTGTTGAATTTTCTCATGAAGTACATGCAA 234329

Qy       3909 AACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGT 3968
              |||||  |||||||  ||  |||||||||| ||  | |  |||| || |||| |      |
Db     234328 AACCA-CTTTGAACTTTGGAAGGTACTGGAACCGTCGTGTTTTACTGTCTTGTAAGTGTT 234270

Qy       3969 TAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTA-GAA 4027
```

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                ||   |  |||  |||| || ||||||||| ||  || ||| |||||||| |||| |
Db     234269 AAAGAGGCAAAAAGATAAAAACTAACCAACCGTGAGTAGTAGGTTTGGGTCTTTTAGGGC 234210

Qy       4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTG-TTATCAGT 4086
              ||  | || || | |  || ||||||||| |  |||||| |||||||||| ||| ||
Db     234209 ACCCAAGAATTCCTCTGTATCTTGTAATCTGTACTTATAACACTACTACTGTTTAACAAG 234150

Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAA-AC 4145
              |||||||||| ||||||   |||||||||||||  | ||||||||||||||||| ||| |
Db     234149 AATGCTAAATATGTAAT-CCGTAACATGATTTCTTTACAGAGAAAGCACAATTAAAACAA 234091

Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
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Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
              ||||| ||||||||   ||||||  |||||  | ||||||  ||||    |   ||||||  ||
Db     234030 TTCTCAATAAAGTA---TAATAGGTTTAGCGGATTAAAGTTAGCAAACACTAGAGAGCAG 233974

Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
              |||  |||||||  |    |        |  ||||    |||  ||  |  ||  |||| ||
Db     233973 AGTGTAAGTAGTTATCCAGAAAGTCAAACCTTTTTGTTTTGTTCTAAGCAGTCTCCCTAA 233914

Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Db     233913 TCCAAGGCACTAGGAA--CAGTTAATGACCTCTGAAGTACTGGGATAAGCAAAGCAGAAA 233856

Qy       4386 ACTCTT--AAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTT 4443
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Qy       4444 CTCA---TGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Db     233795 CTCACGCTGTGTGCGACCTTCTGGAAGAGACTCATTCACAAAAAGGACTCAGATGGGCAG 233736

Qy       4501 AAGTTTTTTTTTTTTTTCTTC--ATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTA 4558
              ||  |   |    |    ||  ||| ||      | |  ||    |   ||  ||
Db     233735 AATGTCCATCAGATGGGACTCAGATGTCTCTCCTGACCAGTGATGGCTTGGATGGATCCC 233676

Qy       4559 TTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCT--T 4616
                 |   |   |   |          |   |  |||||||    |||||||  | |  |
Db     233675 GCCCATACCTACTTTTAAAGTCTGTGACTTTTAAGGATGCTTCAACATCAGCACCTTACT 233616

Qy       4617 CTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTC-GAGACCATAAAGATATTCTT 4675
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Db     233615 TTTTCTCTCTTGTCTCAGACGAGAAAGAACTGCAAACCCTGAGACCACAATGGTGCTGTT 233556

Qy       4676 TAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCA 4735
              | || |||||   || |||| ||| ||| || ||  |||  ||     |   |
Db     233555 GAATGAAGGCTATGTGGGCATCAGCTTGGCTCTTCCCTTCCCACCATTAACTACAGCTAC 233496

Qy       4736 GGATGACTAGATCCTGGGTTTCCATCCTT-------GAGATTCTGAAGTATGAAGTCTGA 4788
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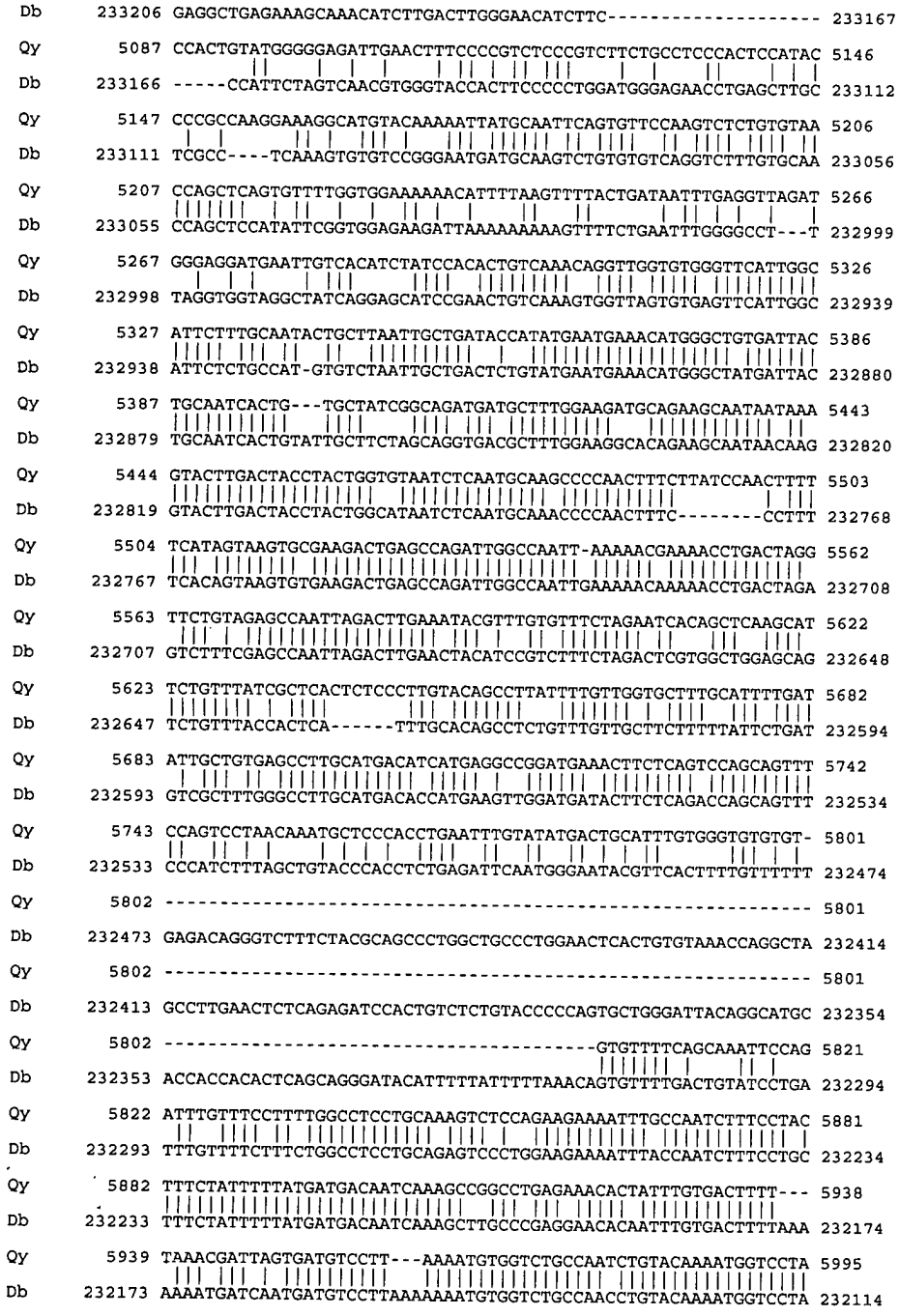
Qy       4789 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 4848
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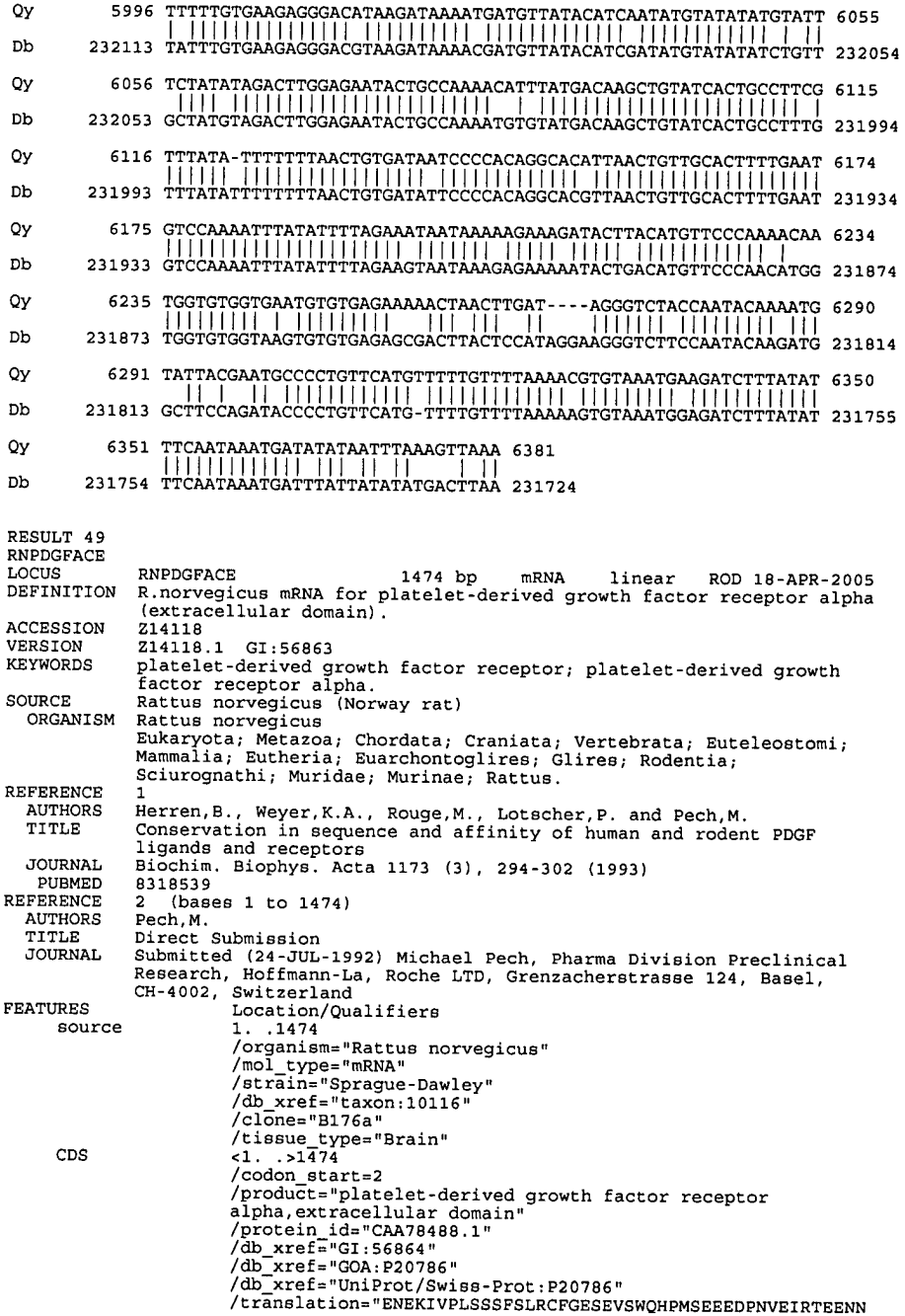
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Qy       4909 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 4968
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Qy       4969 ACAT-TTAATGCCATCTAGCTAGCAATTGCGA-CCTTAATTTAACTTTCCAGTCTTAGCT 5026
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Qy       5027 GAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTC 5086
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RESULT 49
RNPDGFACE
LOCUS       RNPDGFACE              1474 bp    mRNA    linear   ROD 18-APR-2005
DEFINITION  R.norvegicus mRNA for platelet-derived growth factor receptor alpha
            (extracellular domain).
ACCESSION   Z14118
VERSION     Z14118.1  GI:56863
KEYWORDS    platelet-derived growth factor receptor; platelet-derived growth
            factor receptor alpha.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE   1
  AUTHORS   Herren,B., Weyer,K.A., Rouge,M., Lotscher,P. and Pech,M.
  TITLE     Conservation in sequence and affinity of human and rodent PDGF
            ligands and receptors
  JOURNAL   Biochim. Biophys. Acta 1173 (3), 294-302 (1993)
   PUBMED   8318539
REFERENCE   2  (bases 1 to 1474)
  AUTHORS   Pech,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-1992) Michael Pech, Pharma Division Preclinical
            Research, Hoffmann-La, Roche LTD, Grenzacherstrasse 124, Basel,
            CH-4002, Switzerland
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                     /db_xref="GOA:P20786"
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RGRTFKTSEFNVYALKATSELNLEMDTRQTVYKAGETIVVTCAVFNNEVVDLQWTYPG
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GSGGGQTVRCTAEGTPLPNIEWMICKDIKKCNNDTSWTVLASNVSNIITEFHQRGRST
VEGRVSFAKVEETIAVRCLAKNDLGIGNRELKLVAPTLRSE"

ORIGIN

Query Match 16.7%; Score 1073; DB 9; Length 1474;
Best Local Similarity 83.0%; Pred. No. 4.3e-209;
Matches 1223; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

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Qy       237 TGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAG 296
Db         1 TGAGAATGAGAAGATTGTGCCGCTGAGTTCGTCCTTCTCTCTGAGATGCTTCGGGGAGAG 60

Qy       297 TGAAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAA 356
Db        61 CGAAGTGAGCTGGCAGCACCCCATGTCTGAAGAAGAGGACCCCAACGTGGAAATCAGAAC 120

Qy       357 TGAAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGC 416
Db       121 CGAGGAGAACAACAGTAGCCTCTTTGTCACGGTGCTGGAAGTGGTCAACGCCTCAGCGGC 180

Qy       417 CCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGA 476
Db       181 CCACACCGGATGGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAGTGAGATCGA 240

Qy       477 AGGCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAAT 536
Db       241 AGGCAGGCACATTTATATCTATGTACCAGACCCAGACATGGCCTTCGTGCCTCTCGGCAT 300

Qy       537 GACGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAAC 596
Db       301 GACGGATTCTTTAGTCATTGTGGAAGAGGACGATTCTGCCATCATACCCTGCCGCACCAC 360

Qy       597 TGATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGA 656
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Qy       657 CAGCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGT 716
Db       421 CAGCAGGCAGGGCTTCAACGGAACCTTCAGTGTGGGGCCTTACATCTGTGAGGCCACCGT 480

Qy       717 CAAAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGA 776
Db       481 CAGAGGGAGGACGTTCAAGACCAGCGAGTTTAACGTTTATGCCTTGAAAGCCACGTCAGA 540

Qy       777 GCTGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGT 836
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Qy       837 CACCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGT 896
Db       601 GACCTGCGCCGTCTTTAACAATGAGGTGGTTGACCTGCAGTGGACTTACCCTGGAGAGGT 660

Qy       897 GAAAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTA 956
Db       661 GAGAAACAAAGGCATCACCATGCTGGAGGAGATCAAACTCCCGTCCATCAAACTGGTGTA 720

Qy       957 CACTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCG 1016
Db       721 CACGCTGACCGTCCCCAAGGCCACGGTGAAGGACAGCGGAGATTATGAATGTGCTGCCCG 780

Qy      1017 CCAGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGG 1076
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Qy      1077 TTTCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAA 1136
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Qy      1137 ACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAA 1196
Db       901 AGAGTTCGTGGTGGAGGTGCAGGCCTACCCGACCCCCAGGATATCCTGGCTGAAGGACAA 960

Qy      1197 TCTGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAAT 1256
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Qy      1257 AAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATAC 1316
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Qy      1317 TATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGT 1376
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Qy      1377 TCCTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGT 1436
Db       1141 TCCTGCCTCCATTCTGGAGCTTGTGGATGACCACCATGGCTCTGGCGGGGGACAGACTGT 1200

Qy      1437 GAGGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATAT 1496
Db       1201 GAGGTGCACGGCTGAAGGCACCCCTCTTCCGAACATCGAGTGGATGATCTGCAAGGATAT 1260

Qy      1497 TAAGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCAT 1556
Db       1261 TAAGAAATGTAATAATGACACTTCATGGACAGTTTTGGCCAGCAACGTCTCGAATATTAT 1320

Qy      1557 CACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGT 1616
Db       1321 CACGGAGTTCCACCAGCGAGGCAGGAGTACAGTGGAGGGACGAGTGTCCTTCGCCAAGGT 1380

Qy      1617 GGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGA 1676
Db       1381 GGAAGAGACCATCGCAGTTCGGTGCTTGGCAAAGAACGACCTTGGCATTGGGAACAGAGA 1440

Qy      1677 GCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGA 1709
Db       1441 GCTGAAGCTGGTGGCTCCCACCCTGCGATCTGA 1473
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RESULT 50
AC114072/c
LOCUS AC114072 235304 bp DNA linear HTG 13-MAY-2003
DEFINITION Rattus norvegicus clone CH230-64M8, WORKING DRAFT SEQUENCE, 2 unordered pieces.
ACCESSION AC114072
VERSION AC114072.4 GI:30580532
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 235304)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,

Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 235304)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 235304)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On May 13, 2003 this sequence version replaced gi:22857471.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GLGS
Center clone name: CH230-64M8
---------- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 208311 bases at least Q40
Consensus quality: 212093 bases at least Q30
Consensus quality: 214818 bases at least Q20
Estimated insert size: 217886; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 234012: contig of 234012 bp in length
* 234013 234112: gap of unknown length
* 234113 235304: contig of 1192 bp in length.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 16.5%; Score 1060; DB 14; Length 235304;
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Matches 2263; Conservative 0; Mismatches 775; Indels 328; Gaps 41;

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Qy       3436 TTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAG 3495
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Db     191864 TCTGGGAGCCTCCTCGGGATCCCCTTAAGAAAACCACTTCATTGCAATGCAAAGGTTGA- 191806

Qy       3496 AGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCT 3555
                 |||||||  ||||||  |  |  ||||||||||  ||||||||  ||  |||  |||  |
Db     191805 -----GACTTGGGTGATGTGGAGACAGAAGTTCCCGGCCAAGGGTCTTGGGAAGCCT--- 191754

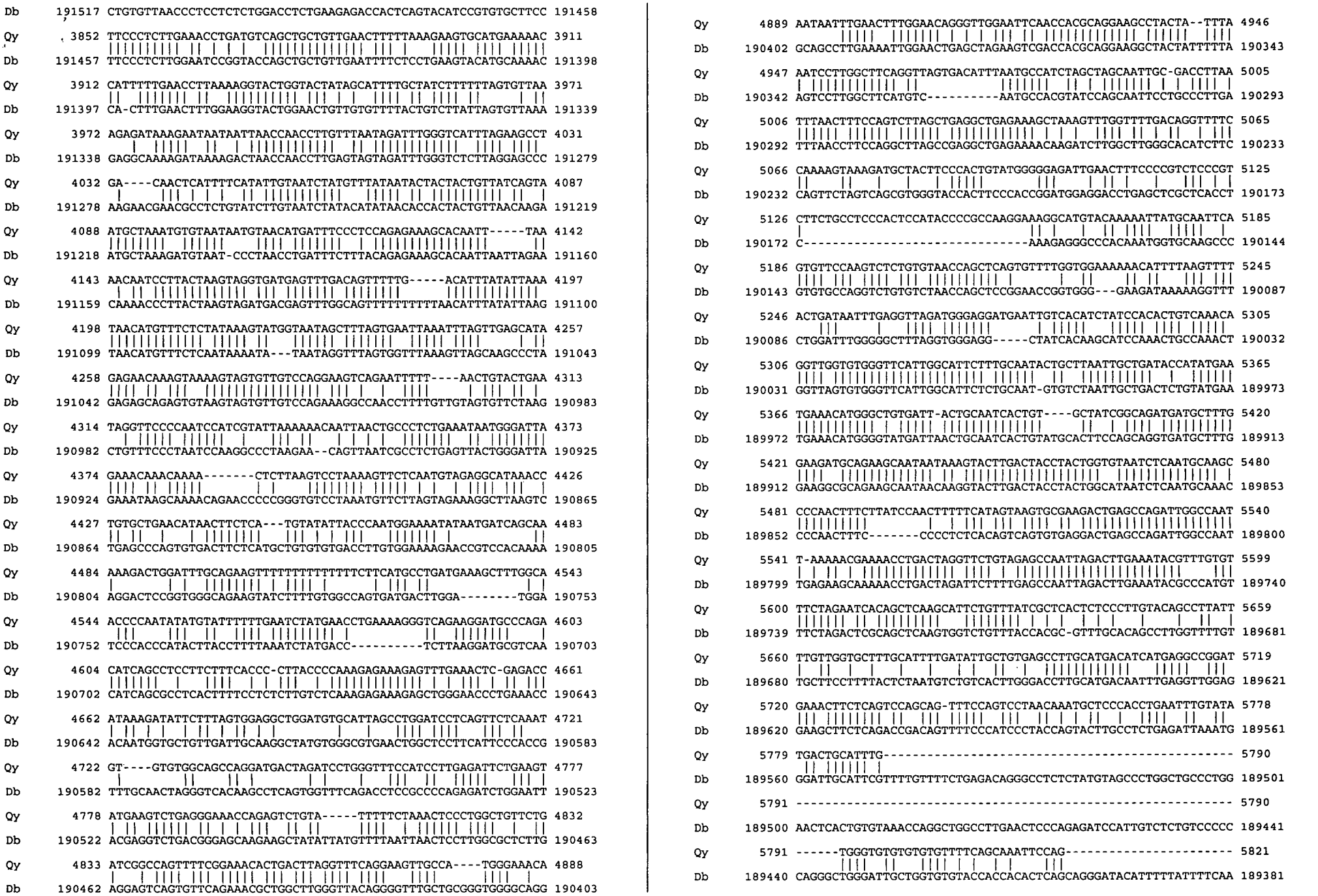
Qy       3556 AAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCC 3615
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Db     191753 --CTGTGAATGACTGGGATA-CTCGGATCGAACGTTGTCCATGCTGCCCCTTGCAATCCG 191697

Qy       3616 TCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCC 3675
             ||||||||||||||  ||  ||||||  |||||||  ||  ||  |||  ||||||  |  |  ||||
Db     191696 TCAGTAGCATCTCAGCGGCGTGTGAGGTTTGGAAATGGACGGACAAGGGAGTGACTGGCC 191637

Qy       3676 ACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATA 3735
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Db     191636 ACAGAAGACGGGCTTTGTGTTTCCGGGGCATTGGTGAGATTCCCACACGCGCAACTTGTA 191577

Qy       3736 CTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGA 3795
             ||||  |  |  ||||  |||||||||||||||||||||||||  |||  ||  |||  |||||
Db     191576 CTGC-AGACAACTCCAGCATTGTAATTATGTAAATAACCCTAGCCGAGGACGTGTTAGAT 191518

Qy       3796 TTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATG----TAC 3851
                 |||  |||||  ||  |||  |||||  ||||||||||||||||||  |  |||||  ||     | |
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Qy       5822 ------------------ATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAA 5863
                                  | ||||| ||||||||||||||| |||| |  |||| |||
Db     189380 ACAGTGTTTTGACTGTATCCTGGTTTCTTTTTGGCCTCCTGCAGAGTCCCTGGAAGGAAA 189321

Qy       5864 TTTGCCAATCTTTCCTACTTTC------TATTTTTATGATGACAATCAAAGCCGGCCTGA 5917
              ||| ||||| ||  || |||||      |||||||||||||||||||||||| |||| ||
Db     189320 TTTACCAATTTTCTCTGCTTTCTATTCTTATTTTTATGATGACAATCAAAGCTGGCCCGA 189261

Qy       5918 GAAACACTATTTGTGAC------TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCT 5971
                ||||| |||||||||      ||||||||  || ||||||||||||||||||||||
Db     189260 AGAACACAATTTGTGACTTTTTTTTTTTTAAATAATCAGTGATGTCCTTAAAATGTGGTCT 189201

Qy       5972 GCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTA 6031
              ||||| |||||||||||||||||| ||| |||||||||| | ||||||||||||||||
Db     189200 GCCAACCTGTACAAAATGGTCCTATATTTTTGAAGAGGGACGTGAGATAAAATGATGTTA 189141

Qy       6032 TACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTA 6091
              |||||| |||||||||||| | || |||| |||||||||||||||||||||||| | ||
Db     189140 TACATCGATATGTATATATCTGTTGCTATGTAGACTTGGAGAATACTGCCAAAACGTGTA 189081

Qy       6092 TGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCA 6151
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Db     189080 TGACAAGCTGTATCACTGCCTTTGTTTATATTTTTTTAACTGTGATATTCCCCACAGGCA 189021

Qy       6152 CATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAG 6211
              | |||||||||||||||||||||||||||||||||||||||||  |||||| |||||
Db     189020 CGTTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAGGAATAAAGAGAAAA 188961

Qy       6212 ATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAG 6271
              |||||||||||||||||| |   ||||||||| ||||||||||  ||||   | || ||
Db     188960 ATACTTACATGTTCCCAACATGGTGGTGTGGTAAATGTGTGAGAGCAACTCCATAGAGAG 188901

Qy       6272 GGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAA----- 6326
              ||||| ||||| ||| |||   || |  || ||| ||||||||||||  ||  |||
Db     188900 GGTCTTCCAATCCAAGATGGCTTCCAGATACCCGTGTTCATGTTTTGTTTAAAAAAAAAA 188841

Qy       6327 -ACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAA 6385
               | ||||||||| |||||||||||||||||||||||||| ||| || ||   ||  |||
Db     188840 GAAGTGTAAATGGAGATCTTTATATTTCAATAAATGATTTATGATATATGATTTTAAAGT 188781

Qy       6386 AAAAAA 6391
                |  ||
Db     188780 TATGAA 188775
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Search completed: May 15, 2006, 14:38:53
Job time : 20944 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 08:49:32 ; Search time 3430 Seconds
(without alignments)
12460.838 Million cell updates/sec

Title: US-08-439-095-2
Perfect score: 6413
Sequence: 1 ccattactgttggagctaca.....aaaaaaaaaaaaaaaaaaaa 6413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6385	99.6	6412	2	AAQ05989	Aaq05989 TR4 cDNA
2	6373.2	99.4	6428	5	ADL63502	Adl63502 Human ova
3	6364.4	99.2	6378	6	ABK35520	Abk35520 Human end
4	6364.4	99.2	6378	6	ABL68519	Abl68519 Kidney ca
5	6364.4	99.2	6378	6	ABL62372	Abl62372 Colon ade
6	6364.4	99.2	6378	10	ADF90648	Adf90648 Human hep
7	6364.4	99.2	6378	11	ADI31868	Adi31868 Human cDN
8	6364.4	99.2	6378	12	ADQ17832	Adq17832 Human sof
9	6364.4	99.2	6378	13	ADS83935	Ads83935 Human lym
10	6364.4	99.2	6633	10	ADG89389	Adg89389 Cancer de
11	6364.4	99.2	6633	12	ADM69011	Adm69011 Human pla
12	6364.4	99.2	6633	14	ADY59388	Ady59388 Human PDG
13	6362.8	99.2	6633	12	ADM69030	Adm69030 Human PDG
14	6362.8	99.2	6633	12	ADM69013	Adm69013 Human PDG
15	6359.6	99.2	6633	12	ADM69034	Adm69034 Human PDG
16	6348.4	99.0	6639	12	ADM69019	Adm69019 Human PDG
17	6334.8	98.8	6624	12	ADM69017	Adm69017 Human PDG
18	6332.6	98.7	6633	14	ADZ13914	Adz13914 Human can
19	6330.4	98.7	6621	12	ADM69015	Adm69015 Human PDG
20	6327.6	98.7	7067	12	ADQ22465	Adq22465 Human sof
21	6327	98.7	6633	13	ADQ38813	Adq38813 Human SNP
22	6324.4	98.6	6618	12	ADM69032	Adm69032 Human PDG
23	6319.6	98.5	6618	12	ADM69021	Adm69021 Human PDG
24	6310.4	98.4	6633	12	ADM69036	Adm69036 Human PDG
25	6224.2	97.1	6240	12	ADQ59531	Adq59531 Human can
26	4160.8	64.9	6075	2	AAQ27451	Aaq27451 Type A hu
27	3837.2	59.8	4054	2	AAQ06869	Aaq06869 Sequence
28	3585	55.9	6576	14	ADZ61190	Adz61190 Murine Pd
29	3581.2	55.8	6556	14	ADZ13909	Adz13909 Murine ca
30	3576.8	55.8	6499	12	ADQ59528	Adq59528 Human can
31	3270	51.0	3270	10	ABS57780	Abs57780 cDNA enco
32	3270	51.0	3270	14	ADV42434	Adv42434 Human psy
33	3268.4	51.0	3270	10	ABS57784	Abs57784 Human pla
34	3268.4	51.0	3270	10	ABS57781	Abs57781 Human pla
35	3268.4	51.0	3270	10	ABS57783	Abs57783 Human pla
36	3266.8	50.9	3270	10	ABS57782	Abs57782 Human pla
37	3260.6	50.8	6264	14	ADZ60757	Adz60757 Rat Pdgfr
38	3108	48.5	89210	14	ADZ13911	Adz13911 Human can
39	3106.4	48.4	59475	12	ADQ59530	Adq59530 Human can
40	2561.2	39.9	3270	14	ADV44174	Adv44174 Human psy
41	1836.4	28.6	1842	3	AAC77955	Aac77955 Human can
42	1767	27.6	1767	10	ABS57785	Abs57785 Truncated
43	1522.8	23.7	2427	12	ADJ93556	Adj93556 NM_030917
44	1522.8	23.7	2472	12	ADJ93555	Adj93555 NM_030917
45	1522.8	23.7	2496	12	ADJ93554	Adj93554 Coding se
46	1522.8	23.7	2541	12	ADJ93553	Adj93553 Coding se
47	1094.6	17.1	65952	12	ADQ59527	Adq59527 Human can
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49	736	11.5	1047	14	ADZ13912	Adz13912 Human can
50	734.8	11.5	1047	13	ADQ38814	Adq38814 Human SNP
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53	667.6	10.4	3321	10	ABS57790	Abs57790 Human pla
54	667.6	10.4	4544	2	AAT34552	Aat34552 Platelet-
55	666	10.4	3321	10	ABS57786	Abs57786 Human pla
56	666	10.4	3321	14	ADV42435	Adv42435 Human psy
57	666	10.4	4544	1	AAN90355	Aan90355 cDNA enco
58	666	10.4	5570	6	ABZ34916	Abz34916 Human gen
59	666	10.4	5570	6	ABV94218	Abv94218 Breast ca
60	666	10.4	5570	10	ADK61411	Adk61411 Ovarian c
61	666	10.4	5570	11	ADI31867	Adi31867 Human cDN
62	666	10.4	5570	13	ADS83934	Ads83934 Human lym
63	666	10.4	5598	14	ADY59380	Ady59380 Human PDG
64	666	10.4	5622	10	ADJ56358	Adj56358 Human cDN
65	666	10.4	5707	13	ABD32965	Abd32965 Human can
66	666	10.4	6315	12	ADQ22601	Adq22601 Human sof
67	664.6	10.4	5602	5	AAS84940	Aas84940 DNA encod
68	664.4	10.4	3321	10	ABS57787	Abs57787 Human pla
69	664.4	10.4	3321	10	ABS57789	Abs57789 Human pla
70	662.8	10.3	3321	10	ABS57788	Abs57788 Human pla
71	661.4	10.3	5084	13	ABD32963	Abd32963 Human can
72	651.6	10.2	5719	1	AAN90388	Aan90388 cDNA enco
73	622	9.7	3739	13	ABD32960	Abd32960 Mouse can
74	622	9.7	5111	13	ABD32961	Abd32961 Mouse can
75	620.4	9.7	3297	14	ADV44175	Adv44175 Human psy
76	620.4	9.7	5110	6	ABI99825	Abi99825 Mouse isc
77	620.4	9.7	5110	14	ADZ61992	Adz61992 Murine Pd
78	573	8.9	2463	2	AAX89336	Aax89336 Platelet-
79	539.4	8.4	1176	11	ADI32078	Adi32078 Human cDN
80	539.4	8.4	1176	13	ADS84145	Ads84145 Human lym
81	526.4	8.2	528	6	ABV78160	Abv78160 Human PDG
82	526.4	8.2	528	6	ABZ35736	Abz35736 Human PDG
83	526.4	8.2	528	6	ABX09979	Abx09979 Human PDG
84	526.4	8.2	528	6	ABL91701	Abl91701 Human pol
85	514.8	8.0	572	6	ABQ55423	Abq55423 Human ova
86	461	7.2	461	14	AEB53111	Aeb53111 Human pro
c 87	453.4	7.1	492	14	ADV75853	Adv75853 Human col
88	439.4	6.9	475	9	ACH25748	Ach25748 Human adu
89	434.2	6.8	477	9	ACH25895	Ach25895 Human adu
90	406.2	6.3	506	5	ADL44417	Adl44417 Human ova
91	404	6.3	477	9	ACH38437	Ach38437 Human end
92	403.6	6.3	477	9	ACH25203	Ach25203 Human adu

	93	391.8	6.1	427	14	ADV75852 Adv75852 Human col
c	94	391	6.1	629	10	ADB57552 Adb57552 Toxicity-
c	95	391	6.1	629	10	ABT41568 Abt41568 Toxicity
	96	390.8	6.1	6390	5	AAS79665 Aas79665 DNA encod
	97	390.8	6.1	6390	5	AAS84936 Aas84936 DNA encod
	98	346	5.4	2928	14	ADV44168 Adv44168 Human psy
	99	344.4	5.4	5098	4	AAD13425 Aad13425 Murine Ki
	100	344.4	5.4	5132	14	AEA19288 Aea19288 Mouse c-k
	101	344.4	5.4	5132	14	AEA80341 Aea80341 Mouse KIT
	102	333.8	5.2	3816	14	AEA80343 Aea80343 Rat KIT t
	103	331.6	5.2	2931	12	ADI33411 Adi33411 Human KIT
	104	331.6	5.2	2931	14	ADV42428 Adv42428 Human psy
	105	331.6	5.2	5021	13	ADS97845 Ads97845 Protein f
	106	331.6	5.2	5084	2	AAV20443 Aav20443 Human c-k
	107	331.6	5.2	5084	4	AAD13426 Aad13426 Human Kit
	108	331.6	5.2	5084	6	ABL64113 Abl64113 Breast ca
	109	331.6	5.2	5084	6	ABL68085 Abl68085 Ovary can
	110	331.6	5.2	5084	10	ADC98647 Adc98647 Human tyr
	111	331.6	5.2	5084	11	ADN39389 Adn39389 Cancer/an
	112	331.6	5.2	5084	11	ADI32009 Adi32009 Human cDN
	113	331.6	5.2	5084	12	ADP10348 Adp10348 Reference
	114	331.6	5.2	5084	13	ADQ82891 Adq82891 Human cKI
	115	331.6	5.2	5084	13	ADP55987 Adp55987 Human PRO
	116	331.6	5.2	5084	13	ADS92936 Ads92936 v-kit Har
	117	331.6	5.2	5084	13	ADU06246 Adu06246 Novel bro
	118	331.6	5.2	5084	13	ADV35109 Adv35109 Human cDN
	119	331.6	5.2	5084	13	ADS84076 Ads84076 Human lym
	120	331.6	5.2	5084	14	ADY15473 Ady15473 DNA encod
	121	331.6	5.2	5084	14	AEA80339 Aea80339 Human KIT
	122	326.2	5.1	3868	12	ADO26905 Ado26905 cDNA enco
	123	323.2	5.0	3069	3	AAZ44718 Aaz44718 Bovine c-
	124	322.8	5.0	2919	2	AAV80687 Aav80687 Hampshire
	125	322.6	5.0	32203	14	ADZ59521 Adz59521 Secondary
	126	322.6	5.0	191150	12	ADM69029 Adm69029 Human pla
	127	319.6	5.0	3952	13	ADT55099 Adt55099 Nucleotid
	128	319.4	5.0	495	3	AAC04186 Aac04186 Human sec
	129	303.2	4.7	3475	13	ADQ39165 Adq39165 Human SNP
	130	303.2	4.7	4225	13	ADQ39164 Adq39164 Human SNP
	131	302.6	4.7	2982	9	ADA02632 Ada02632 Human FLT
	132	302.6	4.7	2982	10	ADB72370 Adb72370 Human FLT
	133	302.6	4.7	2982	10	ADE95880 Ade95880 Human FLT
	134	302.6	4.7	2982	12	ADI33417 Adi33417 Human FMS
	135	302.6	4.7	2982	14	ADV42432 Adv42432 Human psy
	136	302.6	4.7	3422	14	AEA19274 Aea19274 Human Flt
	137	302.6	4.7	3475	2	AAT00802 Aat00802 Human Flk
	138	302.6	4.7	3475	9	ADA02631 Ada02631 Human FLT
	139	302.6	4.7	3475	10	ADB72369 Adb72369 Human FLT
	140	302.6	4.7	3475	10	ADE95879 Ade95879 Human DNA
	141	302.6	4.7	3475	12	ADP10390 Adp10390 Reference
	142	302.6	4.7	3476	2	AAQ91536 Aaq91536 Human STK
	143	302.6	4.7	3489	6	AAD42484 Aad42484 Human rec
	144	302.6	4.7	3501	2	AAQ35250 Aaq35250 Human flk
	145	302.6	4.7	3501	2	AAQ40915 Aaq40915 Human flk
	146	302.6	4.7	3501	2	AAQ53503 Aaq53503 Human flk
	147	302.6	4.7	3501	2	AAQ79069 Aaq79069 Human flk
	148	302.6	4.7	3501	2	AAQ81013 Aaq81013 Flk2 rece
	149	302.6	4.7	3501	2	AAT38734 Aat38734 Murine fo
	150	302.6	4.7	3501	2	AAT72117 Aat72117 Human flk
	151	302.6	4.7	3501	2	ADP90722 Adp90722 Human foe
	152	302.6	4.7	3501	2	AAX77515 Aax77515 Human flk
	153	302.6	4.7	3501	6	ABS55045 Abs55045 Human cDN
	154	302.6	4.7	3501	14	ADW87788 Adw87788 Human fet
	155	302.6	4.7	3501	14	AEB46053 Aeb46053 Human flk
	156	302.6	4.7	4225	14	ADZ12551 Adz12551 Human can
	157	299.6	4.7	3270	10	ADE47735 Ade47735 Human NOV
	158	299.6	4.7	3270	12	ADJ79005 Adj79005 Human NOV
	159	299.4	4.7	3120	2	AAQ49756 Aaq49756 pTK gene
	160	299.4	4.7	3120	2	AAT03096 Aat03096 Protein t
	161	295.8	4.6	2958	2	AAV39042 Aav39042 Human rec
	162	293.6	4.6	3521	2	AAT00801 Aat00801 Flk2/flt3
	163	291	4.5	291	2	AAH87564 Aah87564 Human sin
	164	290.8	4.5	2958	2	AAV39040 Aav39040 Human rec
	165	290.8	4.5	2982	2	AAV39039 Aav39039 Human rec
	166	289.2	4.5	3986	13	ADQ39079 Adq39079 Human SNP
	167	289.2	4.5	3993	13	ADQ39080 Adq39080 Human SNP
	168	288.2	4.5	2092	14	ADY52604 Ady52604 Human tra
	169	288.2	4.5	2949	2	AAV39041 Aav39041 Human rec
	170	288	4.5	2919	14	ADV42426 Adv42426 Human psy
	171	288	4.5	2920	11	ADM29261 Adm29261 Human nov
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	175	288	4.5	3985	12	ADQ19494 Adq19494 Human sof
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	177	288	4.5	3985	14	AEB31948 Aeb31948 Macrophag
	178	288	4.5	3992	5	AAS79666 Aas79666 DNA encod
	179	288	4.5	3992	6	ABV94301 Abv94301 Breast ca
	180	288	4.5	3992	6	ABK48105 Abk48105 Human mac
	181	288	4.5	3992	8	ACA89951 Aca89951 Gene diff
	182	288	4.5	3992	10	ADF81619 Adf81619 Leukaemia
	183	288	4.5	3992	11	ADM29259 Adm29259 Human nov
	184	288	4.5	3992	13	ADR83438 Adr83438 Human c-f
	185	288	4.5	4008	6	ABZ35433 Abz35433 Human gen
	186	286.4	4.5	2978	10	ADE95877 Ade95877 Mouse Flt
	187	286.4	4.5	2979	9	ADA02629 Ada02629 Mouse Flt
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	189	286.4	4.5	3426	9	ADA02628 Ada02628 Mouse Flt
	190	286.4	4.5	3426	10	ADB72366 Adb72366 Mouse Flt
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	192	286.4	4.5	3440	6	AAD42483 Aad42483 Murine re
	193	286.4	4.5	3453	2	AAQ35249 Aaq35249 Murine fl
	194	286.4	4.5	3453	2	AAQ40914 Aaq40914 Murine fl
	195	286.4	4.5	3453	2	AAQ53502 Aaq53502 Murine fl
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	198	286.4	4.5	3453	2	AAT38733 Aat38733 Human foe
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	202	286.4	4.5	3453	6	ABS55044 Abs55044 Mouse cDN
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	205	283.2	4.4	3453	2	AAQ29954 Aaq29954 Murine fl
	206	282.4	4.4	2978	2	AAV39038 Aav39038 Human rec
	207	280.8	4.4	2083	14	ADY52605 Ady52605 Human tra
	208	277.4	4.3	1290	11	ADM29267 Adm29267 Human nov
	209	277.4	4.3	1290	11	ADM29269 Adm29269 Human nov
	210	277.4	4.3	1290	11	ADM29263 Adm29263 Human nov
	211	277.4	4.3	1290	11	ADM29265 Adm29265 Human nov
c	212	266.2	4.2	534	12	ACH69819 Ach69819 Human gen
c	213	265.2	4.1	272	12	ACH83519 Ach83519 Human gen
	214	263	4.1	4240	12	ADQ23697 Adq23697 Human sof
	215	260.4	4.1	467	5	ADI72894 Adi72894 Human ova
	216	260.4	4.1	467	5	ADL38033 Adl38033 Human ova
	217	258	4.0	2931	14	ADV44166 Adv44166 Human psy
	218	250.6	3.9	251	2	AAX12370 Aax12370 Human bia
	219	243.6	3.8	1911	6	ABV78161 Abv78161 Human PDG
	220	243.6	3.8	1911	6	ABZ35737 Abz35737 Human PDG
	221	243.6	3.8	1911	6	ABX09980 Abx09980 Human PDG
	222	243.6	3.8	1911	6	ABL91702 Abl91702 Human pol
	223	234	3.6	3685	12	ADH48399 Adh48399 Human KPP
	224	223.2	3.5	4450	3	AAC62210 Aac62210 Nucleotid
	225	221.6	3.5	4113	10	ADC64991 Adc64991 Human VEG
	226	221.6	3.5	4450	8	ABX12554 Abx12554 Human vas
	227	221.6	3.5	4450	11	ADN95353 Adn95353 Human BEC
	228	221.6	3.5	4450	12	ADQ91190 Adq91190 Human cDN
	229	221.6	3.5	4450	13	ADR05212 Adr05212 Human fms
	230	221.6	3.5	4450	14	ADY16408 Ady16408 DNA encod
	231	221.6	3.5	5470	2	AAQ64049 Aaq64049 Sequence
	232	220	3.4	3277	10	ADE54108 Ade54108 Human pro
	233	220	3.4	3897	6	ABV78212 Abv78212 Human Flt
	234	220	3.4	3897	6	ABZ35788 Abz35788 Human Flt
	235	220	3.4	3897	6	ABX10031 Abx10031 Human Flt
	236	220	3.4	3897	6	ABL91753 Abl91753 Human pol
	237	220	3.4	4111	3	AAC62405 Aac62405 Human Flt
	238	220	3.4	4111	4	AAC68952 Aac68952 Human Flt

	239	220	3.4	4195	2	AAT12068 Aat12068 FLT4 rece
	240	220	3.4	4195	2	ADP90835 Adp90835 Human fms
	241	220	3.4	4195	3	AAA37815 Aaa37815 Human Flt
	242	220	3.4	4195	3	AAZ52333 Aaz52333 Human tyr
	243	220	3.4	4195	6	ABS52553 Abs52553 Human Flt
	244	220	3.4	4195	10	ADD08955 Add08955 Human VEG
	245	220	3.4	4195	14	ADZ00447 Adz00447 VEGFR-3 c
	246	220	3.4	4425	2	AAT03090 Aat03090 Protein t
	247	220	3.4	4425	11	ADI31563 Adi31563 Human cDN
	248	220	3.4	4425	13	ADS83630 Ads83630 Human lym
	249	220	3.4	4795	2	ADP90837 Adp90837 Human fms
	250	220	3.4	4795	3	AAA37816 Aaa37816 Human Flt
	251	220	3.4	4795	3	AAZ52334 Aaz52334 Human tyr
	252	220	3.4	4795	6	ABS52554 Abs52554 Human Flt
	253	220	3.4	5363	6	AAD42485 Aad42485 Murine re
	254	220	3.4	5390	10	ACF80603 Acf80603 Murine Fl
	255	220	3.4	5403	14	ADW87790 Adw87790 Murine fe
	256	220	3.4	5404	2	AAT38735 Aat38735 Murine fo
	257	220	3.4	5404	2	AAX77516 Aax77516 Murine fl
	258	220	3.4	5404	14	AEB46055 Aeb46055 Murine fl
	259	220	3.4	5406	2	AAQ29957 Aaq29957 flk-1 cDN
	260	220	3.4	5406	2	AAQ35251 Aaq35251 Human flk
	261	220	3.4	5406	2	AAQ40916 Aaq40916 Murine fl
	262	220	3.4	5406	2	AAQ53504 Aaq53504 Murine fl
	263	220	3.4	5406	2	AAQ79070 Aaq79070 Mouse flk
	264	220	3.4	5406	2	AAQ81014 Aaq81014 Flk1 rece
	265	220	3.4	5406	2	AAT72119 Aat72119 Murine fl
	266	220	3.4	5406	2	ADP90724 Adp90724 Mouse foe
	267	220	3.4	5406	6	ABS55046 Abs55046 Mouse cDN
	268	220	3.4	5470	8	ACC71720 Acc71720 Murine va
c	269	220	3.4	6827	2	AAQ49753 Aaq49753 pTK gene
c	270	220	3.4	6827	2	AAT03101 Aat03101 Protein t
	271	220	3.4	9108	2	AAT03104 Aat03104 Plasmid p
	272	216	3.4	993	12	ADI79353 Adi79353 Colony st
	273	216	3.4	1035	12	ADI79352 Adi79352 Colony st
	274	215.6	3.4	5505	13	ADS17399 Ads17399 Nucleotid
	275	215.6	3.4	5789	10	ADD93315 Add93315 Zebrafish
	276	215	3.4	4017	6	ABV78211 Abv78211 Human Flt
	277	215	3.4	4017	6	ABZ35787 Abz35787 Human Flt
	278	215	3.4	4017	6	ABX10030 Abx10030 Human Flt
	279	215	3.4	4017	6	ABL91752 Abl91752 Human pol
	280	215	3.4	4017	10	ACF80602 Acf80602 Human VEG
	281	215	3.4	4017	14	ADY59382 Ady59382 Human VEG
	282	213.4	3.3	5777	12	ADP07278 Adp07278 Human FLT
	283	213.4	3.3	5777	14	ADZ26558 Adz26558 Human VEG
	284	213.4	3.3	7680	5	AAS70286 Aas70286 DNA encod
	285	213.4	3.3	7680	8	ACC86708 Acc86708 Human vas
	286	213.4	3.3	7680	10	AAD63204 Aad63204 Human DNA
	287	213.4	3.3	7680	10	AAD62805 Aad62805 Human DNA
	288	213.4	3.3	7680	10	ABX08846 Abx08846 Angiogene
	289	213.4	3.3	7680	11	ADN95711 Adn95711 Human BEC
	290	213.4	3.3	7680	11	ADN95934 Adn95934 Human BEC
	291	213.4	3.3	7680	11	ADP88300 Adp88300 Metastati
	292	213.4	3.3	7680	13	ADR24850 Adr24850 Breast ca
	293	213.4	3.3	7680	14	ADY61786 Ady61786 Human gen
	294	213.4	3.3	7718	12	ADL12515 Adl12515 Human ste
	295	213	3.3	1894	2	AAQ54036 Aaq54036 Flk-2ws g
	296	212.4	3.3	2463	13	ADR32353 Adr32353 GST-rat K
	297	212.4	3.3	5693	13	ADR32337 Adr32337 Rat optim
	298	212.4	3.3	5892	10	ADB58183 Adb58183 Toxicity-
	299	204.2	3.2	6055	8	ACC86715 Acc86715 Mouse vas
	300	199.4	3.1	4044	6	ABV78210 Abv78210 Human Flk
	301	199.4	3.1	4044	6	ABZ35786 Abz35786 Human Flk
	302	199.4	3.1	4044	6	ABX10029 Abx10029 Human Flk
	303	199.4	3.1	4044	6	ABL91751 Abl91751 Human pol
	304	199.4	3.1	4071	2	AAV99829 Aav99829 Human rec
	305	199.4	3.1	4071	6	ABV78213 Abv78213 Human KDR
	306	199.4	3.1	4071	6	ABZ35789 Abz35789 Human KDR
	307	199.4	3.1	4071	6	ABX10032 Abx10032 Human KDR
	308	199.4	3.1	4071	6	ABL91754 Abl91754 Human pol
	309	199.4	3.1	4071	10	ACF80601 Acf80601 Human VEG
	310	199.4	3.1	4071	10	AAL56271 Aal56271 Human KDR
	311	199.4	3.1	4225	4	AAF83308 Aaf83308 Human VEG
	312	199.4	3.1	5200	13	ADQ38978 Adq38978 Human SNP
	313	199.4	3.1	5830	8	ACC71713 Acc71713 Human vas
	314	199.4	3.1	5830	10	ADD08953 Add08953 Human VEG
	315	199.4	3.1	5830	10	ADK61446 Adk61446 Ovarian c
	316	199.4	3.1	5830	12	ADJ97234 Adj97234 Human Flk
	317	199.4	3.1	5830	13	ADR46590 Adr46590 Cancer-as
	318	199.4	3.1	5830	13	ADT92352 Adt92352 Human vas
	319	199.4	3.1	5830	14	ADY59384 Ady59384 Human VEG
	320	199.4	3.1	5830	14	ADZ26560 Adz26560 Human VEG
	321	199.4	3.1	5830	14	AEB22583 Aeb22583 Vascular
	322	199.4	3.1	5832	13	ADQ38980 Adq38980 Human SNP
	323	199.4	3.1	5841	10	ADI02728 Adi02728 Human cDN
	324	198.2	3.1	504	6	ABL99491 Abl99491 Target ca
	325	198	3.1	4071	2	AAQ28272 Aaq28272 A novel t
	326	198	3.1	4230	14	ADZ00445 Adz00445 VEGFR-2 c
	327	198	3.1	4236	2	AAV34763 Aav34763 Human KDR
	328	198	3.1	5832	9	ACH03813 Ach03813 Human cDN
	329	193.4	3.0	2085	14	ADW38878 Adw38878 T-cell me
	330	193.4	3.0	2184	6	ABK94963 Abk94963 Human nov
	331	193.4	3.0	2184	12	ADO49090 Ado49090 Human ded
	332	193.4	3.0	2421	6	ABV78202 Abv78202 Human FGF
	333	193.4	3.0	2421	6	ABZ35778 Abz35778 Human FGF
	334	193.4	3.0	2421	6	ABX10021 Abx10021 Human FGF
	335	193.4	3.0	2421	6	ABL91743 Abl91743 Human pol
	336	193.4	3.0	2421	9	ADA02848 Ada02848 Human FGF
	337	193.4	3.0	2421	10	ADB72586 Adb72586 Human FGF
	338	193.4	3.0	2421	10	ADC85327 Adc85327 Human Fgf
	339	193.4	3.0	2421	12	ADM74443 Adm74443 Human car
	340	193.4	3.0	2427	5	AAA54420 Aaa54420 Mutant (N
	341	193.4	3.0	2427	5	AAA54425 Aaa54425 Mutant (P
	342	193.4	3.0	2427	5	AAA54423 Aaa54423 Mutant (G
	343	193.4	3.0	2427	5	AAA54422 Aaa54422 Mutant (G
	344	193.4	3.0	2427	5	AAA54411 Aaa54411 Mutant (S
	345	193.4	3.0	2427	5	AAA54421 Aaa54421 Mutant (G
	346	193.4	3.0	2427	5	AAA54412 Aaa54412 Mutant (Y
	347	193.4	3.0	2427	5	AAA54424 Aaa54424 Mutant (A
	348	193.4	3.0	2427	5	AAA54407 Aaa54407 Mutant (R
	349	193.4	3.0	2427	5	AAA54418 Aaa54418 Mutant (X
	350	193.4	3.0	2427	5	AAA54414 Aaa54414 Mutant (X
	351	193.4	3.0	2427	5	AAA54417 Aaa54417 Mutant (X
	352	193.4	3.0	2427	5	AAA54410 Aaa54410 Mutant (K
	353	193.4	3.0	2427	5	AAA54419 Aaa54419 Mutant (N
	354	193.4	3.0	2427	5	AAA54406 Aaa54406 Fibroblas
	355	193.4	3.0	2427	5	AAA54409 Aaa54409 Mutant (G
	356	193.4	3.0	2427	5	AAA54413 Aaa54413 Mutant (K
	357	193.4	3.0	2427	5	AAA54408 Aaa54408 Mutant (S
	358	193.4	3.0	2427	5	AAA54415 Aaa54415 Mutant (X
	359	193.4	3.0	2427	5	AAA54416 Aaa54416 Mutant (X
	360	193.4	3.0	2427	11	ADK51039 Adk51039 Human NOV
	361	193.4	3.0	2469	13	ADR14979 Adr14979 Rat elect
	362	193.4	3.0	2469	13	ADV41310 Adv41310 Rat cardi
	363	193.4	3.0	2490	11	ADK51037 Adk51037 Human NOV
	364	193.4	3.0	2520	8	AAD55411 Aad55411 Human FGF
	365	193.4	3.0	2520	14	ADV73163 Adv73163 Human col
	366	193.4	3.0	3391	14	ADZ12668 Adz12668 Human can
	367	193.4	3.0	3727	14	ADZ12674 Adz12674 Human can
	368	193.4	3.0	3733	14	ADZ12678 Adz12678 Human can
	369	193.4	3.0	3757	13	ACF91644 Acf91644 Human SIR
	370	193.4	3.0	3767	14	ADZ12682 Adz12682 Human can
	371	193.4	3.0	3837	14	ADZ12680 Adz12680 Human can
	372	193.4	3.0	4093	9	ADA02847 Ada02847 Human FGF
	373	193.4	3.0	4093	10	ADB72585 Adb72585 Human FGF
	374	193.4	3.0	4093	10	ADC85326 Adc85326 Human Fgf
	375	193.4	3.0	4093	12	ADM74442 Adm74442 Human car
	376	193.4	3.0	4093	13	ADR44003 Adr44003 Human bre
	377	193.4	3.0	4093	13	ACF91643 Acf91643 Human SIR
	378	193.4	3.0	4093	14	AEB29665 Aeb29665 Human fib
	379	193.4	3.0	4103	14	ADZ12684 Adz12684 Human can
	380	193.4	3.0	4118	12	ADQ23177 Adq23177 Human sof
	381	193.4	3.0	4173	14	ADZ12672 Adz12672 Human can
	382	193.4	3.0	5993	5	AAD34801 Aad34801 Human fib
	383	192	3.0	5050	13	ADQ38979 Adq38979 Human SNP
	384	191.8	3.0	3829	6	ABL68525 Abl68525 Kidney ca

385	191.8	3.0	3829	6	ABQ88193	Abq88193 Human ost
386	191.8	3.0	3829	8	AAD55418	Aad55418 Human FGF
387	191.8	3.0	4106	13	ACN42510	Acn42510 Human dia
388	185	2.9	2049	5	AAD21622	Aad21622 Sheep fib
389	184.4	2.9	933	2	AAV26249	Aav26249 Protein t
390	184.4	2.9	1056	2	AAV26250	Aav26250 Fibroblas
391	184.4	2.9	2202	10	ADL13668	Adl13668 Osteoarth
392	184.4	2.9	2360	11	ADI31962	Adi31962 Human cDN
393	184.4	2.9	2360	13	ADS84029	Ads84029 Human lym
394	184.4	2.9	2463	13	ADS18124	Ads18124 Human fib
395	184.4	2.9	2463	13	ADS18121	Ads18121 Human FGF
396	184.4	2.9	2463	13	ADS18123	Ads18123 Human FGF
397	184.4	2.9	2469	2	AAQ13311	Aaq13311 Basic FGF
398	184.4	2.9	2469	6	ABV78187	Abv78187 Human FGF
399	184.4	2.9	2469	6	ABZ35763	Abz35763 Human FGF
400	184.4	2.9	2469	6	ABX10006	Abx10006 Human FGF
401	184.4	2.9	2469	6	ABL91728	Abl91728 Human pol
402	184.4	2.9	2469	13	ADS18135	Ads18135 Human FGF
403	184.4	2.9	2469	13	ADS18136	Ads18136 Human FGF
404	184.4	2.9	2470	12	ADO42156	Ado42156 Human NOV
405	184.4	2.9	2662	2	AAQ21003	Aaq21003 flg recep
406	184.4	2.9	2662	8	AAD52780	Aad52780 Human FGF
407	184.4	2.9	2662	13	ADS18134	Ads18134 Human FGF
408	184.4	2.9	2731	12	ADO42158	Ado42158 Human NOV
409	184.4	2.9	2733	2	AAT31051	Aat31051 Human fib
410	184.4	2.9	2733	10	ACC42967	Acc42967 Human Fib
411	184.4	2.9	2737	12	ADO42154	Ado42154 Human NOV
412	184.4	2.9	2771	13	ACN41762	Acn41762 Human dia
413	184.4	2.9	2855	13	ACN41761	Acn41761 Human dia
414	184.4	2.9	2856	2	AAQ10448	Aaq10448 Human bas
415	184.4	2.9	2858	13	ACN41760	Acn41760 Human dia
416	184.4	2.9	3313	2	AAX87177	Aax87177 ZNF198-FG
417	184.4	2.9	3328	2	AAQ20914	Aaq20914 Human bFG
418	184.4	2.9	3328	6	ABZ35187	Abz35187 Human gen
419	184.4	2.9	3328	10	ADE84879	Ade84879 Farnesyl
420	184.4	2.9	3343	2	AAX87179	Aax87179 Fibroblas
421	184.4	2.9	3343	11	ADP65617	Adp65617 Human fib
422	184.4	2.9	3343	11	ADP65619	Adp65619 Human fib
423	184.4	2.9	3343	12	ADO49086	Ado49086 Human ded
424	184.4	2.9	3343	13	ADS18133	Ads18133 Human FGF
425	184.4	2.9	3365	10	ADL13667	Adl13667 Osteoarth
426	184.4	2.9	3449	14	ADZ12918	Adz12918 Human can
427	184.4	2.9	3454	8	ABX63048	Abx63048 Human cDN
428	184.4	2.9	3459	14	ADZ12916	Adz12916 Human can
429	184.4	2.9	3481	13	ACN41759	Acn41759 Human dia
430	184.4	2.9	3525	2	AAQ27658	Aaq27658 N-sam cDN
431	184.4	2.9	3722	14	ADZ12912	Adz12912 Human can
432	184.4	2.9	3726	3	AAF18252	Aaf18252 Lung canc
433	184.4	2.9	3782	13	ACF91623	Acf91623 Human SIR
434	184.4	2.9	3786	13	ACF91624	Acf91624 Human SIR
435	184.4	2.9	3981	11	ADP65620	Adp65620 Human N-s
436	184.4	2.9	3981	11	ADP65618	Adp65618 Human N-s
437	184.4	2.9	3981	12	ADQ17657	Adq17657 Human sof
438	184.4	2.9	4043	13	ACF91622	Acf91622 Human SIR
439	184.4	2.9	4049	11	ADP65062	Adp65062 Human fib
440	184.4	2.9	4049	11	ADP65063	Adp65063 Human fib
441	184.4	2.9	4049	13	ACF91621	Acf91621 Human SIR
442	184.4	2.9	4049	14	ADY16515	Ady16515 DNA encod
443	184.4	2.9	4444	12	ADQ22324	Adq22324 Human sof
444	184.4	2.9	5438	12	ADQ23077	Adq23077 Human sof
445	182.2	2.8	2526	6	ABA01689	Aba01689 Mouse fib
446	182.2	2.8	3203	14	ADZ12905	Adz12905 Murine ca
447	182.2	2.8	3573	14	ADZ12903	Adz12903 Murine ca
448	180.4	2.8	1875	2	AAV19075	Aav19075 Truncated
449	180.4	2.8	1875	2	AAX85613	Aax85613 Truncated
450	180.2	2.8	2403	9	ADA02845	Ada02845 Mouse Fgf
451	180.2	2.8	2403	10	ADB72583	Adb72583 Mouse Fgf
452	180.2	2.8	2403	10	ADC85324	Adc85324 Mouse Fgf
453	180.2	2.8	2403	12	ADM74440	Adm74440 Murine ca
454	180.2	2.8	2887	9	ADA02844	Ada02844 Mouse Fgf
455	180.2	2.8	2887	10	ADB72582	Adb72582 Mouse Fgf
456	180.2	2.8	2887	10	ADC85323	Adc85323 Mouse Fgf
457	180.2	2.8	2887	12	ADM74439	Adm74439 Murine ca
458	178.6	2.8	1038	12	ADO60027	Ado60027 CRH signa
459	178.6	2.8	1038	12	ADO44547	Ado44547 Fibroblas
460	178.6	2.8	1978	11	ACN44601	Acn44601 Mouse mRN
461	178.6	2.8	2345	2	AAQ14049	Aaq14049 Human ect
462	178.6	2.8	2345	2	AAQ10868	Aaq10868 KGF recep
463	178.6	2.8	3104	14	ADZ13041	Adz13041 Murine ca
464	178.6	2.8	3306	10	ADH63056	Adh63056 Murine fi
465	178.6	2.8	3836	14	ADZ12663	Adz12663 Murine ca
466	178.6	2.8	4206	14	ADZ12665	Adz12665 Murine ca
467	177.4	2.8	3503	2	AAV44041	Aav44041 Mouse bFG
468	176	2.7	1739	2	AAQ27539	Aaq27539 Tyrosine
469	176	2.7	2409	6	ABV78188	Abv78188 Human FGF
470	176	2.7	2409	6	ABZ35764	Abz35764 Human FGF
471	176	2.7	2409	6	ABX10007	Abx10007 Human FGF
472	176	2.7	2409	6	ABL91729	Abl91729 Human pol
473	176	2.7	2418	14	ADX44440	Adx44440 Human col
474	176	2.7	2418	14	ADY39351	Ady39351 Human col
475	176	2.7	2479	13	ADU83385	Adu83385 Human rec
476	176	2.7	2895	10	ACC72775	Acc72775 Human can
477	176	2.7	2895	13	ACN38368	Acn38368 Tumour-as
478	176	2.7	2895	13	ACF91646	Acf91646 Human SIR
479	176	2.7	2915	10	ADE38382	Ade38382 Human pro
480	176	2.7	3015	6	ABV94047	Abv94047 Breast ca
481	176	2.7	3015	10	ACC72774	Acc72774 Human can
482	176	2.7	3015	12	ADO49092	Ado49092 Human ded
483	176	2.7	3015	12	ADQ84136	Adq84136 Human tum
484	176	2.7	3015	13	ADQ84946	Adq84946 Human tum
485	176	2.7	3015	13	ACN38367	Acn38367 Tumour-as
486	176	2.7	3015	13	ACF91645	Acf91645 Human SIR
487	176	2.7	3015	14	ADY28147	Ady28147 Receptor
488	175.2	2.7	478	10	ADK11795	Adk11795 Breast ca
489	174.4	2.7	2383	12	ADL57064	Adl57064 Human NOV
490	174.4	2.7	2383	12	ADL57076	Adl57076 Human NOV
491	174.4	2.7	2383	12	ADL57086	Adl57086 Human NOV
492	174.4	2.7	2383	12	ADL57084	Adl57084 Human NOV
493	174.4	2.7	2383	12	ADL57090	Adl57090 Human NOV
494	174.4	2.7	2383	12	ADL57088	Adl57088 Human NOV
495	174.4	2.7	2383	12	ADL57058	Adl57058 Human NOV
496	174.4	2.7	2383	12	ADL57068	Adl57068 Human NOV
497	174.4	2.7	2383	12	ADL57080	Adl57080 Human NOV
498	174.4	2.7	2383	12	ADL57082	Adl57082 Human NOV
499	174.4	2.7	2383	12	ADL57056	Adl57056 Human NOV
500	174.4	2.7	2383	12	ADL57066	Adl57066 Human NOV

ALIGNMENTS

```
RESULT 1
AAQ05989
ID   AAQ05989 standard; cDNA; 6412 BP.
XX
AC   AAQ05989;
XX
DT   25-MAR-2003  (revised)
DT   16-JAN-1991  (first entry)
XX
DE   TR4 cDNA clone related to T11 gene encoding alpha type PDGF rceptor.
XX
KW   Platelet derived growth factor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             139. .3408
FT                   /*tag=  a
FT   sig_peptide     139. .207
FT                   /*tag=  b
FT   mat_peptide     208. .3405
FT                   /*tag=  c
FT                   /product= "T11 receptor"
FT   exon            2701. .2812
FT                   /*tag=  d
```

```
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FT                      /*tag=  e
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FT   exon               2913. .3018
FT                      /*tag=  f
FT                      /label= exon c
FT   polyA_signal       6353. .6358
FT                      /*tag=  g
FT   polyA_site         6376. .6412
FT                      /*tag=  h
XX
PN   WO9010013-A.
XX
PD   07-SEP-1990.
XX
PF   09-FEB-1989;   89US-00308282.
XX
PR   09-FEB-1989;   89US-00308282.
XX
PA   (USDC ) US SEC OF COMMERCE.
PA   (USSH ) US NAT CANCER INST.
XX
PI   Matsui T,  Aaronson SA,  Pierce J;
XX
DR   WPI; 1990-290306/38.
DR   P-PSDB; AAR06910.
XX
PT   Type alpha platelet-derived growth factor receptor gene - useful for
PT   transforming cells to express novel protein receptor and also susceptible
PT   to genetic engineering.
XX
PS   Claim 3; Fig 3; 64pp; English.
XX
CC   The TR4 clone is the largest cDNA clone related to the T11 genomic clone,
CC   isolated from a library prepd. from human thymus DNA. The T4 cDNA clone
CC   was isolated from a M426 human embryo fibroblast cDNA library. The exons
CC   shown were determined from the T11 genomic clone. The gene has bee mapped
CC   to chromosome 4 at location q 11-12, which is within the same region as
CC   the c-kit proto-oncogene. The coding region can be introduced into the
CC   pSV2 gpt vector with a simian sarcoma virus LTR as a promoter and
CC   expressed in a host. The resulting protein is a novel PDGF receptor
CC   designated type alpha (the known receptor is designated type beta). The
CC   cDNA can be used also be used to investigate the mechanisms of PDGF
CC   regulatory processes or in bioassays for detect- ing related genes,
CC   particularly for identification of classes of tumour cells or of genetic
CC   defects in connective tissue and/or healing response. (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 6412 BP; 1885 A; 1299 C; 1443 G; 1785 T; 0 U; 0 Other;

  Query Match            99.6%;  Score 6385;  DB 2;  Length 6412;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 6402;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 60

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATGGGAG 120

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Db        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Db        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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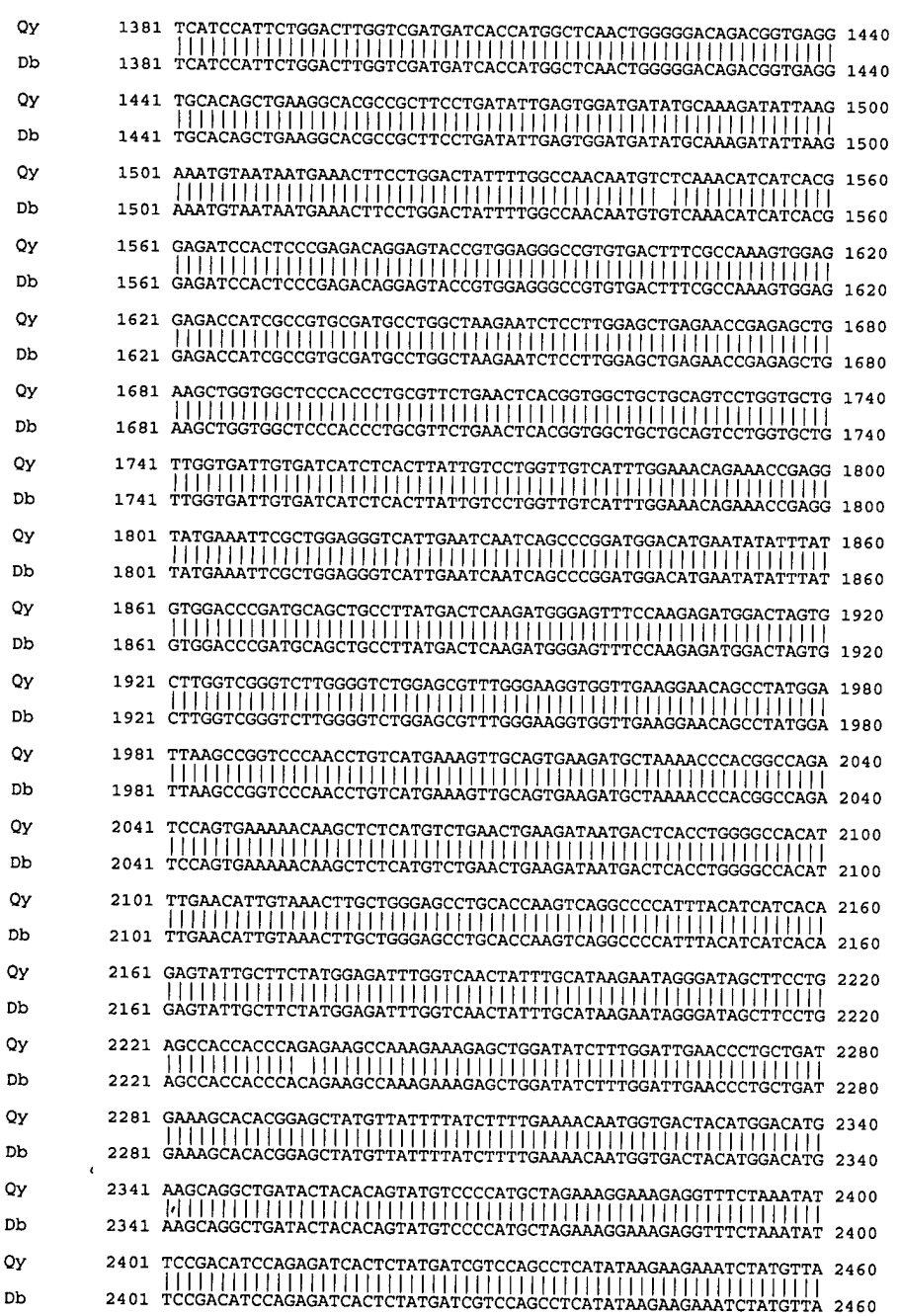
Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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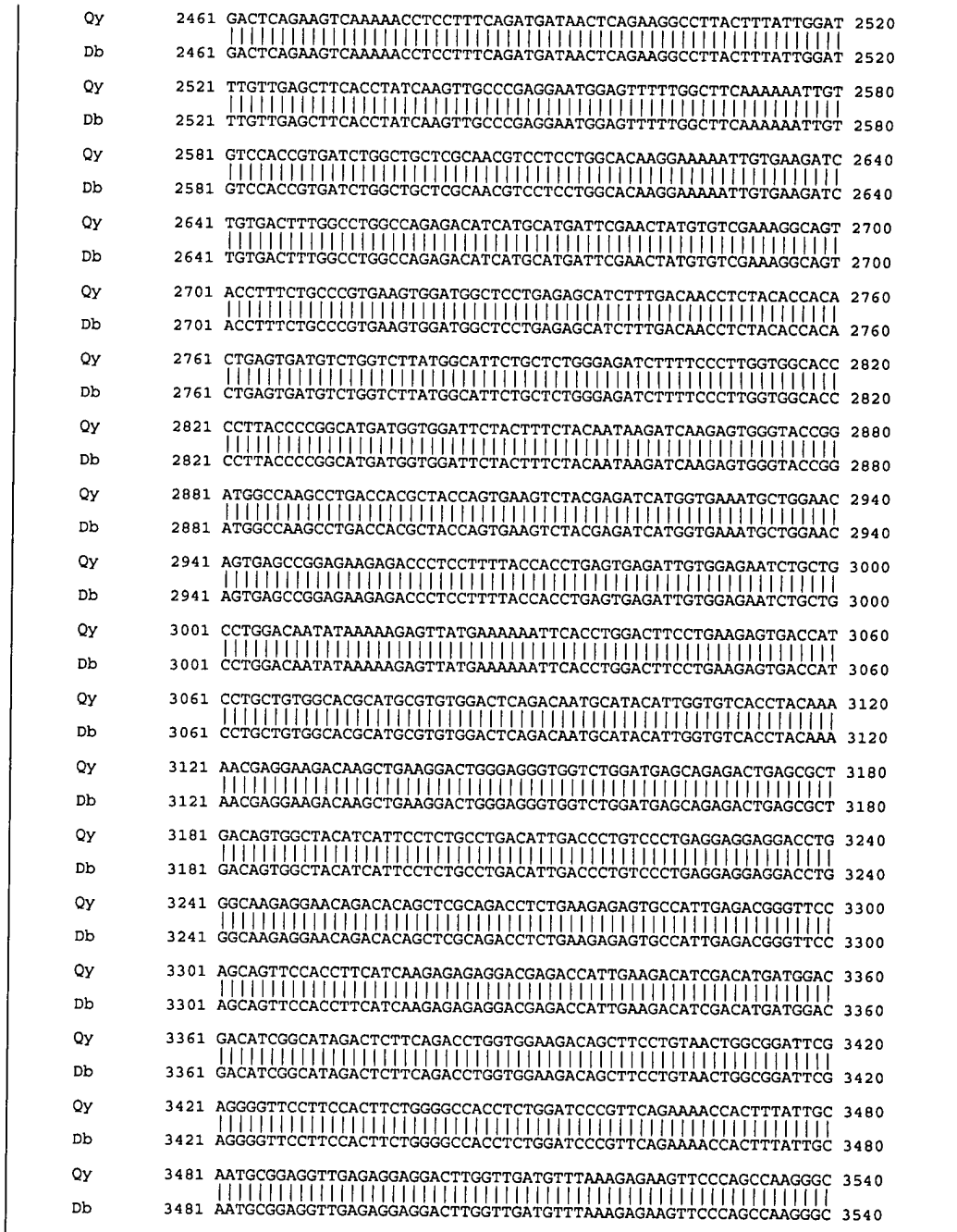
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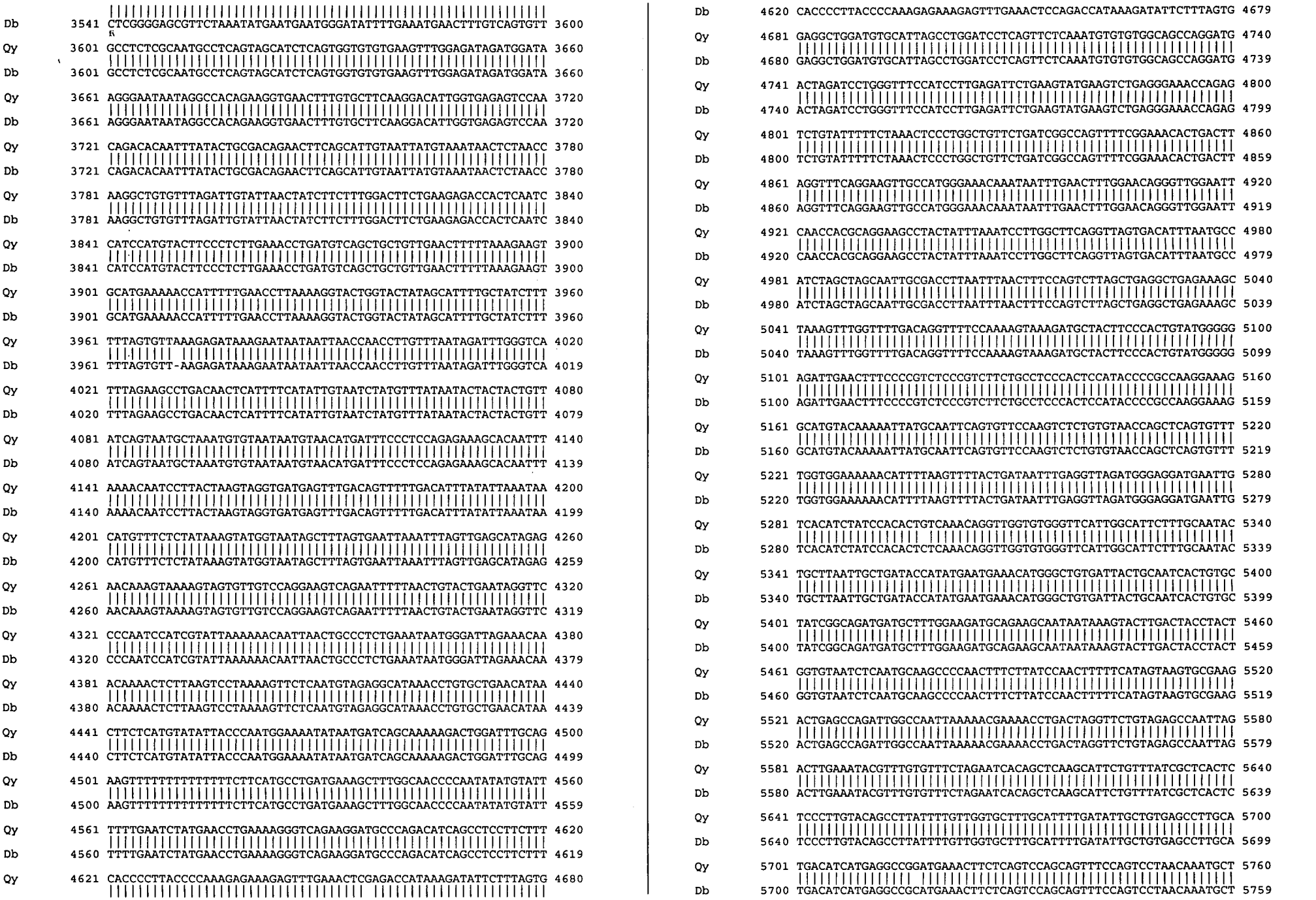
Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Db       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6060 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6119

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Qy       6361 GATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6413
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Db       6360 GATATATAATTTAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6412
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RESULT 2
ADL63502
ID ADL63502 standard; DNA; 6428 BP.
XX
AC ADL63502;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human ovarian cancer DNA marker #21714.
XX
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
XX
OS Homo sapiens.
XX
PN WO200170979-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009126.
XX
PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Lee J, Lillie J;
XX
DR WPI; 2001-611502/70.
XX
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
PS Disclosure; SEQ ID NO 21714; 106pp; English.
XX
CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 6428 BP; 1871 A; 1303 C; 1460 G; 1792 T; 0 U; 2 Other;

Query Match 99.4%; Score 6373.2; DB 5; Length 6428;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6386; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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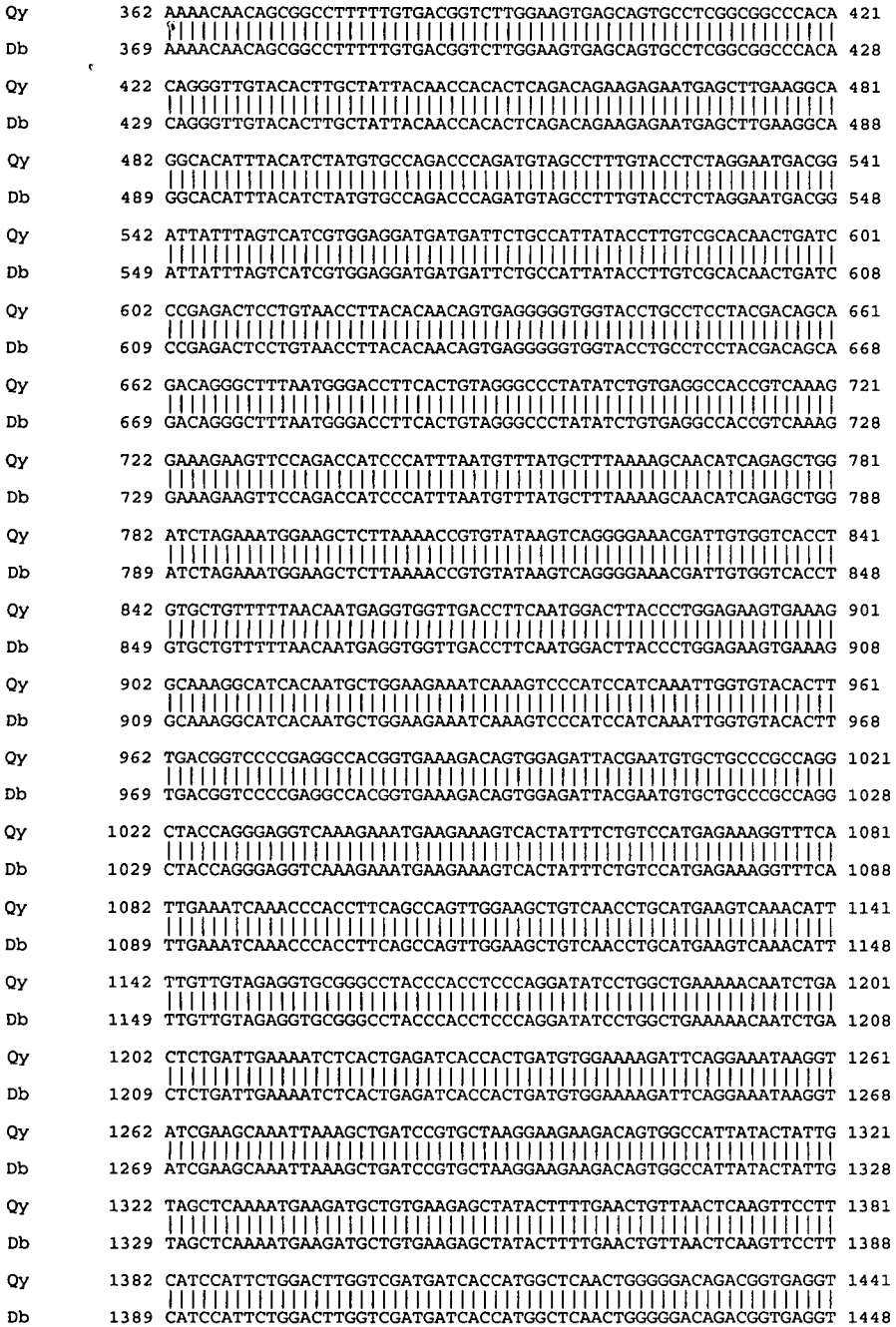
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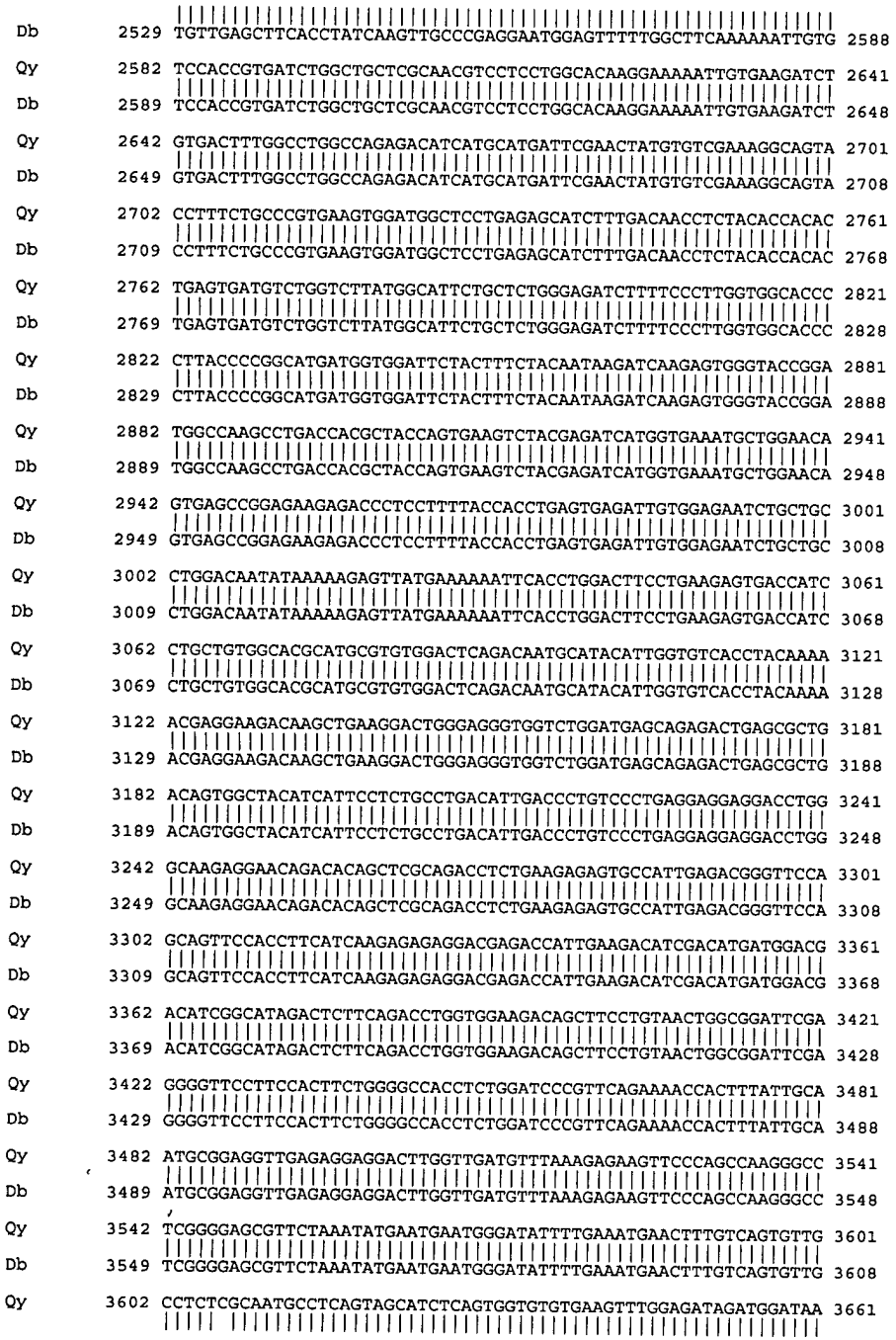
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Db       5708 GACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTC 5767

Qy       5762 CCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAG 5821
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5768 CCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAG 5827

Qy       5822 ATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTAC 5881
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Qy       5882 TTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAA 5941
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Db       5888 TTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAA 5947

Qy       5942 ACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTG 6001
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5948 ACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTG 6007

Qy       6002 TGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATA 6061
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6008 TGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATA 6067

Qy       6062 TAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATA 6121
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Db       6068 TAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATA 6127

Qy       6122 TTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAA 6181
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Qy       6182 ATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTG 6241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6242 GTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATG 6301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6248 GTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATG 6307

Qy       6302 CCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATG 6361
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Db       6308 CCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATG 6367

Qy       6362 ATATATAATTTAAAGTTAAAAAAAAAAAAA 6391
             ||||||||||||||||||||||||||||||
Db       6368 ATATATAATTTAAAGTTAAAAAAAAAAAA 6397
```

RESULT 3
ABK35520
ID ABK35520 standard; DNA; 6378 BP.
XX
AC ABK35520;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human endometrial cancer related gene, PDGFRA.
XX
KW Human; ds; gene; endometrial cancer; differential expression;
KW DNA microarray; protein microarray.
XX
OS Homo sapiens.
XX
PN WO200209573-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US024104.
XX
PR 31-JUL-2000; 2000US-0221735P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI; 2002-179967/23.
DR P-PSDB; AAU84300.
XX
PT Diagnosing endometrial cancer comprises determining expression of nucleic
PT acid molecules or expression products that are differentially expressed

PT in normal and malignant endometrium.
XX
PS Claim 1; Page 109-113; 233pp; English.
XX
CC The invention relates to diagnosing endometrial cancer in a subject
CC suspected of having endometrial cancer comprising determining the
CC expression of a set of nucleic acid molecules or expression products in
CC an endometrial sample suspected of being cancerous, where the set of
CC nucleic acid molecules comprises at least 2 nucleic acid molecules
CC selected from 50 fully defined sequences as given in the specification.
CC The nucleic acids are used as an array of at least 2 of the 50 nucleic
CC acids bound to a solid substrate. Also included is a solid-phase protein
CC microarray comprising at least 2 antibodies or its antigen binding
CC fragments, that specifically bind at least 2 different polypeptides from
CC the 50 fully defined sequences as given in the specification, fixed to a
CC solid substrate. The methods and arrays are useful for the diagnosis of
CC endometrial cancer, selecting and monitoring treatment regimes and
CC identification of lead compounds useful for the treatment of endometrial
CC cancer. The present sequence is one of 50 genes differentially expressed
CC between cancerous and non-cancerous samples
XX
SQ Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

Query Match 99.2%; Score 6364.4; DB 6; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Db       1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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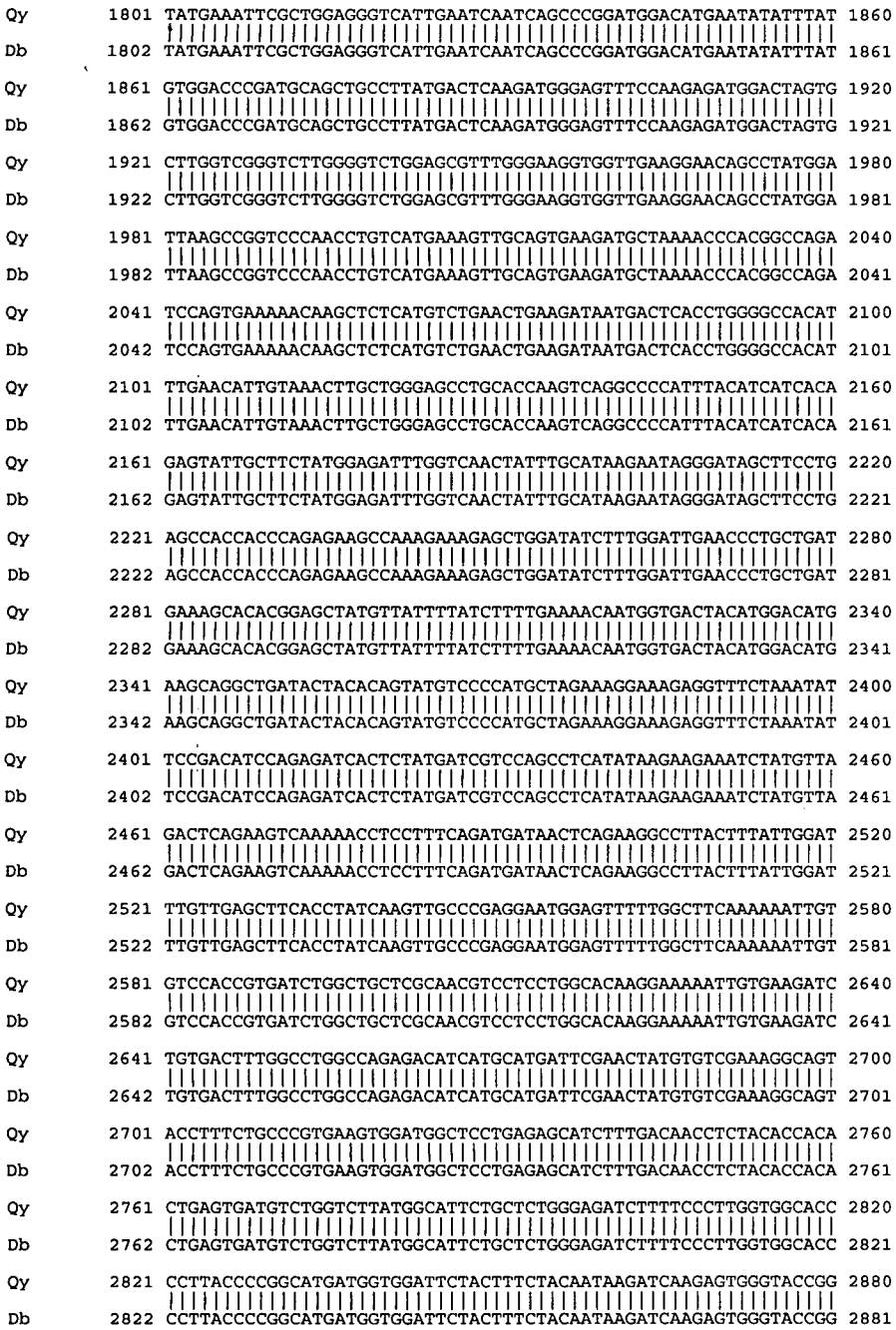
Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561

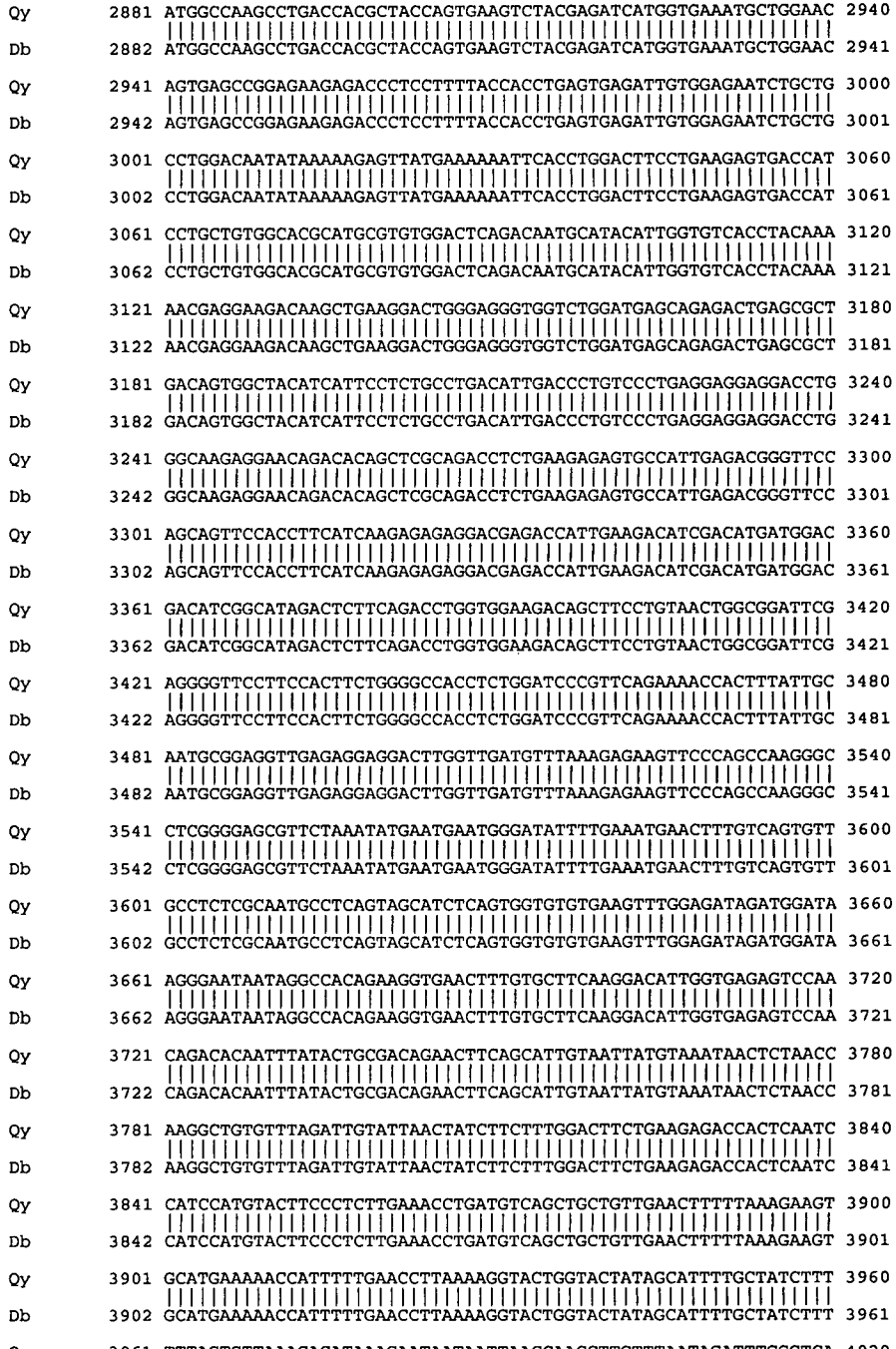
Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621

Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
```


Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1860
Db 1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1861
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041
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Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
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Db 2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Db 2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Db 2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
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Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy       6361 GATATATAATTTAAAGTT 6378
              ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 4
ABL68519
ID ABL68519 standard; DNA; 6378 BP.
XX
AC ABL68519;
XX
DT 15-MAY-2002 (first entry)
XX
DE Kidney cancer related gene sequence SEQ ID NO:6856.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
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XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 6856; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

Query Match 99.2%; Score 6364.4; DB 6; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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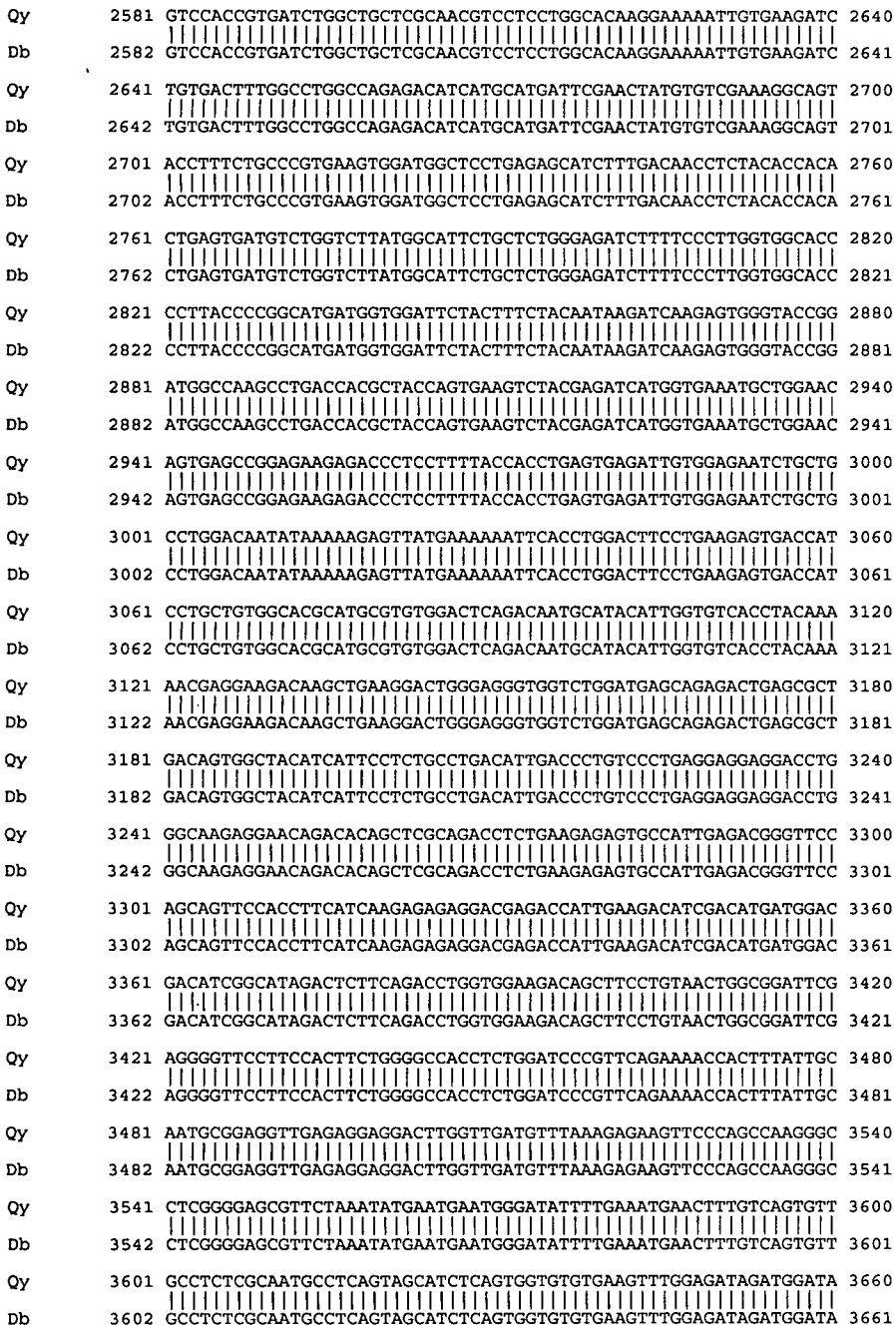
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421
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Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481
Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541
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Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201
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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Qy       2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
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AC ABL62372;
XX
DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:709.
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KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
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PN WO200194629-A2.
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XX
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XX
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XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 709; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

Query Match 99.2%; Score 6364.4; DB 6; Length 6378;
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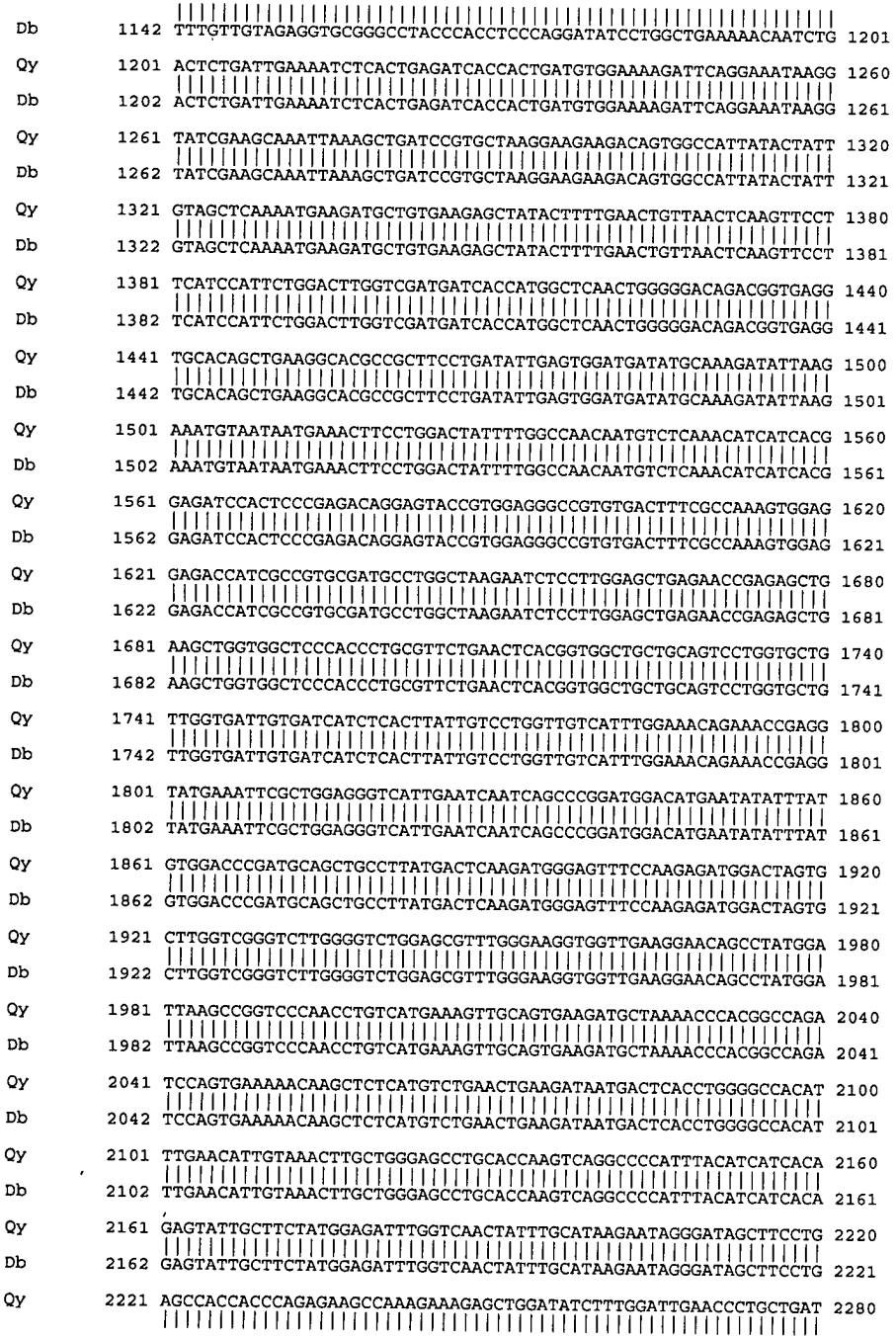
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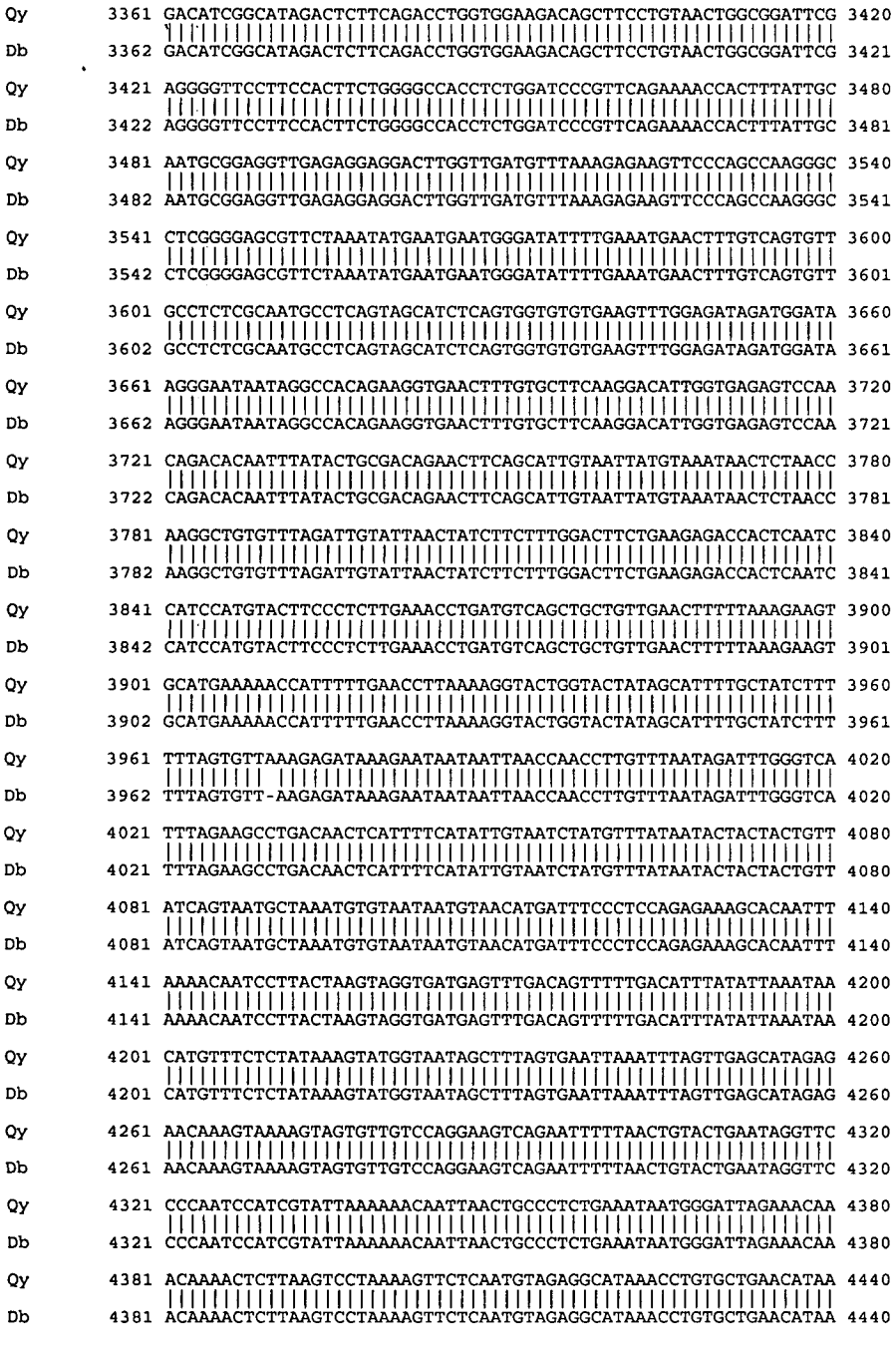
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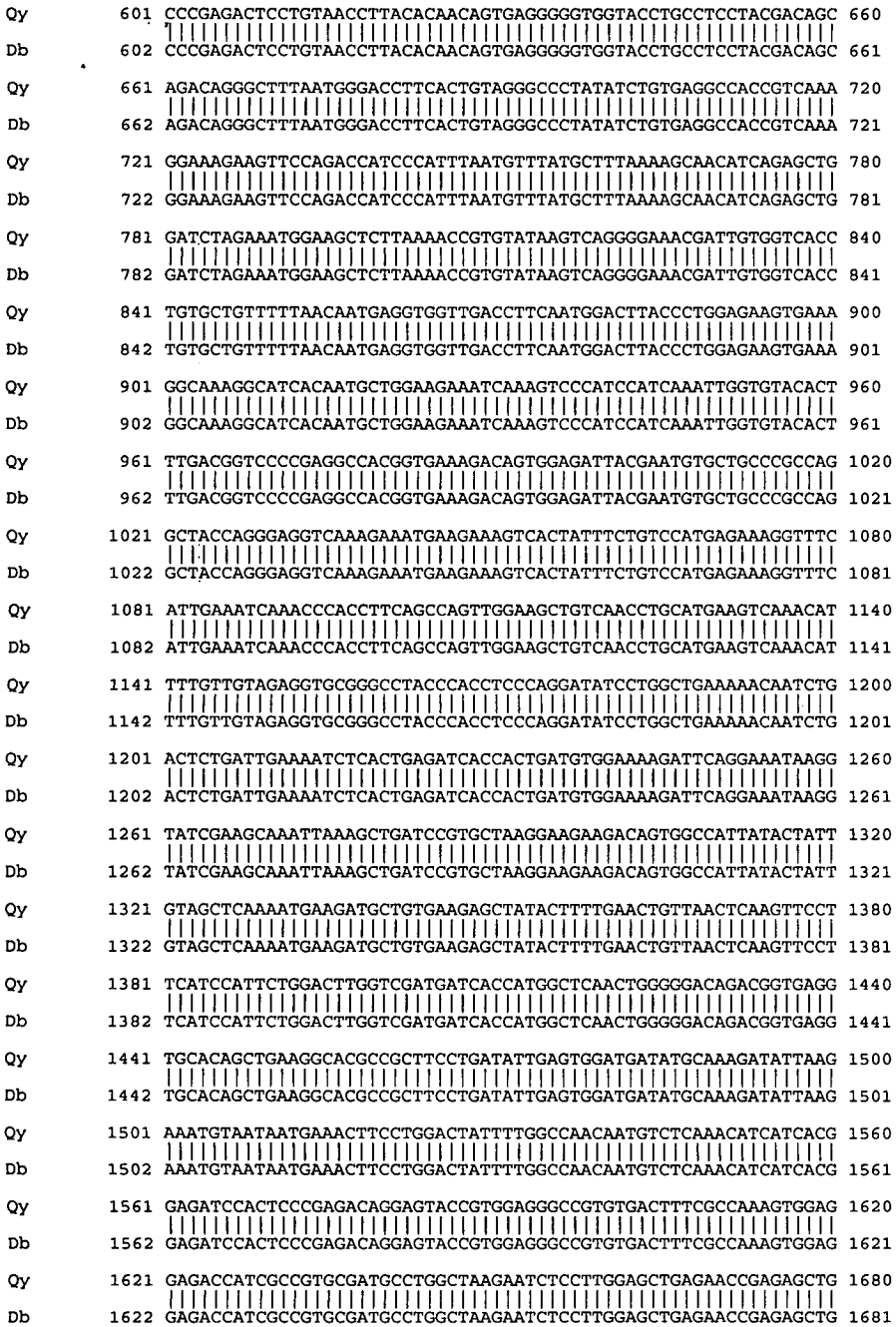
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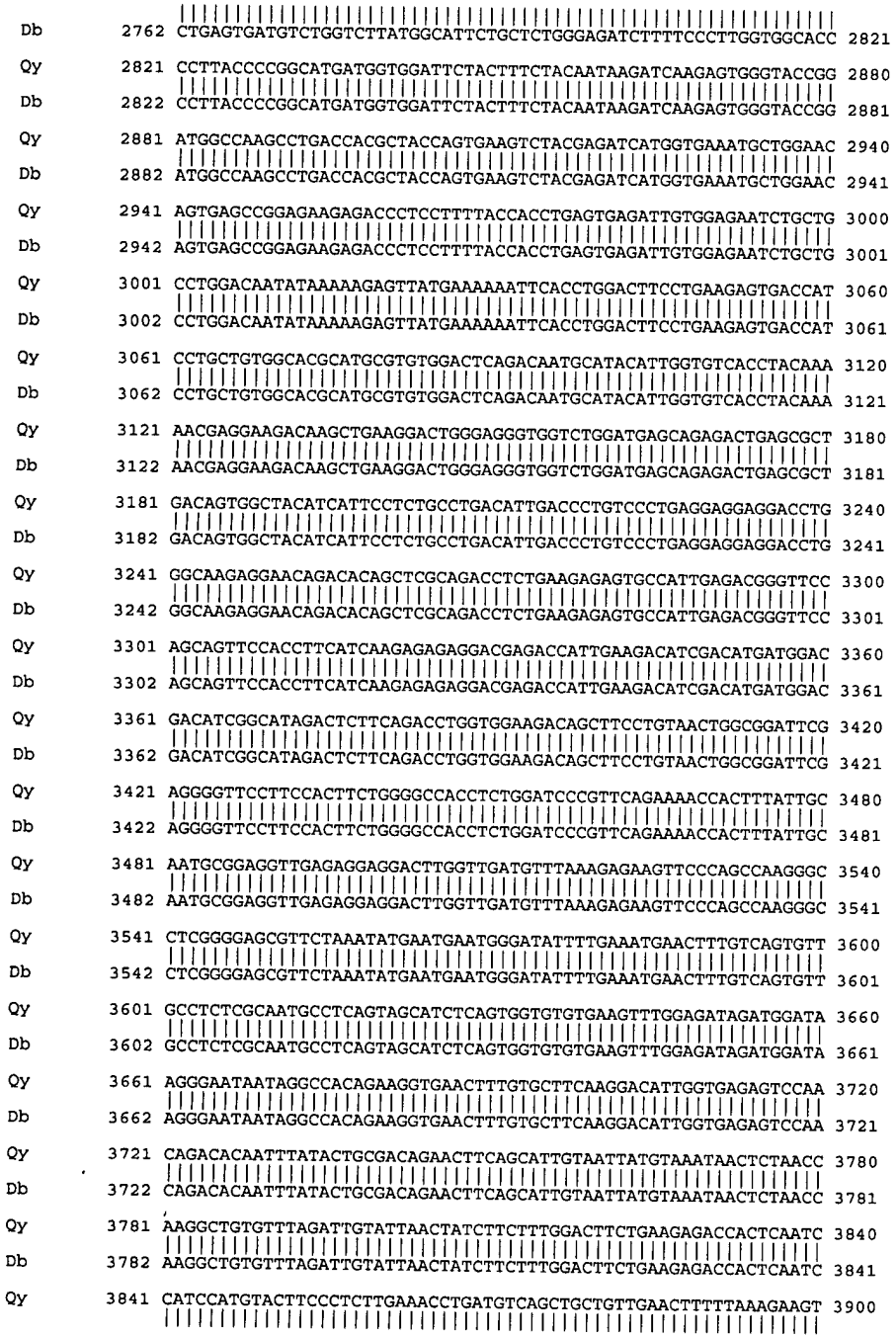
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Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Db 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Qy 4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
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Qy 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Qy 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Qy 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Qy 4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db 4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Qy 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Qy 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Qy 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Qy 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Qy 4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Db 4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Db       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 7
ADI31868
ID ADI31868 standard; cDNA; 6378 BP.
XX
AC ADI31868;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #1194.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 1194; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes

CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

Query Match 99.2%; Score 6364.4; DB 11; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Db       1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561

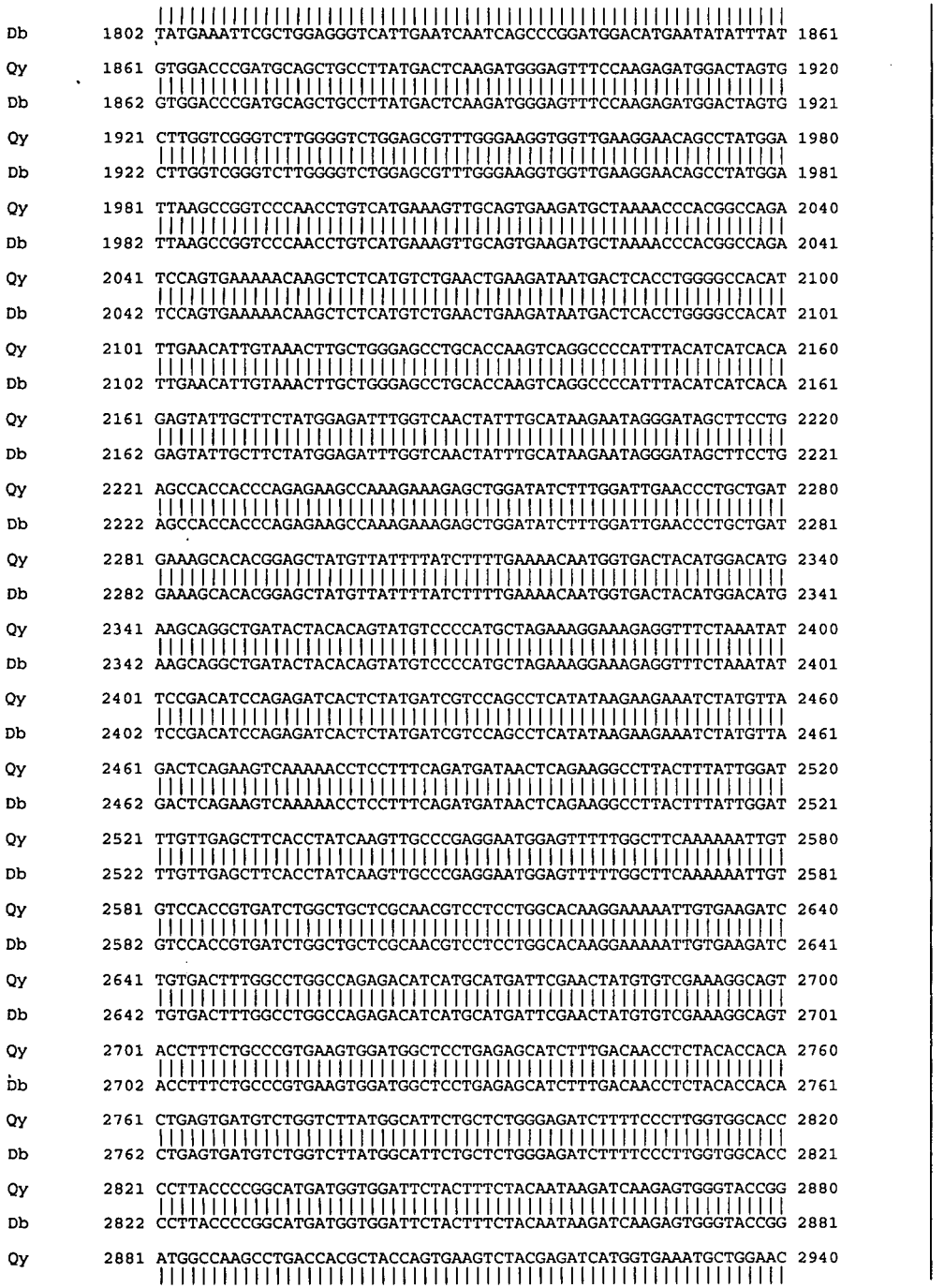
Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621

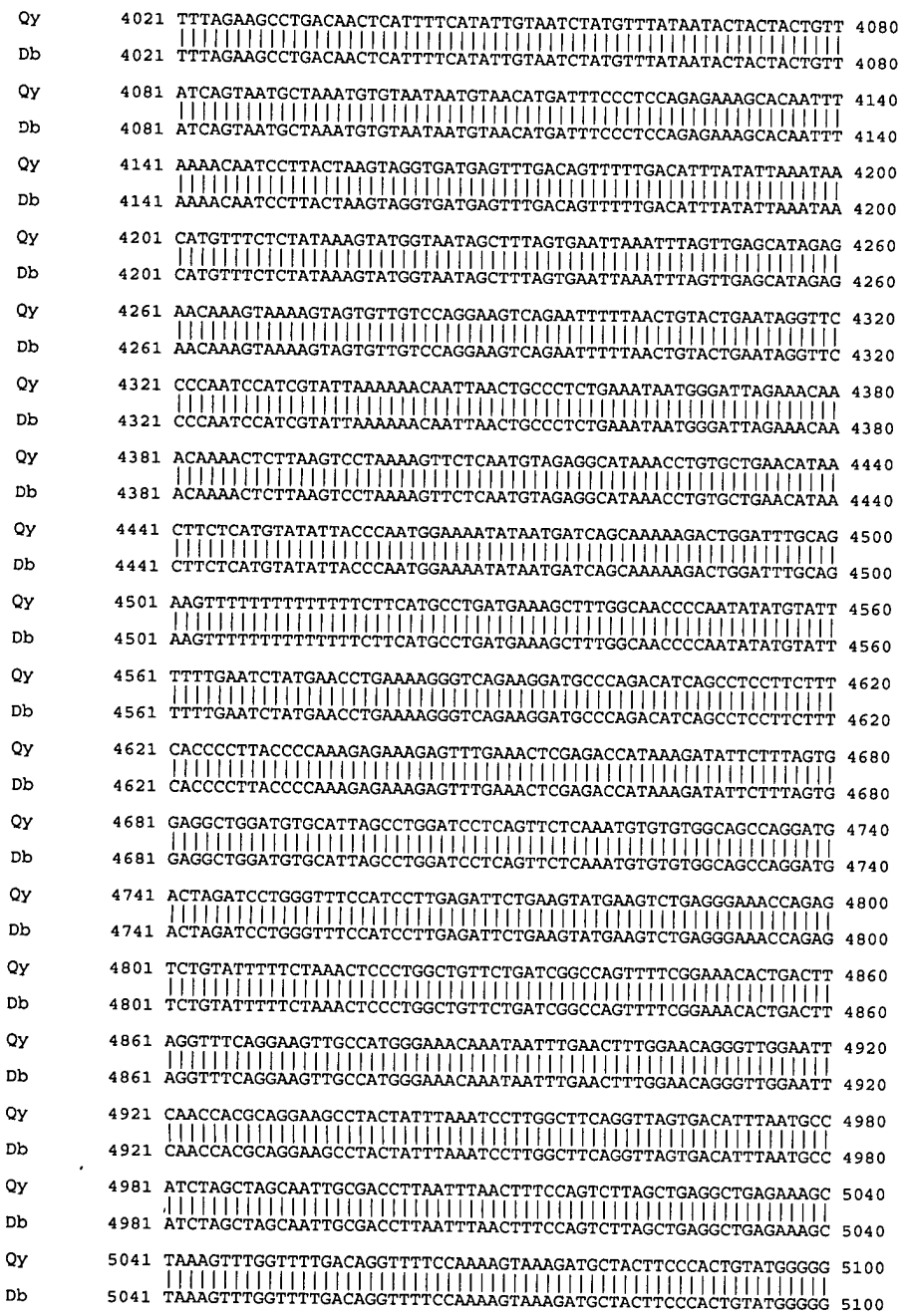
Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801

Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1860
```


Db 1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
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Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db 2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db 2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db 2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db 2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db 2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001
Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
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Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020


Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
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Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Qy 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Qy 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Db 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Qy 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Qy 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Qy 4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Qy 5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Db 5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Qy 5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy 5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Db 5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Qy 5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Db 5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Qy 5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Db 5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Qy 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Qy 6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db 6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
Qy 6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
Db 6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
Qy 6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
                 ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378


RESULT 8
ADQ17832
ID   ADQ17832 standard; DNA; 6378 BP.
XX
AC   ADQ17832;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 649.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 649; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   DNA of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 6364.4;  DB 12;  Length 6378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

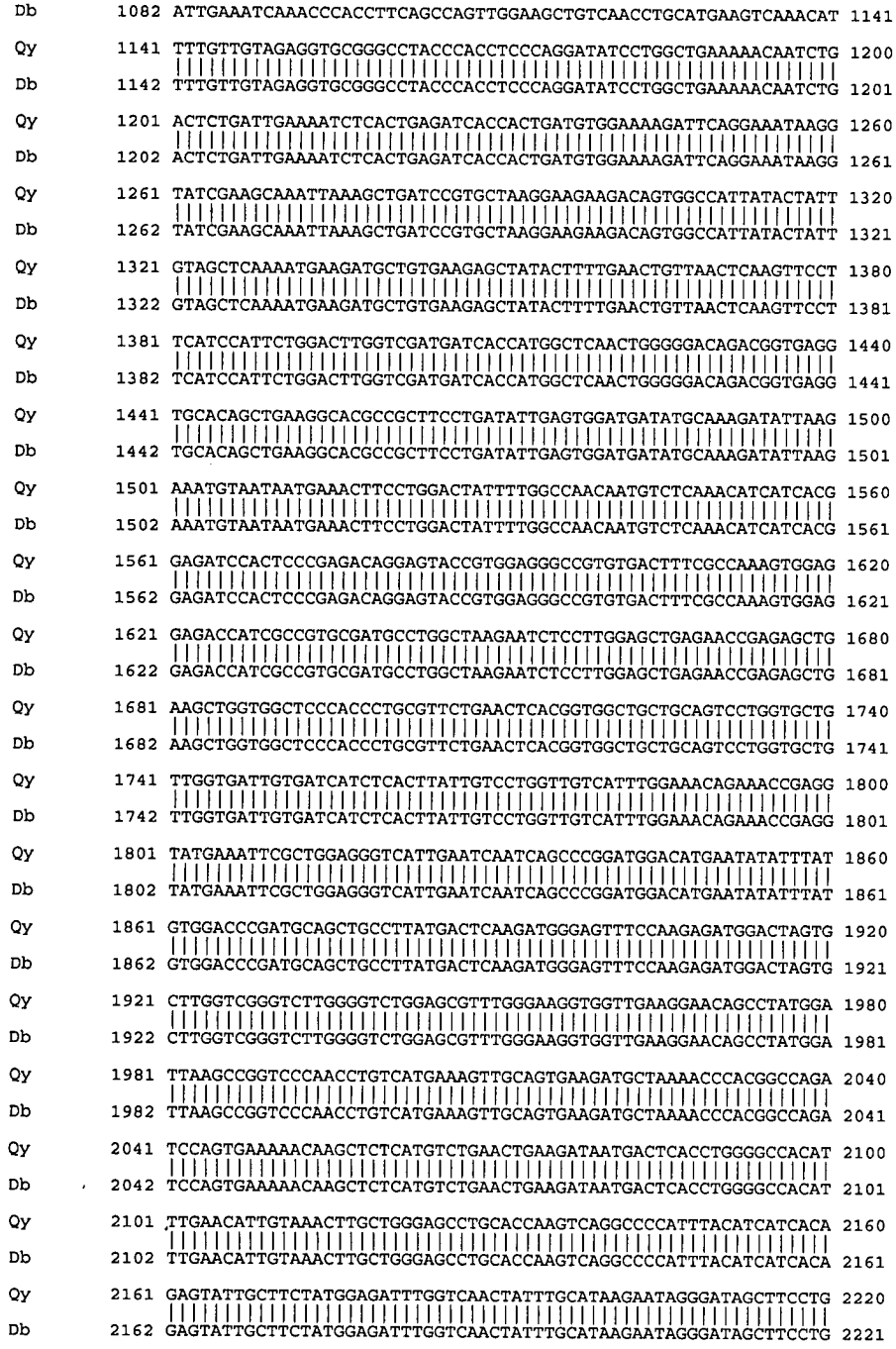
Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141
Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
Db 1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201
Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db 1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261
Qy 1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db 1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db 1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db 1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441
Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db 1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501
Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db 1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561
Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db 1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621
Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db 1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681
Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
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Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
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Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
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Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
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Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
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Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
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Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301

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Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
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Db      3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361

Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db      3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Db      3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541

Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661

Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721

Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781

Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841

Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
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Db      3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901

Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
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Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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Db      3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020

Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
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Db      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080

Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140

Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200

Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260

Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
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Db      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320

Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380

Qy      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440

Qy      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500

Qy      4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560

Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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Db      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620

Qy      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680

Qy      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
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Db      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Db      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

Qy      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Db      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860

Qy      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Db      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920

Qy      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Db      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Db      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160

Qy      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Db      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Db      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280

Qy      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Db      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340

Qy      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy      5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db      5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy      5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             |||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
```

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RESULT 9
ADS83935
ID   ADS83935 standard; cDNA; 6378 BP.
XX
AC   ADS83935;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Human lymph node cDNA #1194.
XX
KW   ss; gene; human; immunological response; blood cell; cancer;
KW   immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW   bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW   osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
OS   Homo sapiens.
XX
PN   US2004077003-A1.
XX
PD   22-APR-2004.
XX
PF   14-AUG-2003; 2003US-00641643.
XX
PR   09-FEB-1998;   98US-00023655.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Cocks BG,  Stuart SG,  Seilhamer JJ;
XX
DR   WPI; 2004-387937/36.
XX
PT   New compositions having a number of first, second and third
PT   polynucleotide probes, useful in research and diagnostic applications in
PT   cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT   infections.
XX
PS   Claim 15; SEQ ID NO 1194; 16pp; English.
XX
CC   The invention relates to polynucleotides which are used as probes to
CC   detect genes differentially expressed in an immunological response,
CC   abundantly expressed in an immunological response and/or coding for a
CC   polypeptide known to regulate blood cell biology. The polynucleotides are
CC   useful in research and diagnostic applications particularly in cancer and
CC   immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC   atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC   sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC   present sequence represents a human lymph node cDNA used to detect blood
CC   cell and immunological response gene expression. Note: The present
CC   sequence does not appear in the printed specification but was obtained in
CC   electronic format from the USPTO web site
CC   (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ   Sequence 6378 BP; 1850 A; 1298 C; 1445 G; 1785 T; 0 U; 0 Other;

  Query Match           99.2%;  Score 6364.4;  DB 13;  Length 6378;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
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Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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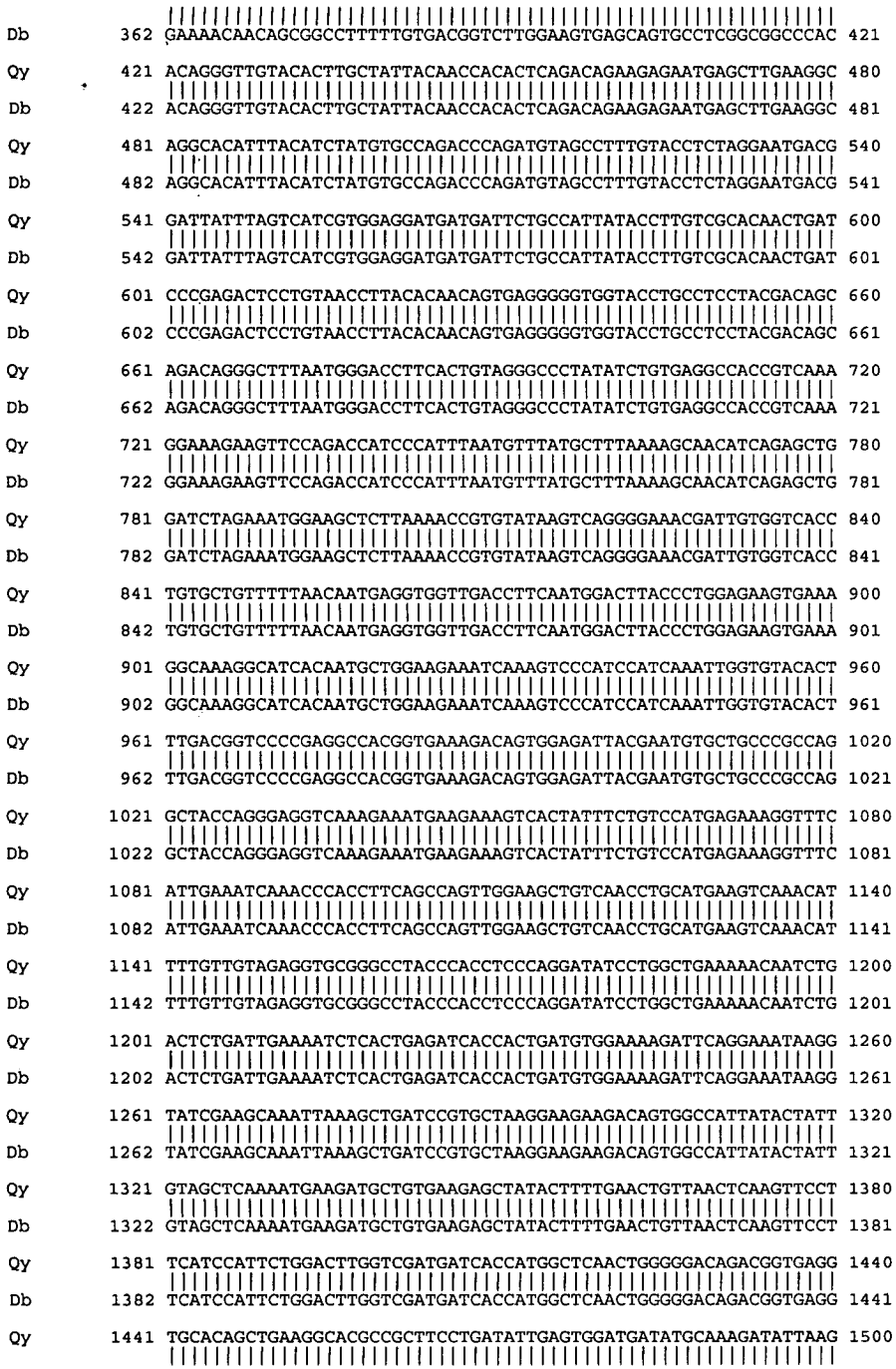
Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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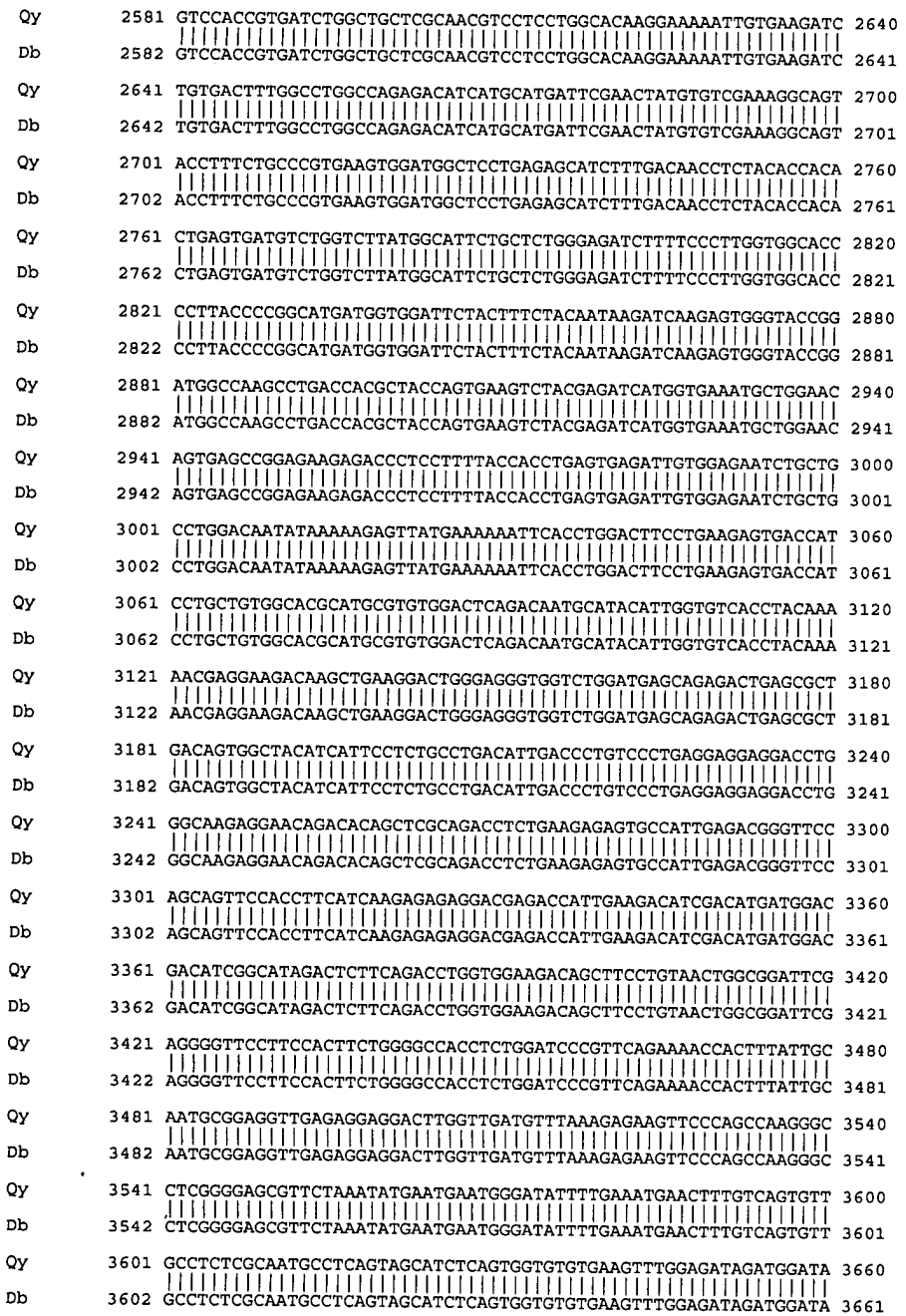
Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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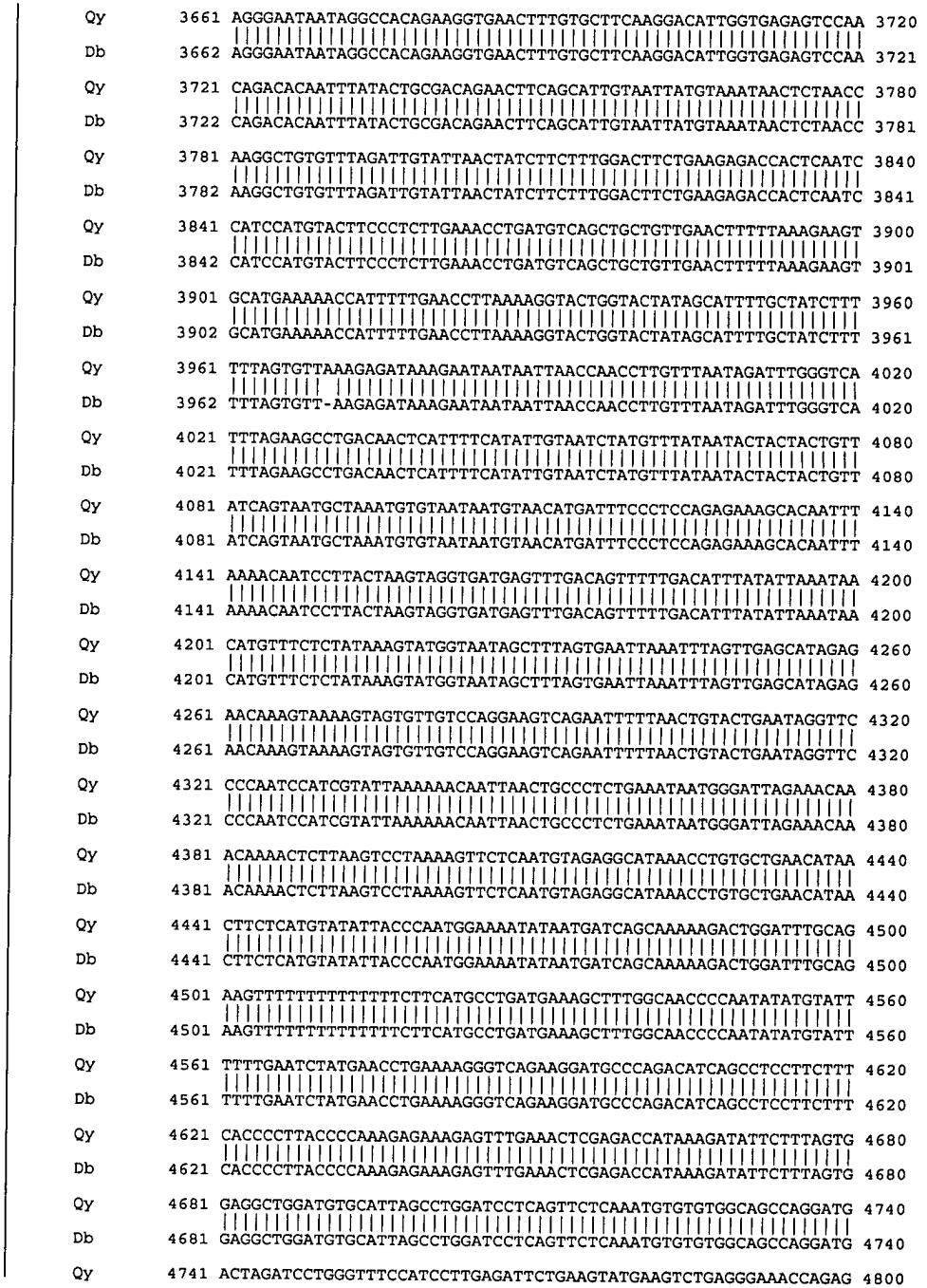
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Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Db 362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421
Qy 421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
Db 422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481
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Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
Db 1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201
Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db 1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261
Qy 1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db 1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
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Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
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Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
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Db 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

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Db       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Db       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
```

RESULT 10
ADG89389
ID ADG89389 standard; DNA; 6633 BP.
XX
AC ADG89389;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cancer detection method related gene #52.
XX
KW ds; cancer; gene expression;
KW estrogen receptor-positive invasive breast cancer.
XX
OS Homo sapiens.
XX
PN WO2003078662-A1.
XX
PD 25-SEP-2003.
XX
PF 12-MAR-2003; 2003WO-US007713.
XX
PR 13-MAR-2002; 2002US-0364890P.
PR 18-SEP-2002; 2002US-0412049P.
XX
PA (GENO-) GENOMIC HEALTH INC.
XX
PI Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;
XX
DR WPI; 2003-767536/72.
XX
PT Predicting clinical outcome for a patient diagnosed with cancer comprises
PT determining the expression level of one or more genes, and compared to
PT the amount found in a reference cancer tissue set.
XX

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PS   Disclosure; SEQ ID NO 337; 198pp; English.
XX
CC   The invention relates to a method of predicting clinical outcome for a
CC   patient diagnosed with cancer by determining the expression level of one
CC   or more genes, or their expression products, selected from p53BP2,
CC   cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer
CC   tissue obtained from the patient, normalized against control gene(s), and
CC   compared to the amount found in a reference cancer tissue set. The
CC   specification also discloses an array comprising polynucleotides
CC   hybridizing to the following genes: FOXMI, PRAME, Bcl2, STKI5, CEGP1, Ki-
CC   67, GSTM1, CA9, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3,
CC   RPS6KB1, Sro, Chk1, ID1, EstR1, p27, CCNBI, XIAP, Chk2, CDC25B, IGFIR,
CC   AK055699, PI3KC2A, TGFB3, BAGI1, CYP3A4, EpCAM, VEGFC, pS2, hENT1, WISP1,
CC   HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENTI, EPHXI, IFIA,
CC   CDHI, HIFlt, IGFBP3, CTSB, Her2 and DIABLO, immobilized on a solid
CC   surface. The methods are useful for predicting clinical outcome for a
CC   patient diagnosed with cancer, classifying cancer, and predicting the
CC   likelihood of long-term survival of a breast cancer patient, or a patient
CC   diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC   positive invasive breast cancer. This sequence corresponds to a gene
CC   sequence whose expression is detected by the method of the invention.
XX
SQ   Sequence 6633 BP; 1919 A; 1344 C; 1518 G; 1852 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 6364.4;  DB 10;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy    .   541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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Db       1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Db       1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Db       1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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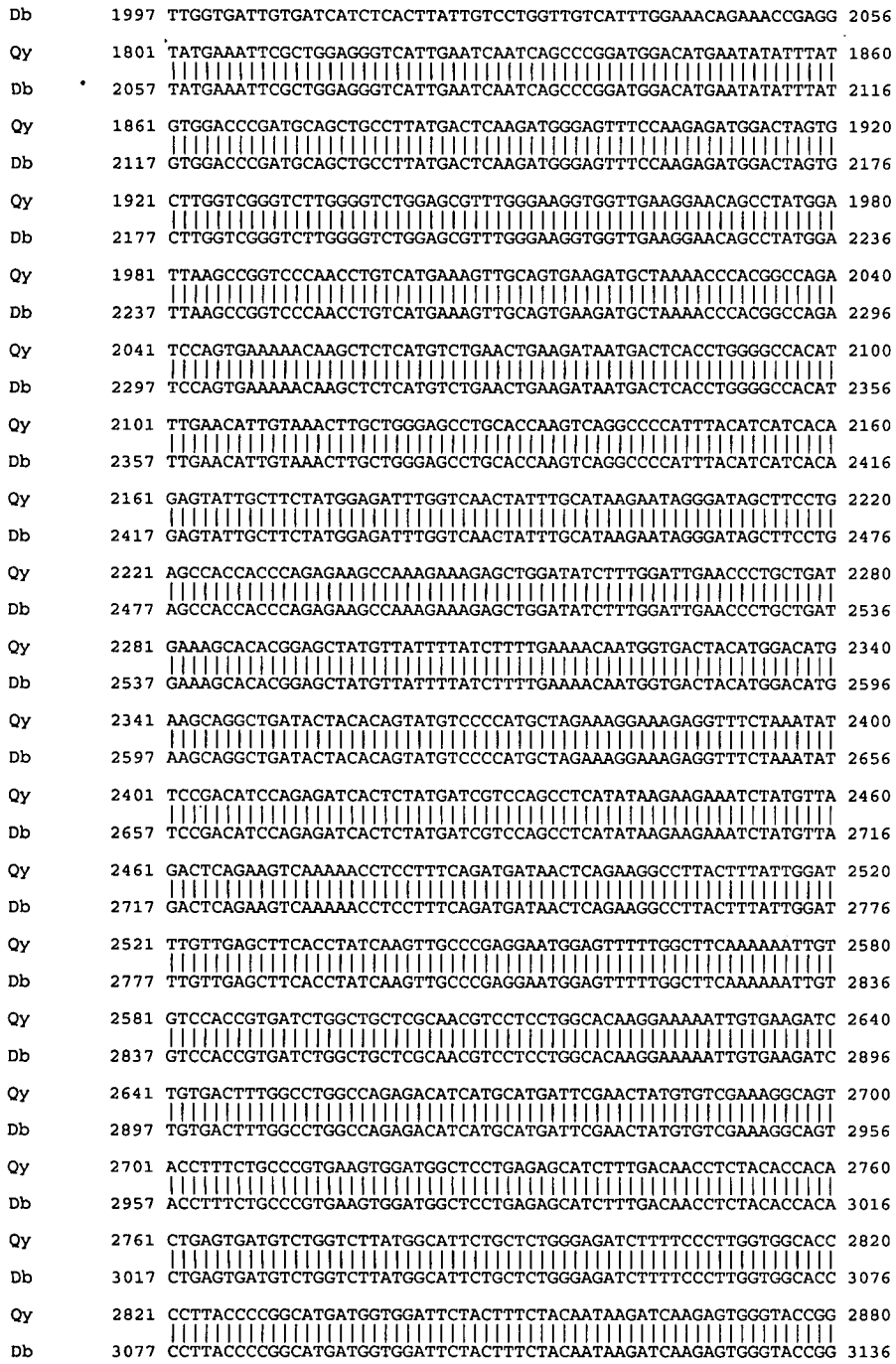
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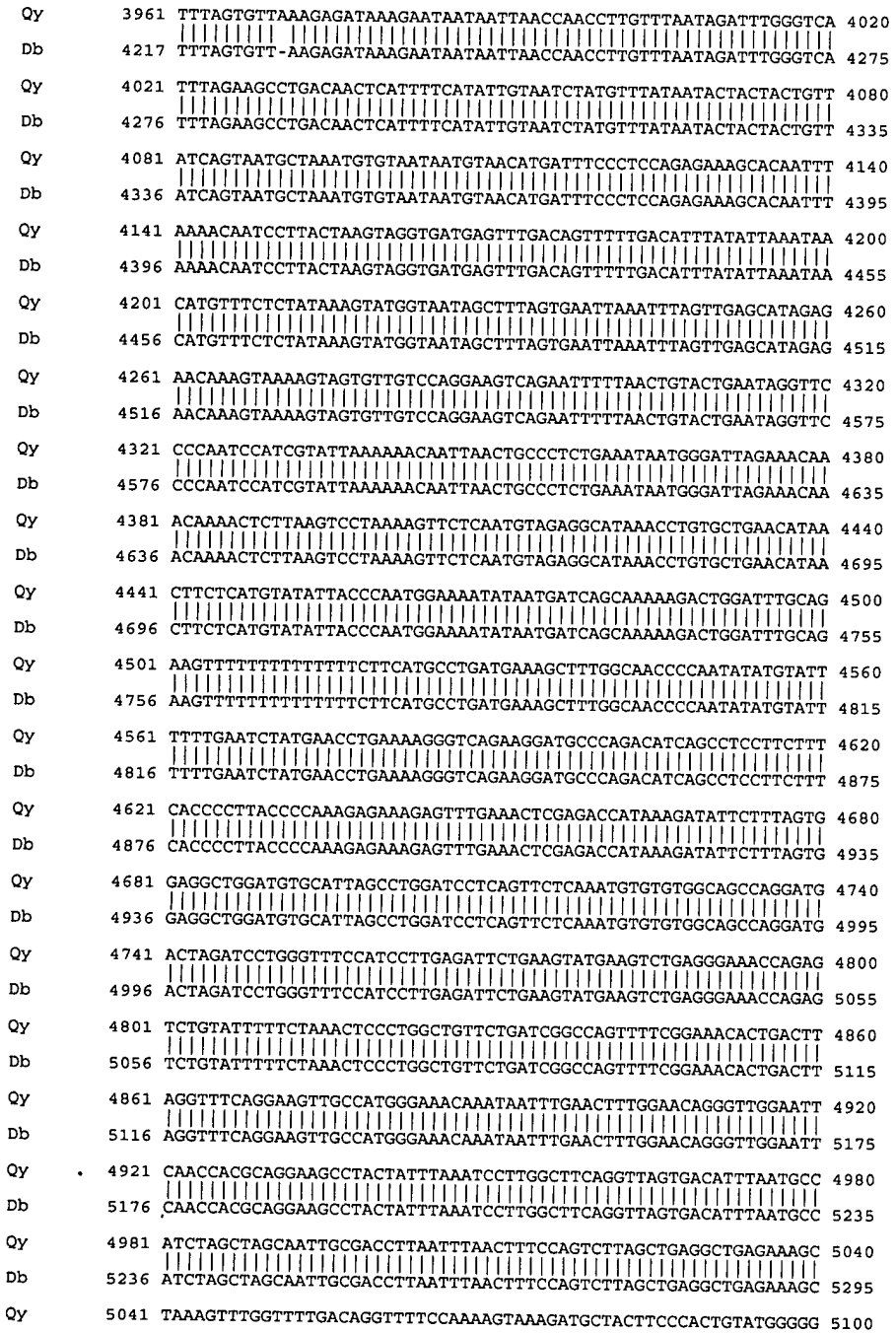
Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876

Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936

Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1860
Db 2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 2116
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
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Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
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Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
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Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216


Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Qy 4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Qy 5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db 6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135
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Qy 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6436 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6495

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6496 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6361 GATATATAATTTAAAGTT 6378
              ||||||||||||||||||
Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 11
ADM69011
ID   ADM69011 standard; cDNA; 6633 BP.
XX
AC   ADM69011;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha wild-type cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   wild-type; type III receptor tyrosine kinase; RTK; ss; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3664
FT                   /*tag=  a
FT                   /product= "Human platelet derived growth factor receptor
FT                   alpha wild-type protein"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69012.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Example 1; SEQ ID NO 1; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA wild-type
CC   cDNA of the invention.
XX
SQ   Sequence 6633 BP; 1919 A; 1344 C; 1518 G; 1852 T; 0 U; 0 Other;
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  Query Match             99.2%;  Score 6364.4;  DB 12;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

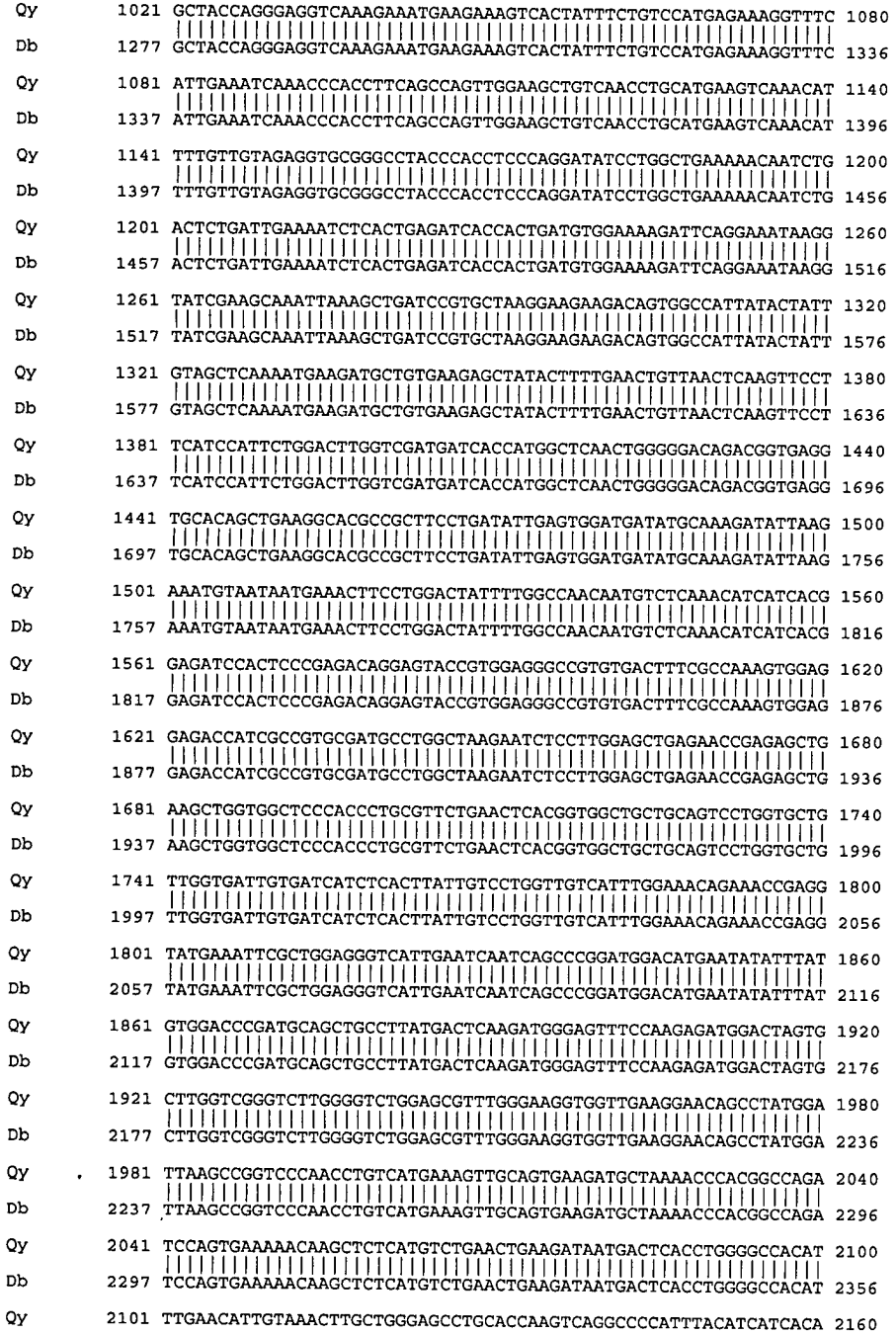
Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276
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Qy 1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
Db 1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336
Qy 1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
Db 1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396
Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
Db 1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456
Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
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Db 2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
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Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
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Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2897 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2956
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2957 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3016
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db 3017 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3076
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db 3077 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3136
Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db 3197 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3256
Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3257 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3316
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240

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Db       3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496

Qy       3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556

Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616

Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676

Qy       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736

Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796

Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856

Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916

Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976

Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036

Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096

Qy       3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156

Qy       3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216

Qy       3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275

Qy       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335

Qy       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395

Qy       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455

Qy       4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4456 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4515

Qy       4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4516 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4575

Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635

Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4636 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4695

Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4696 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4755

Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4756 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4815

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5116 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5175

Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5176 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 5235

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5236 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5295

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5296 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5355

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5356 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5415

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5416 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5475

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5596 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5655
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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5656 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5715

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5716 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5775

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5776 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5835

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5836 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5895

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6016 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6075

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6195

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6315

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6316 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6375

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6376 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6435

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6436 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6495

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6496 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6556 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6615

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 12
ADY59388
ID   ADY59388 standard; DNA; 6633 BP.
XX
AC   ADY59388;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Human PDGFR-A DNA.
XX
KW   PDGF antagonist; VEGF antagonist; ds; psoriasis; rheumatoid arthritis;
KW   age-related macular degeneration; antipsoriatic; dermatological disease;
KW   immune disorder; antiarthritic; antirheumatic; immune disorder;
KW   inflammation; musculoskeletal disease; age related macular degeneration;
KW   ophthalmological; ocular disease; diabetic retinopathy; antidiabetic;
KW   ophthalmological; cardiovascular disease; ocular disease; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3664
FT                   /*tag=  a
FT                   /product= "PDGFR-A"
XX
PN   WO2005020972-A2.
XX
PD   10-MAR-2005.
XX
PF   26-AUG-2004; 2004WO-US027612.
XX
PR   27-AUG-2003; 2003US-0498407P.
PR   26-MAR-2004; 2004US-0556837P.
XX
PA   (EYET-) EYETECH PHARM INC.
XX
PI   Shima D,  Calias P,  Adamis AP;
XX
DR   WPI; 2005-214423/22.
DR   P-PSDB; ADY59389.
XX
PT   Treating an ocular neovascular disorder, comprises administering a
PT   platelet derived growth factor antagonist and a vascular endothelial
PT   growth factor antagonist, simultaneously or within ninety days of each
PT   other.
XX
PS   Disclosure; SEQ ID NO 13; 112pp; English.
XX
CC   The invention relates to a method of treating a patient diagnosed with or
CC   at risk for developing a neovascular disorder, or suppressing a
CC   neovascular disorder in a patient. The method is useful for treating a
CC   patient diagnosed with or at risk for developing a neovascular disorder
CC   or suppressing a neovascular disorder in a patient. The neovascular
CC   disorder is an ocular neovascular disorder, psoriasis or rheumatoid
CC   arthritis. The ocular neovascular disorder is ischemic retinopathy, iris
CC   neovascularization, intraocular neovascularization, age-related macular
CC   degeneration, corneal neovascularization, retinal neovascularization,
CC   choroidal neovascularization, diabetic retinal ischemia, or proliferative
CC   diabetic retinopathy. The present sequence represents human PDGFR DNA.
XX
SQ   Sequence 6633 BP; 1919 A; 1344 C; 1518 G; 1852 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 6364.4;  DB 14;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436
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Qy      181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy      241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy      301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy      361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy      421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy      481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy      541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy      601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy      661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Db      917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy      721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy      781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
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Db     1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy      841 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1097 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy      901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy      961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy     1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336

Qy     1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396

Qy     1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456

Qy     1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1457 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1516

Qy     1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576

Qy     1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636

Qy     1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696

Qy     1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756

Qy     1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
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Qy     1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
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Db     1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996

Qy     1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Qy     1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Qy     1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Db     2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176

Qy     1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
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Db     2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236

Qy     1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296

Qy     2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356

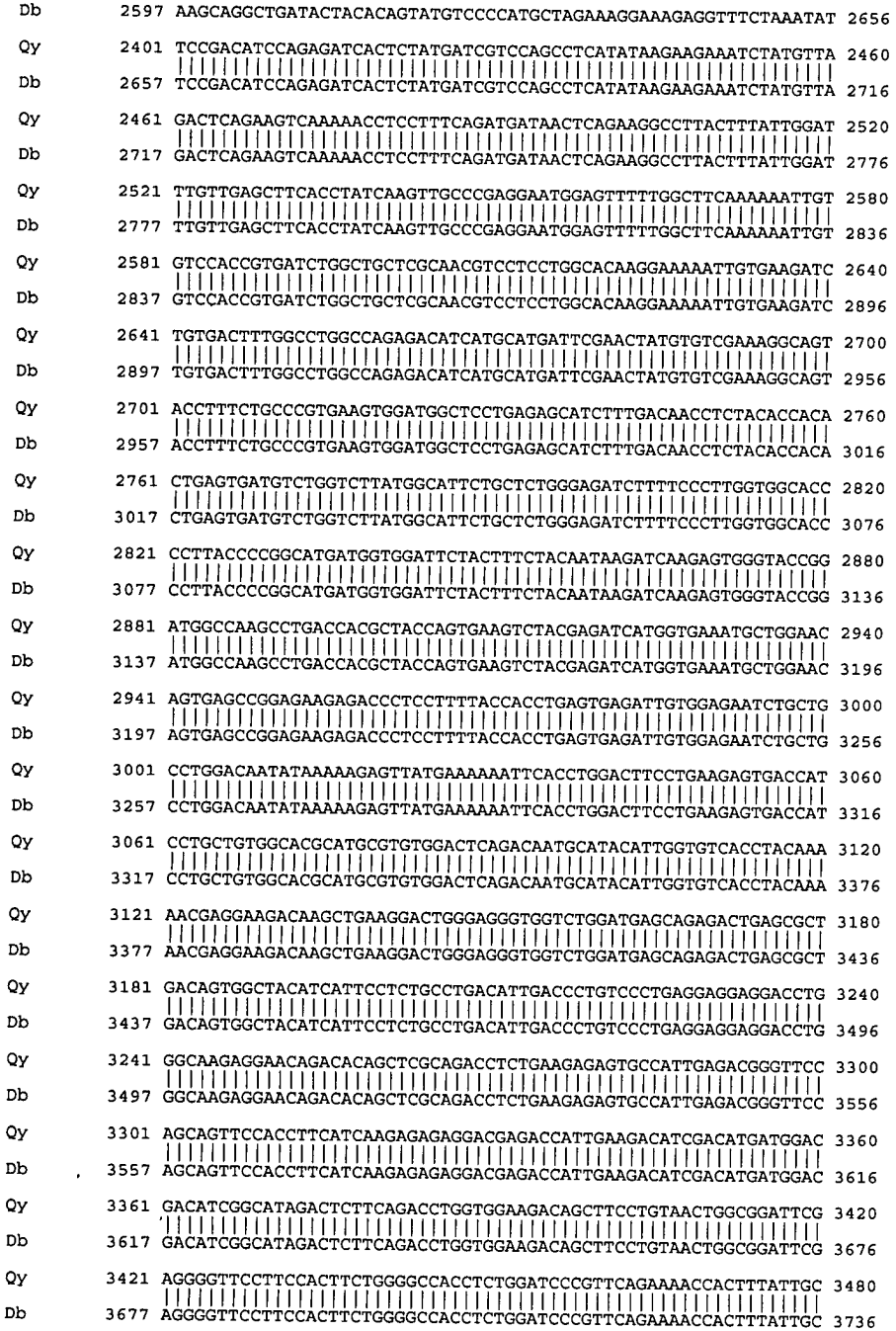
Qy     2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416

Qy     2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476

Qy     2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536

Qy     2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596

Qy     2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
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Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
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Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
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Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Db       5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015

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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Qy       6361 GATATATAATTTAAAGTT 6378
             |||||||||||||||||
Db       6616 GATATATAATTTAAAGTT 6633
```

RESULT 13
ADM69030
ID ADM69030 standard; cDNA; 6633 BP.
XX
AC ADM69030;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant V561D cDNA.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   395. .3664
FT   /*tag= a
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FT misc_difference 2075. .2077

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FT                   /note= "Wild-type GTC substituted by GAC"
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PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69031.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 20; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant V561D cDNA of the invention.
XX
SQ   Sequence 6633 BP; 1920 A; 1344 C; 1518 G; 1851 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 6362.8;  DB 12;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6375;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
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Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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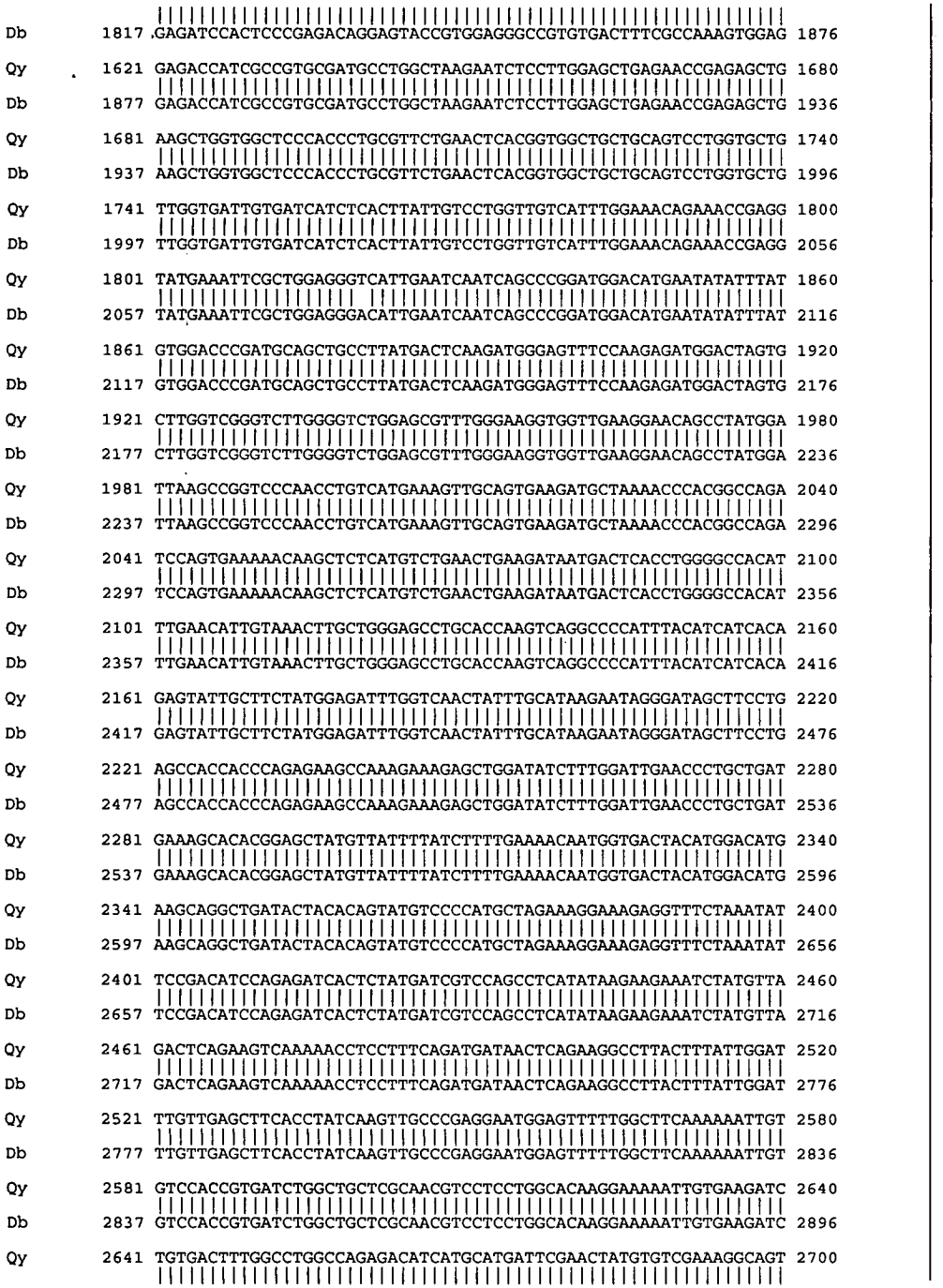
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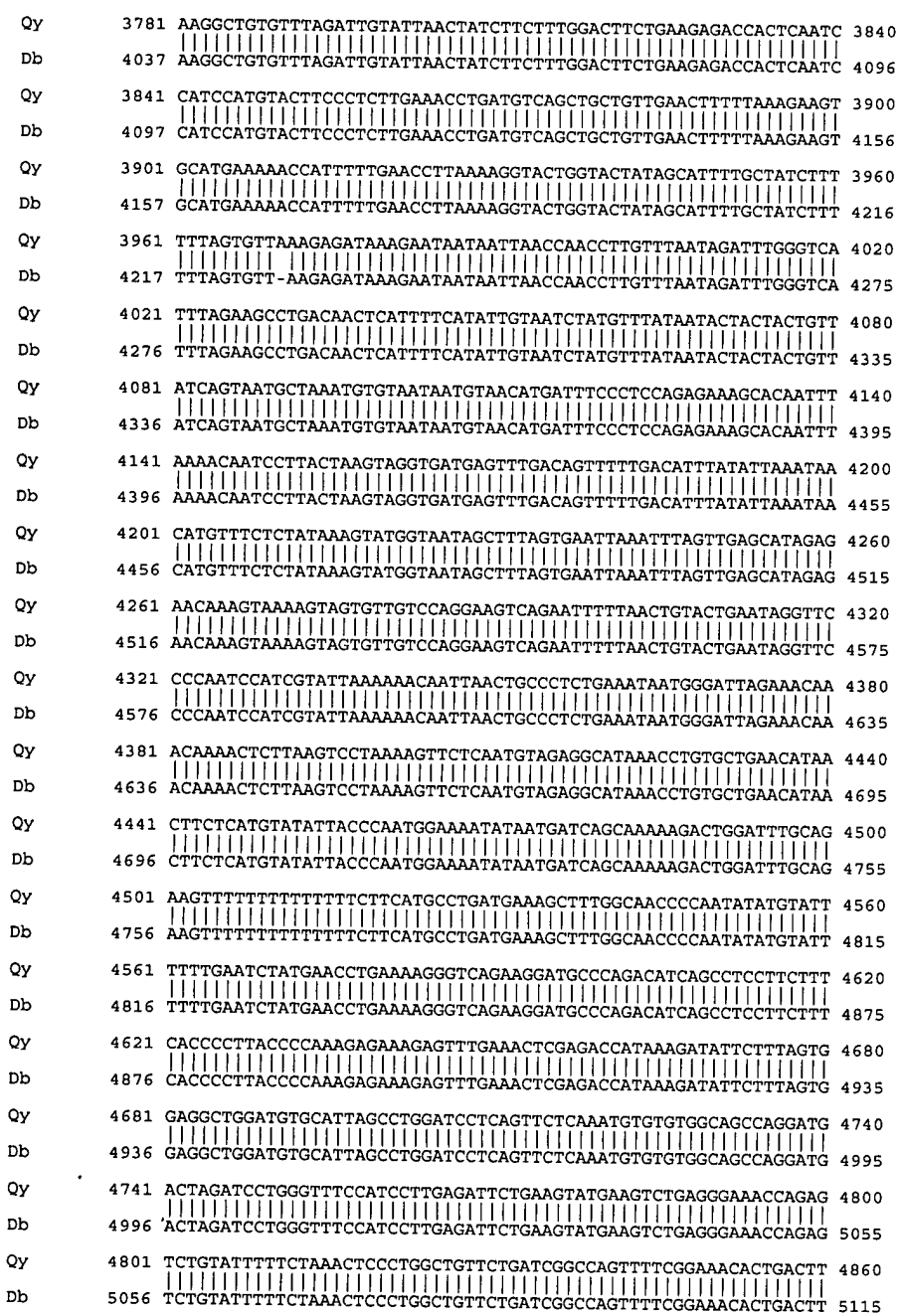
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```


Db 1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876
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Qy        6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Qy        6361 GATATATAATTTAAAGTT 6378
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Db        6616 GATATATAATTTAAAGTT 6633


RESULT 14
ADM69013
ID   ADM69013 standard; cDNA; 6633 BP.
XX
AC   ADM69013;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant D842V cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3664
FT                   /*tag=  a
FT                   /product= "Human PDGFRA cancer-related activating mutant
FT                   D842V protein"
FT   misc_difference 2918. .2920
FT                   /*tag=  b
FT                   /note= "Wild-type GAC substituted by GTC"
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PN   WO2003105773-A2.
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PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69014.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 3; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant D842V cDNA of the invention.
XX
SQ   Sequence 6633 BP; 1918 A; 1344 C; 1518 G; 1853 T; 0 U; 0 Other;

  Query Match             99.2%;  Score 6362.8;  DB 12;  Length 6633;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6375;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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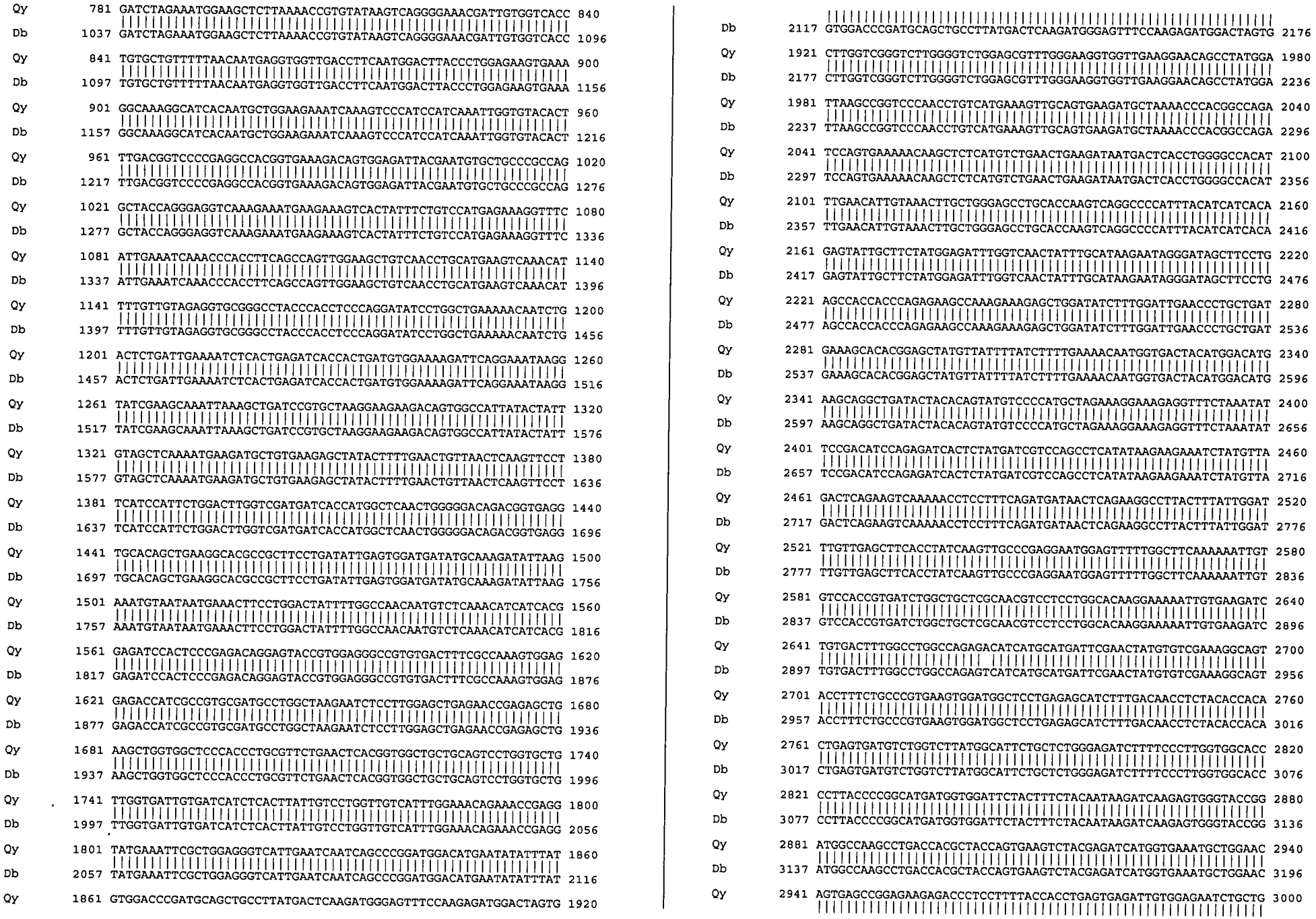
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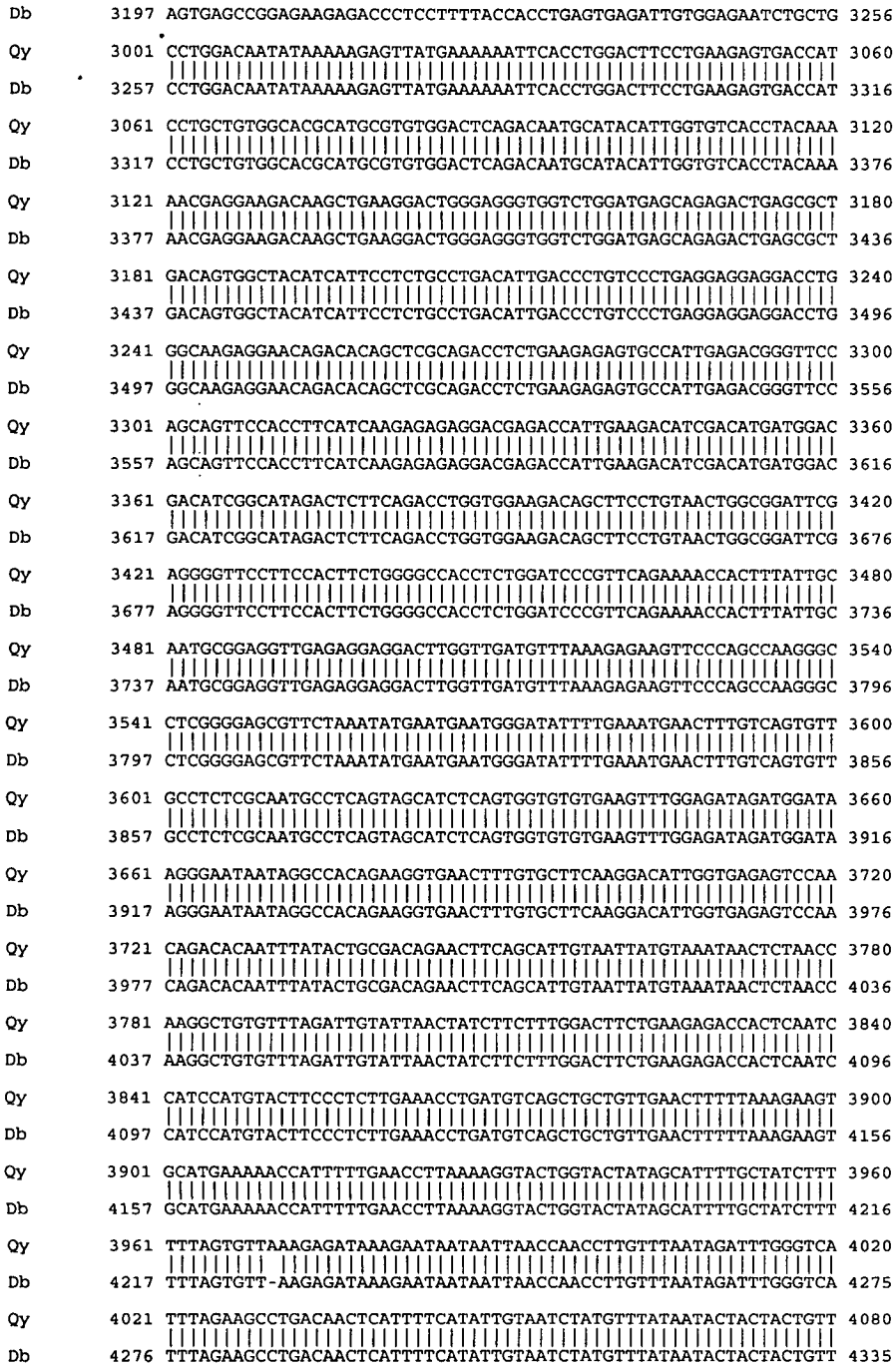
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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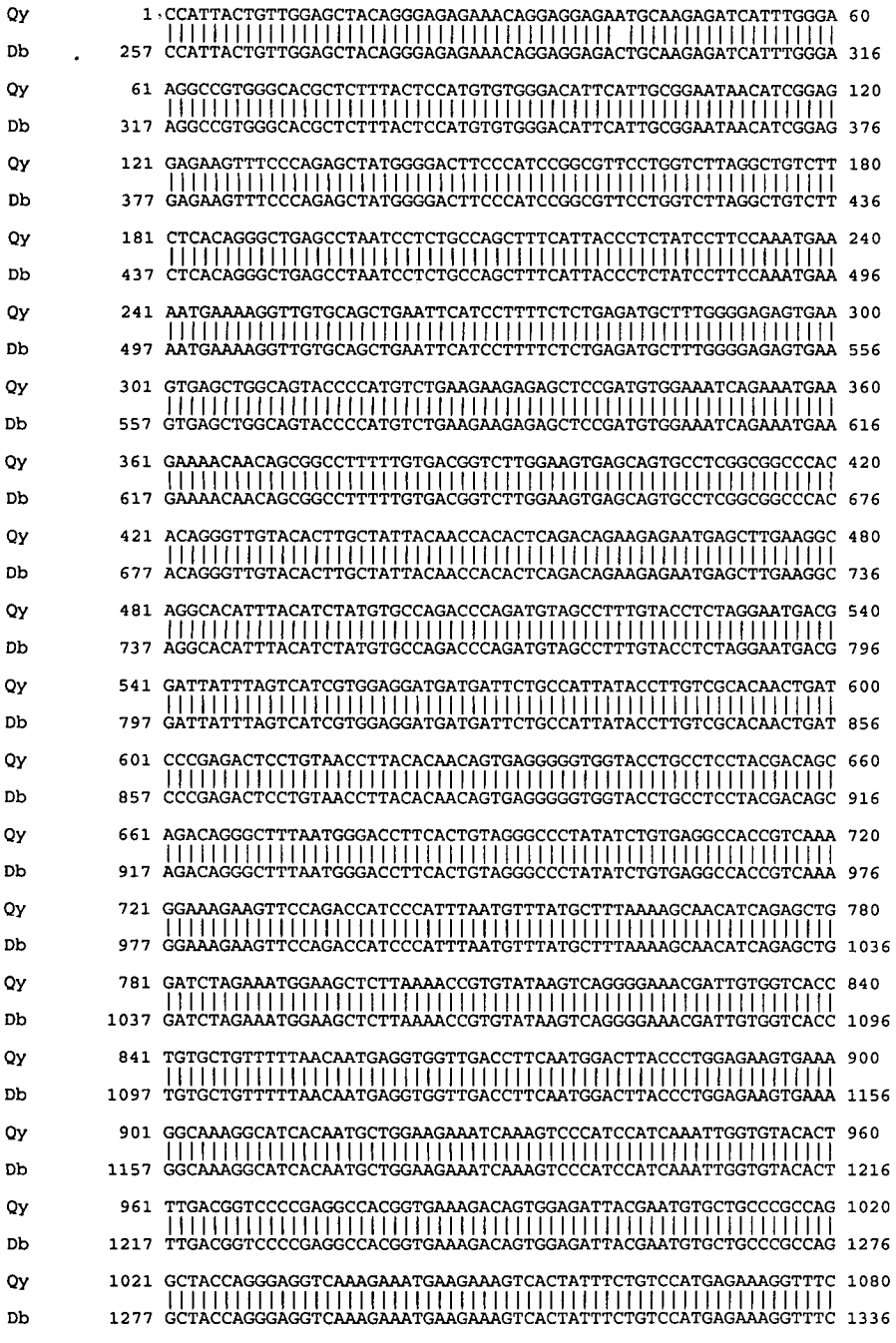
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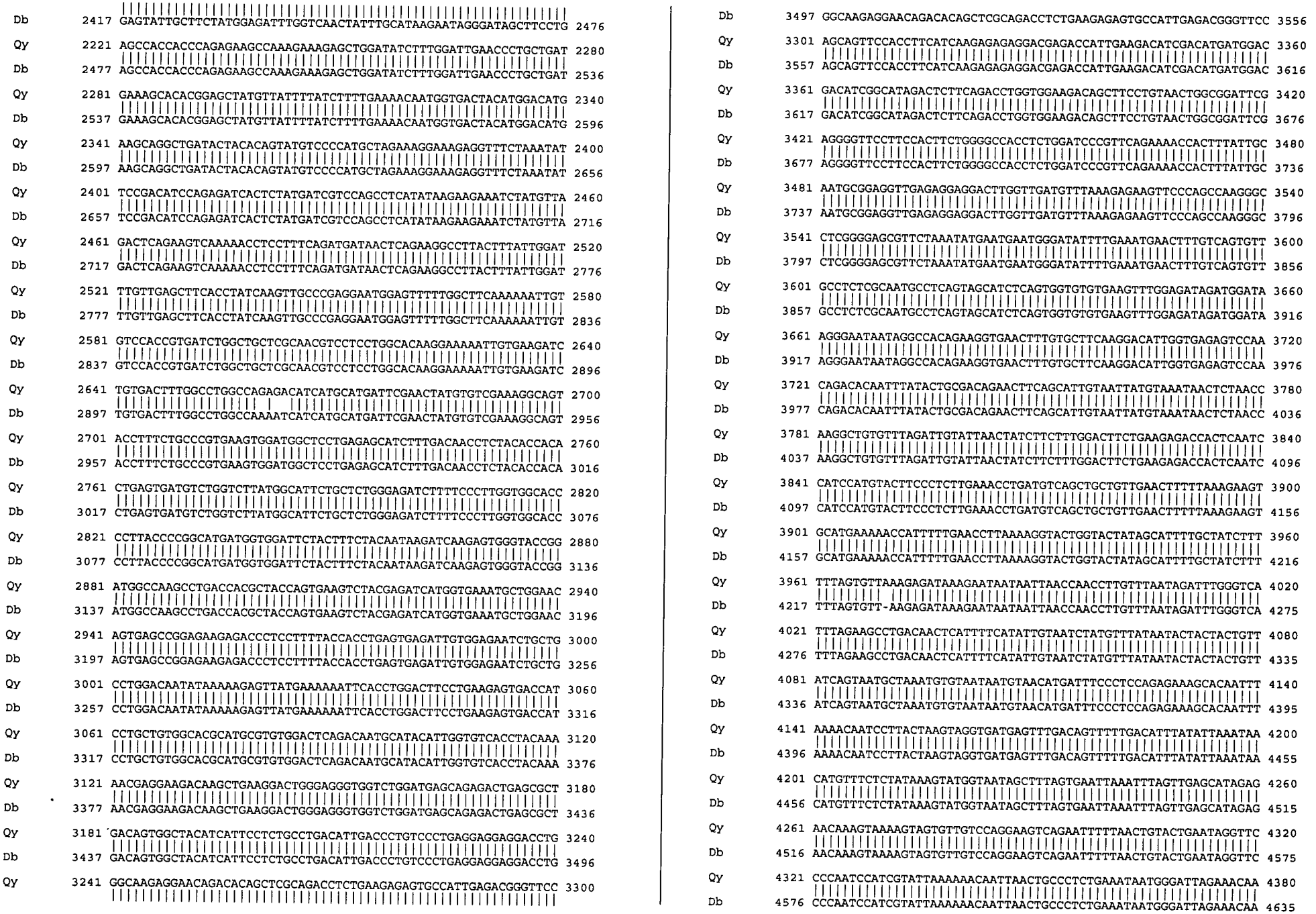
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Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6616 GATATATAATTTAAAGTT 6633
```

RESULT 15
ADM69034
ID ADM69034 standard; cDNA; 6633 BP.
XX
AC ADM69034;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant Deletion RD841-842KI cDNA.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   395. .3664
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FT   /product= "Human PDGFRA cancer-related activating mutant
FT   Deletion RD841-842KI protein"
FT misc_difference 2915. .2920
FT   /*tag= b
FT   /note= "Wild-type AGAGAC substituted by AAAATC"
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PN WO2003105773-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018901.
XX
PR 13-JUN-2002; 2002US-0389107P.
PR 08-JAN-2003; 2003US-0438899P.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
XX
PI Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
DR WPI; 2004-082052/08.
DR P-PSDB; ADM69035.
XX
PT New isolated variant platelet derived growth factor alpha (PDGFRA)
PT polypeptide, useful for screening for a compound useful in influencing
PT PDGFRA-mediated neoplasia in a mammal.
XX
PS Claim 13; SEQ ID NO 24; 302pp; English.
XX
CC The invention relates to a novel isolated variant platelet derived growth
CC factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC for screening for a compound that may influence PDGFRA-mediated neoplasia
CC in a mammal. The current sequence is that of the human PDGFRA cancer-
CC related activating mutant Deletion RD841-842KI cDNA of the invention.
XX
SQ Sequence 6633 BP; 1920 A; 1344 C; 1516 G; 1853 T; 0 U; 0 Other;

Query Match 99.2%; Score 6359.6; DB 12; Length 6633;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6373; Conservative 0; Mismatches 4; Indels 1; Gaps 1;


Qy 1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Db 2897 TGTGACTTTGGCCTGGCCAAAATCATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2956
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Db 2957 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3016
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db 3017 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3076
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
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Db 3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Db 3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
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Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
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Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
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Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
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Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db 4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
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Qy 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Db 4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635

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Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Qy       4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Db       5236 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5295

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db       5356 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5415

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Db       5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Db       5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595

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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Db       6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6256 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6315

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Db       6316 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6375

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6496 GGTGAATGTGTGAGAAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6556 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6615

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 16
ADM69019
ID ADM69019 standard; cDNA; 6639 BP.
XX
AC ADM69019;
XX
DT 03-JUN-2004 (first entry)
XX

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DE   Human PDGFRA cancer-related activating mutant ER561-562 cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3670
FT                   /*tag=  a
FT                   /product= "Human PDGFRA cancer-related activating mutant
FT                   ER561-562 protein"
FT   misc_difference 2075. .2080
FT                   /*tag=  b
FT                   /note= "Absent in wild-type"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69020.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 9; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant ER561-562 cDNA of the invention.
XX
SQ   Sequence 6639 BP; 1921 A; 1344 C; 1522 G; 1852 T; 0 U; 0 Other;

  Query Match             99.0%;  Score 6348.4;  DB 12;  Length 6639;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    7;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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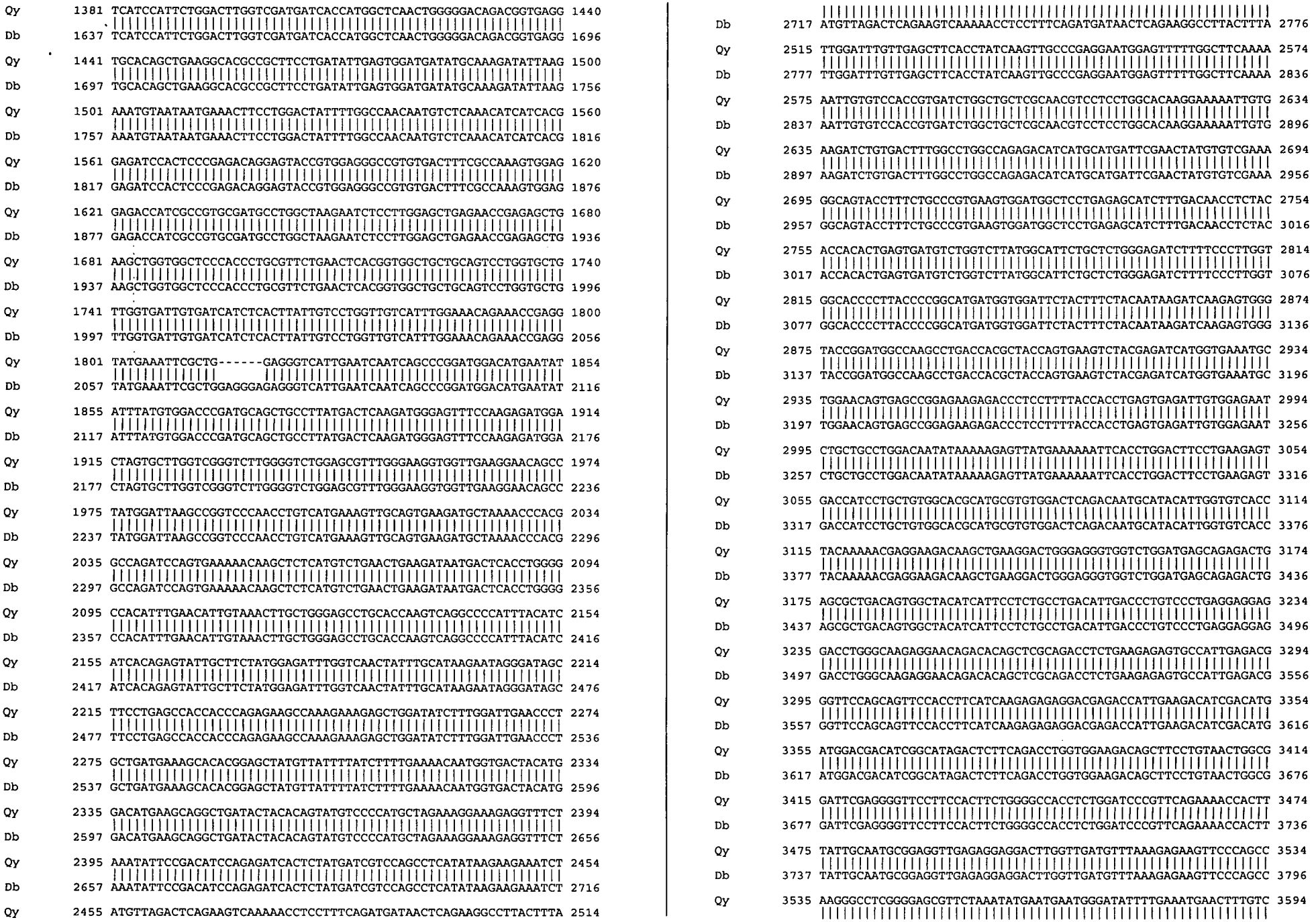
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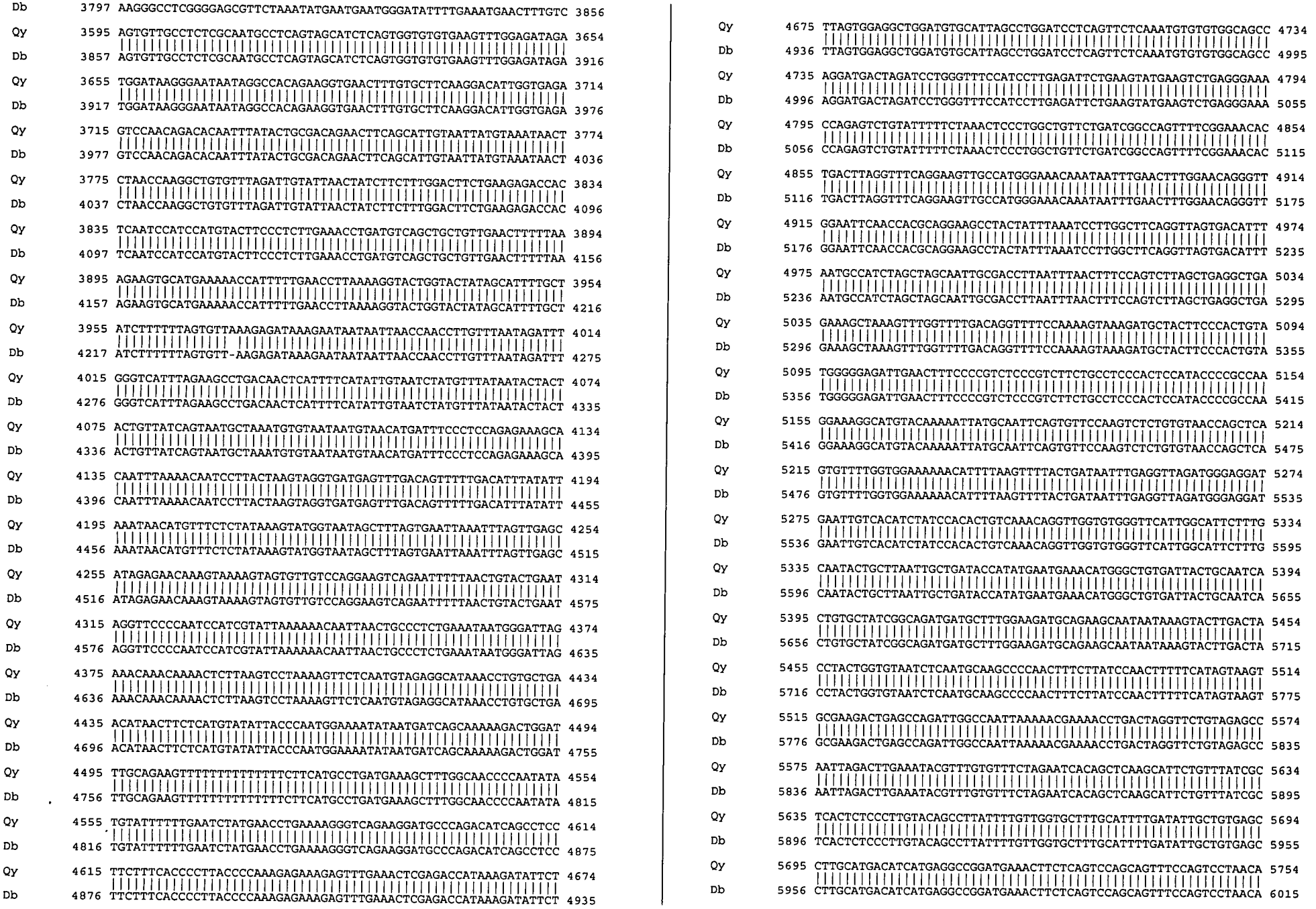
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Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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RESULT 17
ADM69017
ID   ADM69017 standard; cDNA; 6624 BP.
XX
AC   ADM69017;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant HSDN845-848P cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69018.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 7; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant HSDN845-848P cDNA of the invention.
XX
SQ   Sequence 6624 BP; 1915 A; 1344 C; 1516 G; 1849 T; 0 U; 0 Other;
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  Query Match           98.8%;  Score 6334.8;  DB 12;  Length 6624;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 6366;  Conservative    0;  Mismatches    2;  Indels   10;  Gaps    2;

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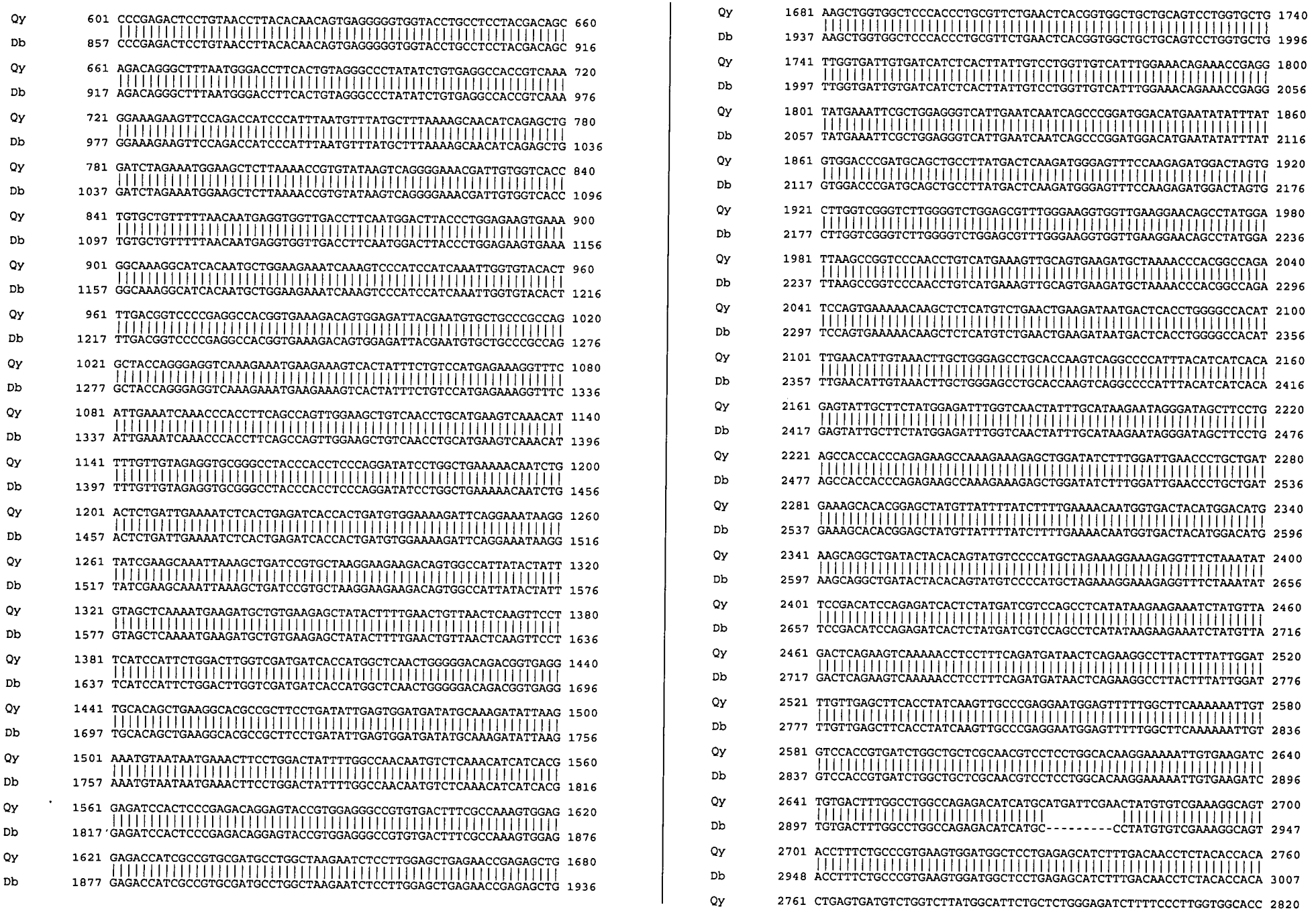
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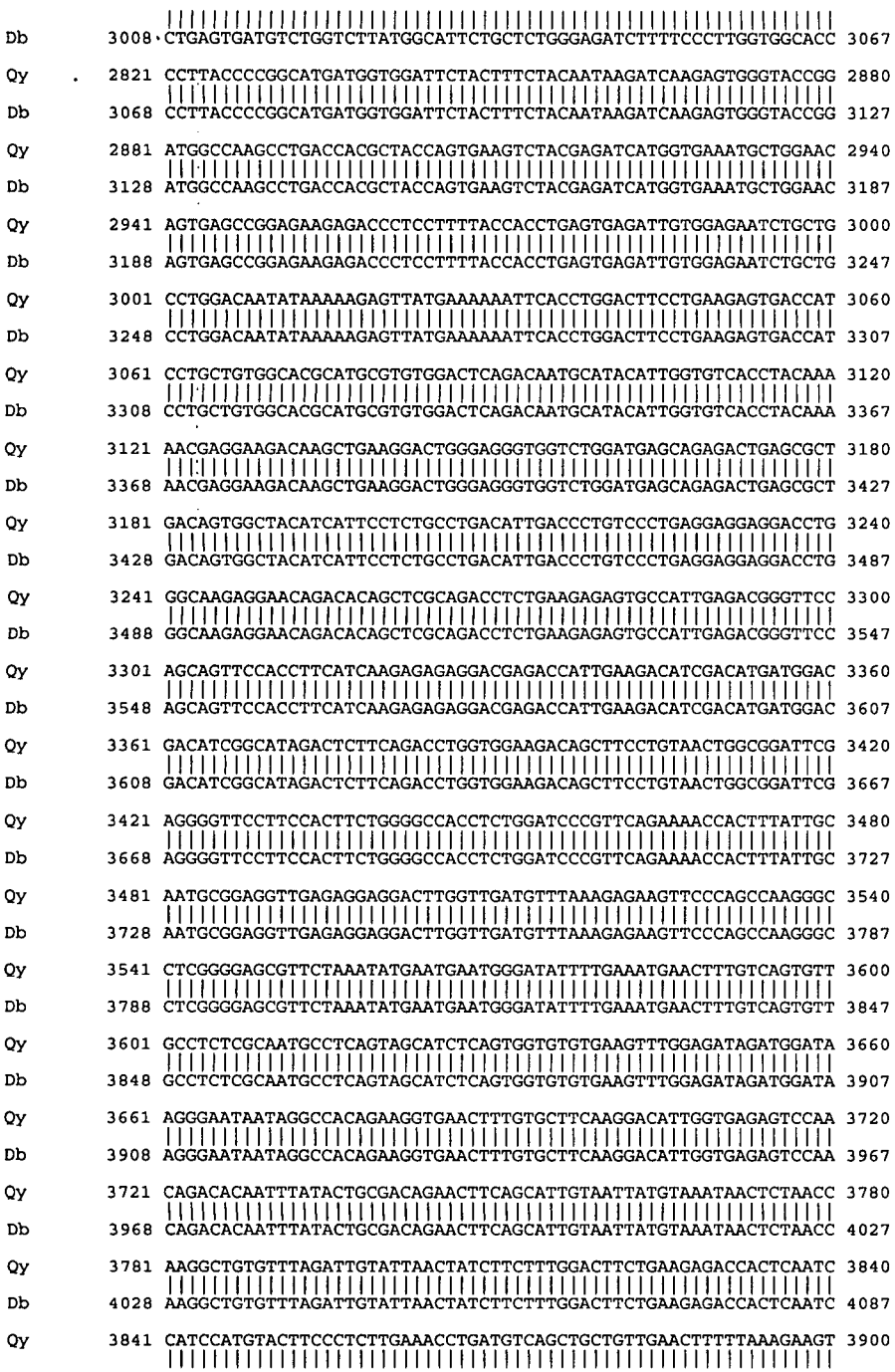
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Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db 2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db 2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db 2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2897 TGTGACTTTGGCCTGGCCAGAGACATCATGC---------CCTATGTGTCGAAAGGCAGT 2947
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2948 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3007
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820


Db 3008 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3067
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db 3068 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3127
Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 3128 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3187
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db 3188 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3247
Qy 3001 CCTGGACAATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3248 CCTGGACAATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3307
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3308 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3367
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3368 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3427
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3428 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3487
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3488 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3547
Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3548 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3607
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3608 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3667
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3668 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3727
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3728 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3787
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3788 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3847
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3848 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3907
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3908 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3967
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3968 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4027
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 4028 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4087
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 4088 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4147
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 4148 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4207
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 4208 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4266
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4267 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4326
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db 4327 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4386
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Db 4387 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4446
Qy 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Db 4447 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4506
Qy 4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
Db 4507 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4566
Qy 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Db 4567 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4626
Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db 4627 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4686
Qy 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db 4687 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4746
Qy 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db 4747 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4806
Qy 4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db 4807 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4866
Qy 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db 4867 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4926
Qy 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db 4927 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4986
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db 4987 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5046
Qy 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db 5047 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5106
Qy 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db 5107 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5166
Qy 4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Db 5167 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 5226

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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5227 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5286

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5287 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5346

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5347 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5406

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5407 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5466

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5467 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5526

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5527 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5586

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5587 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5646

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5647 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5706

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5707 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5766

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5767 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5826

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5827 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5886

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5887 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5946

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5947 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6006

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6007 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6066

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6067 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6126

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6127 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6186

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6187 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6246

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6247 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6306

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6307 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6366

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6367 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6426

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6427 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6486

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6487 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6546

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6547 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6606

Qy       6361 GATATATAATTTAAAGTT 6378
             |||||||||||||||||
Db       6607 GATATATAATTTAAAGTT 6624
```

RESULT 18
ADZ13914
ID ADZ13914 standard; cDNA; 6633 BP.
XX
AC ADZ13914;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated cDNA #436.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
DR P-PSDB; ADZ13915.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1434; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA

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CC   nucleic acids. The antibody is useful for detecting the presence or
CC   absence of cancer cells in an individual which involves contacting cells
CC   from the individual with the antibody and detecting a complex of a CA
CC   protein from the cancer cells and the antibody, where the detection of
CC   the complex correlates with the presence of cancer cells in the
CC   individual. The composition is useful for inhibiting growth of cancer
CC   cells in an individual or for delivering a therapeutic agent to cancer
CC   cells in an individual. The invention is also useful for diagnosing
CC   cancer, for treating cancer and for inhibiting expression of a CA gene in
CC   a cell. This sequence represents human cancer-associated cDNA of the
CC   invention.
XX
SQ   Sequence 6633 BP; 1920 A; 1343 C; 1519 G; 1851 T; 0 U; 0 Other;

  Query Match             98.7%;  Score 6332.6;  DB 14;  Length 6633;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 6371;  Conservative    0;  Mismatches    4;  Indels    6;  Gaps    3;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        779 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 838
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Qy        839 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 898
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Db       1094 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 1153

Qy        899 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 958
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Qy        959 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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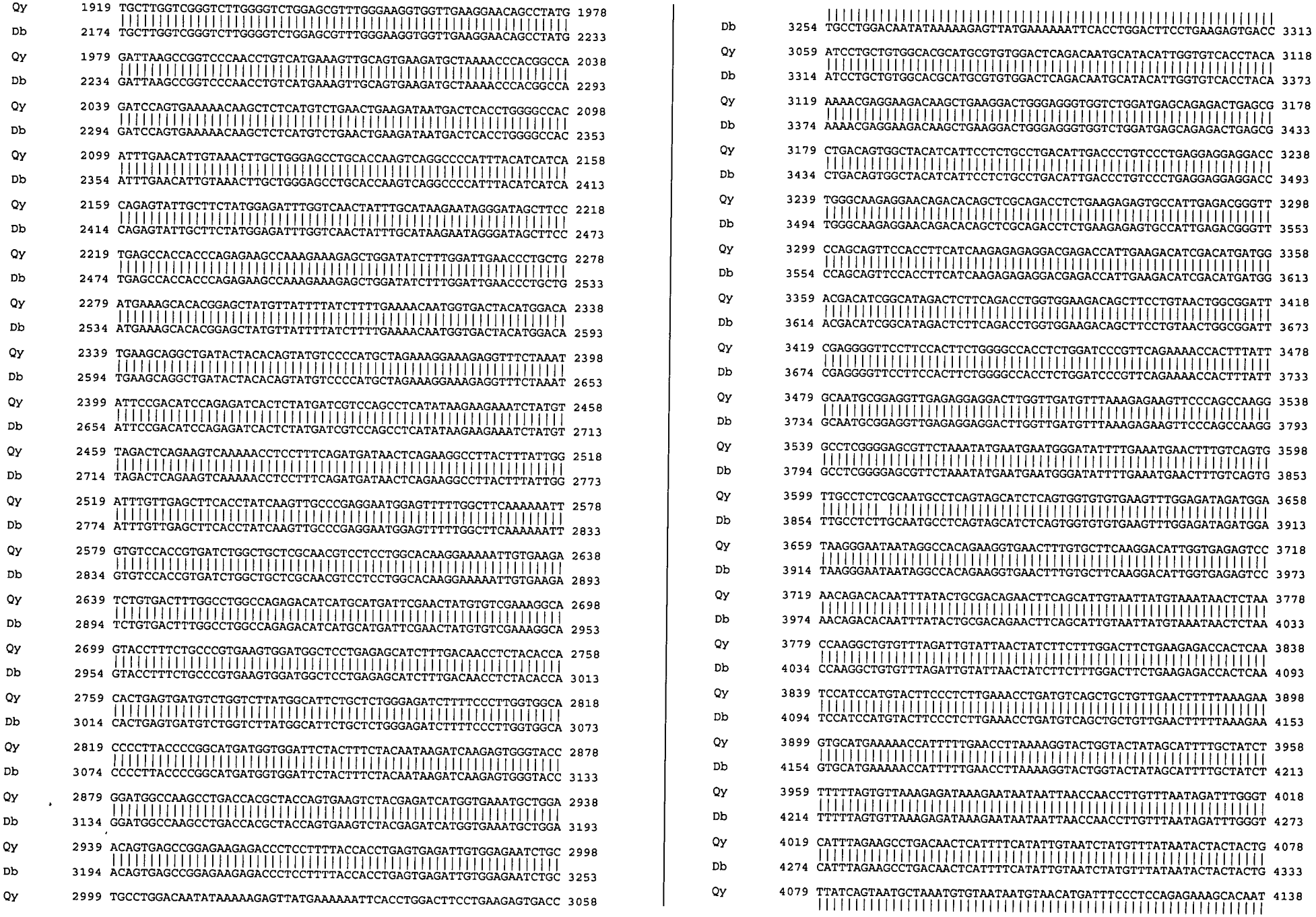
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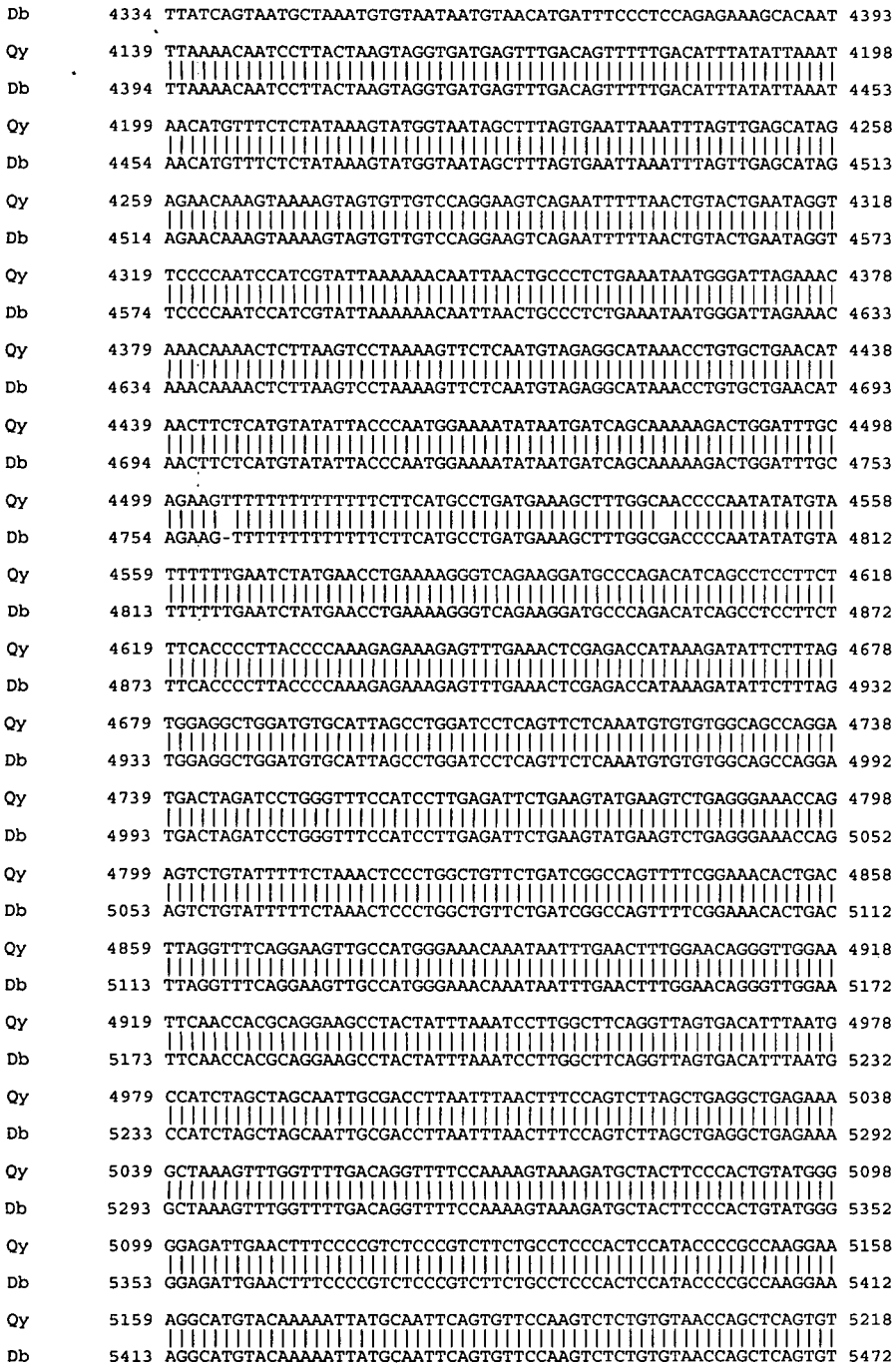
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```


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RESULT 19
ADM69015
ID   ADM69015 standard; cDNA; 6621 BP.
XX
AC   ADM69015;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant DIMH842-845 cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69016.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 5; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant DIMH842-845 cDNA of the invention.
XX
SQ   Sequence 6621 BP; 1915 A; 1341 C; 1516 G; 1849 T; 0 U; 0 Other;

  Query Match'          98.7%;  Score 6330.4;  DB 12;  Length 6621;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 6364;  Conservative    0;  Mismatches    1;  Indels   13;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||

Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

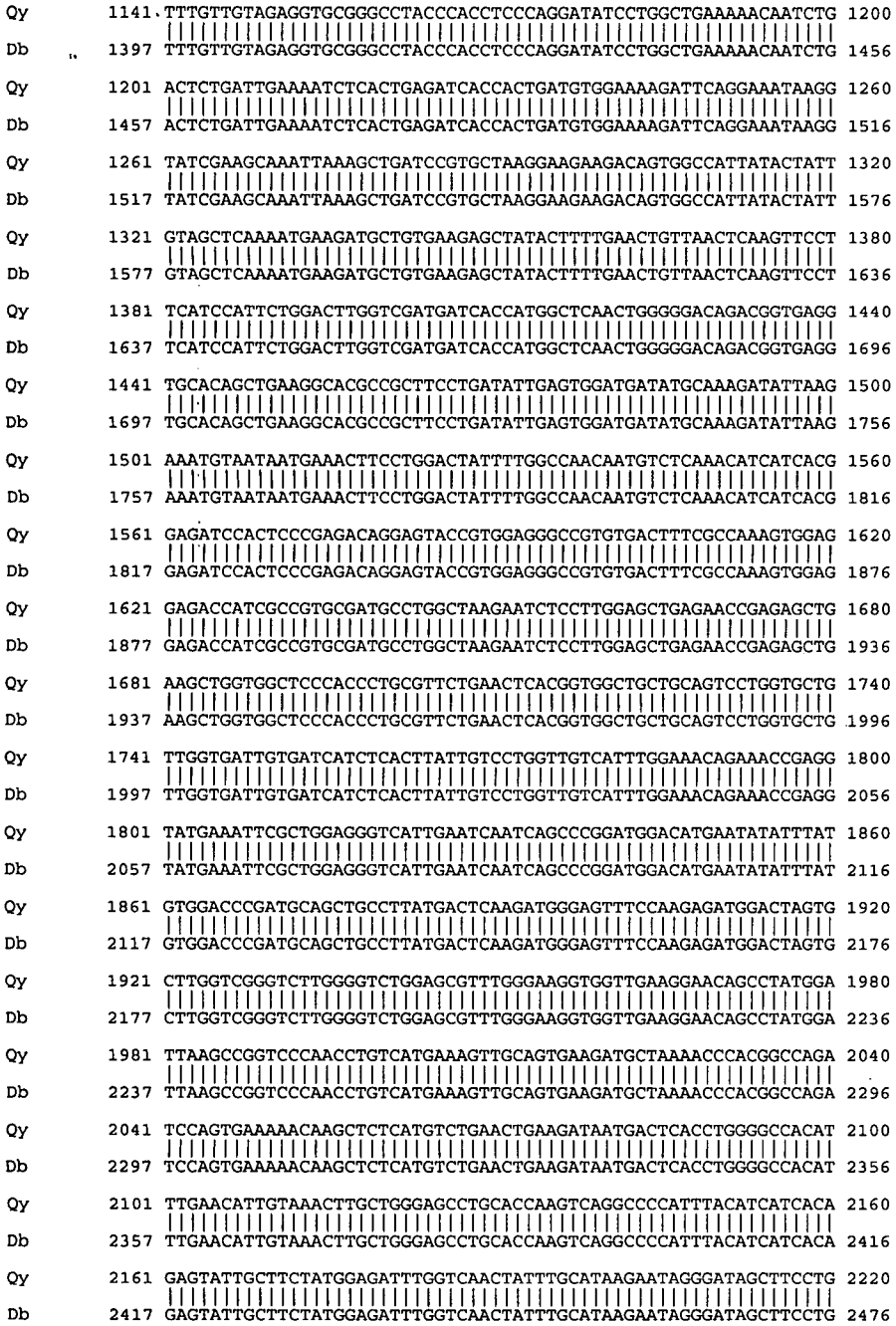
Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396
```


Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
Db 1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456
Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db 1457 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1516
Qy 1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db 1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db 1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636
Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Db 1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756
Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db 1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816
Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db 1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876
Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db 1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936
Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db 2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
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Db 2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2897 TGTGACTTTGGCCTGGCCAGA----------GATTCGAACTATGTGTCGAAAGGCAGT 2944
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
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Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
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Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 3125 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3184
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Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3305 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3364
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3365 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3424
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3425 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3484
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3485 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3544
Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360



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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Db    .  5764 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5823

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5824 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5883

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5884 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5943

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5944 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6003

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6004 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6063

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Db       6064 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6123

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Db       6124 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6183

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6184 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6243

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6244 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6303

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6304 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6363

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6424 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6483

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6484 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6543

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6544 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6603

Qy       6361 GATATATAATTTAAAGTT 6378
             |||||||||||||||||
Db       6604 GATATATAATTTAAAGTT 6621


RESULT 20
ADQ22465
ID   ADQ22465 standard; DNA; 7067 BP.
XX
AC   ADQ22465;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 5285.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 5285; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   DNA of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 7067 BP; 2163 A; 1405 C; 1633 G; 1850 T; 0 U; 16 Other;

  Query Match             98.7%;  Score 6327.6;  DB 12;  Length 7067;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 6367;  Conservative    0;  Mismatches   45;  Indels    2;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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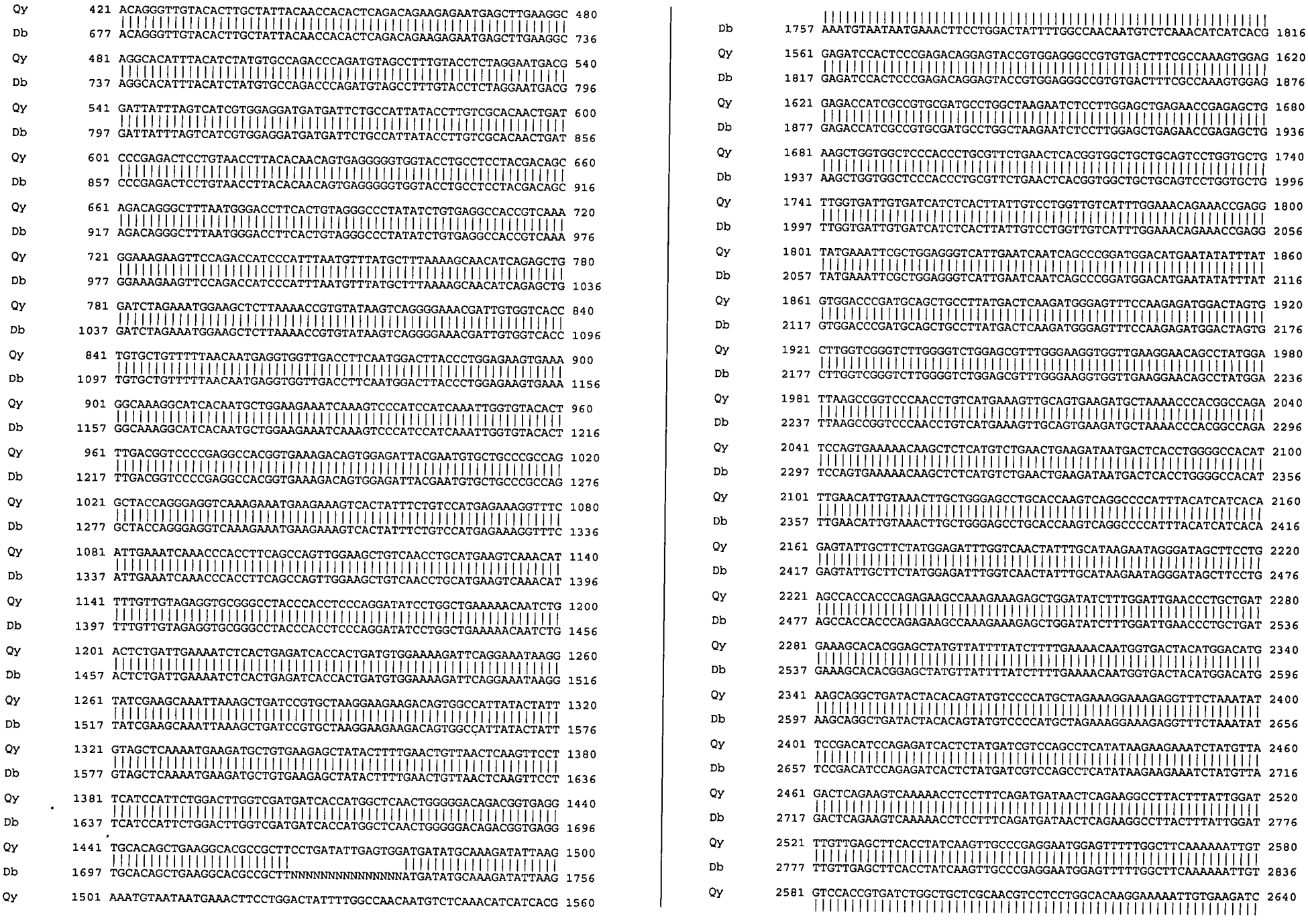
Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676
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Db      2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db      2897 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2956
Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db      2957 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3016
Qy      2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db      3017 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3076
Qy      2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db      3077 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3136
Qy      2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db      3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196
Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db      3197 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3256
Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db      3257 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3316
Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db      3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db      3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db      3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496
Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db      3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556
Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db      3557 AGCAGTTCCACCTTCATCAAGAGAGAGNGTACCCGGCTATAACATGATCAACATGTGGAC 3616
Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db      3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db      3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db      3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796
Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db      3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db      3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db      3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976
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Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db      3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db      4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096
Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db      4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156
Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db      4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216
Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db      4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275
Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db      4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335
Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db      4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395
Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Db      4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455
Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Db      4456 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4515
Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
Db      4516 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4575
Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Db      4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635
Qy      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db      4636 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4695
Qy      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db      4696 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4755
Qy      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCCAATATATGTATT 4560
Db      4756 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCCAATATATGTATT 4815
Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db      4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875
Qy      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db      4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935
Qy      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db      4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995
Qy      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db      4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055
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Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5116 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5175

Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTA-GTGACATTTAATGC 4979
             |||||||||||||||||||||||||||||||||||| |||||| ||||| ||||||||
Db       5176 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTTAGGTTAGGTGACGTTTAATGC 5235

Qy       4980 CATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAG 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5236 CATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAG 5295

Qy       5040 CTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGG 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5296 CTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGG 5355

Qy       5100 GAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAA 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5356 GAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAA 5415

Qy       5160 GGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5416 GGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTT 5475

Qy       5220 TTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATT 5279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5476 TTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATT 5535

Qy       5280 GTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATA 5339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5536 GTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATA 5595

Qy       5340 CTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTG 5399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5596 CTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTG 5655

Qy       5400 CTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTAC 5459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5656 CTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTAC 5715

Qy       5460 TGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAA 5519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5716 TGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAA 5775

Qy       5520 GACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTA 5579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5776 GACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTA 5835

Qy       5580 GACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACT 5639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5836 GACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACT 5895

Qy       5640 CTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGC 5699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5896 CTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGC 5955

Qy       5700 ATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGC 5759
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5956 ATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGC 6015

Qy       5760 TCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCC 5819
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6016 TCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCC 6075

Qy       5820 AGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCT 5879
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6076 AGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCT 6135

Qy       5880 ACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTT 5939
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 ACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTT 6195

Qy       5940 AAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTT 5999
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6196 AAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTT 6255

Qy       6000 TGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTA 6059
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 TGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTA 6315

Qy       6060 TATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTA 6119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6316 TATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTA 6375

Qy       6120 TATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCA 6179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6376 TATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCA 6435

Qy       6180 AAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTG 6239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6436 AAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTG 6495

Qy       6240 TGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAA 6299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6496 TGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAA 6555

Qy       6300 TGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAA 6359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6556 TGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAA 6615

Qy       6360 TGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6413
             ||||||||||||||||||||||||||||||||||||||||| |||| ||| ||| |
Db       6616 TGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAACAAAACAAACAAACA 6669
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RESULT 21
ADQ38813
ID ADQ38813 standard; DNA; 6633 BP.
XX
AC ADQ38813;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 476.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
DR P-PSDB; ADQ39641.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX

PS Claim 7; SEQ ID NO 476; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 6633 BP; 1917 A; 1339 C; 1516 G; 1847 T; 0 U; 14 Other;

Query Match 98.7%; Score 6327; DB 13; Length 6633;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 6357; Conservative 14; Mismatches 4; Indels 6; Gaps 3;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGRCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 778
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGCAACATCAGAGC 1033

Qy        779 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 1093

Qy        839 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1094 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 1153

Qy        899 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 958
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1154 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 1213

Qy        959 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1273

Qy       1019 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTT 1078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db       1274 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGKT 1333

Qy       1079 TCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAAC 1138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 TCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAAC 1393

Qy       1139 ATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATC 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 ATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATC 1453

Qy       1199 TGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAA 1258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 TGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAA 1513

Qy       1259 GGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTA 1318
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 GSTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTA 1573

Qy       1319 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1574 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1633

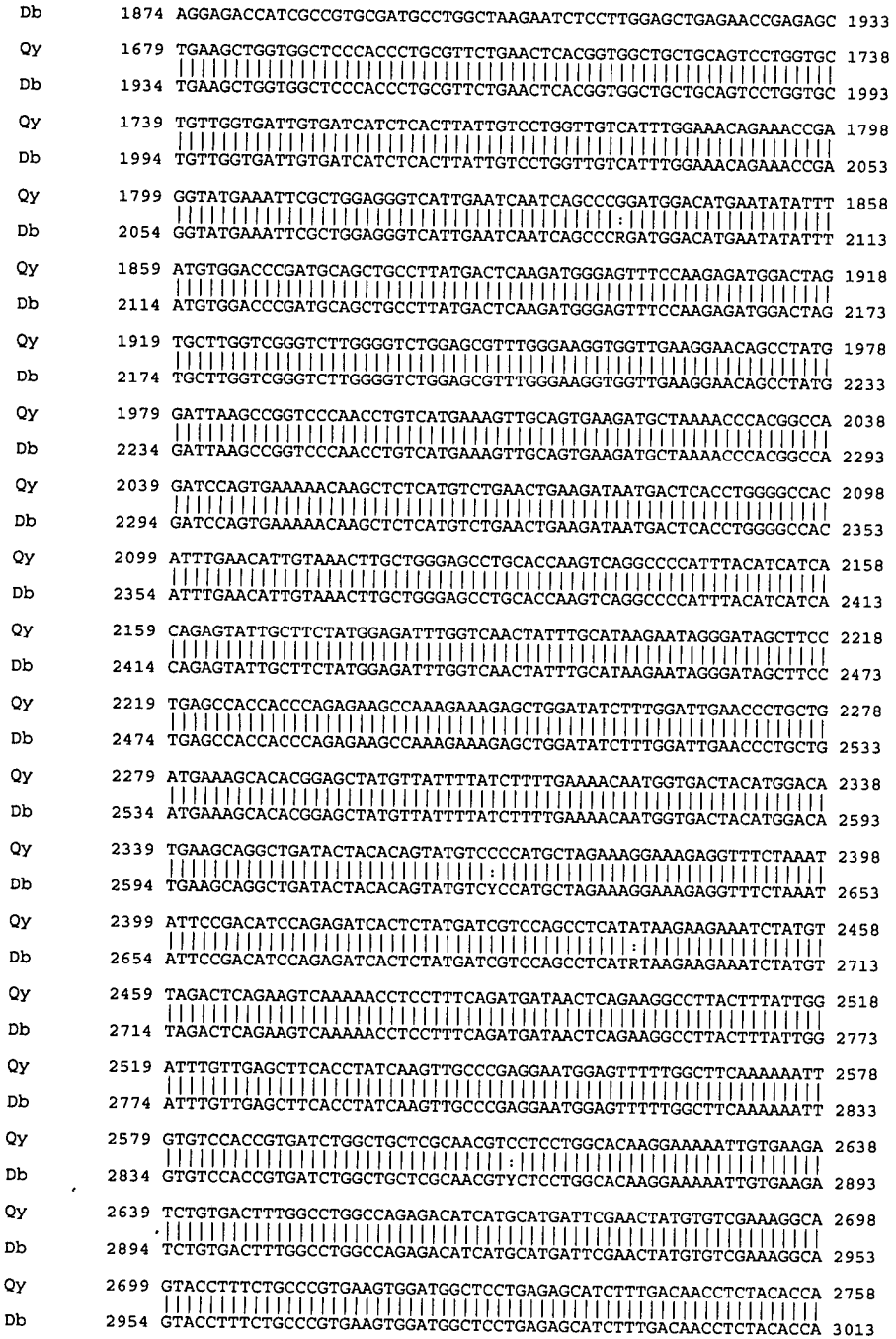
Qy       1379 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1438
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db       1634 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTYAACTGGGGGACAGACGGTGA 1693

Qy       1439 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1753

Qy       1499 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1813

Qy       1559 CGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1618
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 CGGAGATCCACYCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1873

Qy       1619 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1874 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1933
Qy 1679 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1738
Db 1934 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1993
Qy 1739 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 1798
Db 1994 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 2053
Qy 1799 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTT 1858
Db 2054 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCRGATGGACATGAATATATTT 2113
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Db 2174 TGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATG 2233
Qy 1979 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2038
Db 2234 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2293
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Db 2354 ATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCA 2413
Qy 2159 CAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCC 2218
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Qy 2219 TGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTG 2278
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Qy 2459 TAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGG 2518
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Qy 2519 ATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATT 2578
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Qy 2579 GTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGA 2638
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Qy 2639 TCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCA 2698
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Qy 2879 GGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGA 2938
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Qy      4019 CATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTG 4078
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Qy      4859 TTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAA 4918
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Db      5113 TTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGMA 5172

Qy      4919 TTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATG 4978
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Qy      4979 CCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAA 5038
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5233 CCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAA 5292

Qy      5039 GCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGG 5098
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Qy      5279 TGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAAT 5338
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Qy      5339 ACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGT 5398
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Db      6133 TACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTT 6192

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Db      6193 TAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTT 6252

Qy      5999 TTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCT 6058
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Db       6253 TTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCT 6312

Qy       6059 ATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTT 6118
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Qy       6119 ATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCC 6178
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Db       6373 ATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCC 6432

Qy       6179 AAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGT 6238
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Db       6553 ATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAA 6612

Qy       6359 ATGATATATAATTTAAAGTTA 6379
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Db       6613 ATGATATATAATTTAAAGTTA 6633
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RESULT 22
ADM69032
ID ADM69032 standard; cDNA; 6618 BP.
XX
AC ADM69032;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant RVIES560-564 cDNA.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	395. .3649
FT		/*tag= a
FT		/product= "Human PDGFRA cancer-related activating mutant
FT		RVIES560-564 protein"
FT	misc_difference	2071. .2072
FT		/*tag= b
FT		/note= "Wild-type AGGGTCATTGAATCA deleted"

XX
PN WO2003105773-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018901.
XX
PR 13-JUN-2002; 2002US-0389107P.
PR 08-JAN-2003; 2003US-0438899P.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (DAND) DANA FARBER CANCER INST INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (USGO) US DEPT VETERANS AFFAIRS.
XX
PI Heinrich MC, Corless CL, Fletcher JA, Demetri GD;
XX
DR WPI; 2004-082052/08.
DR P-PSDB; ADM69033.
XX
PT New isolated variant platelet derived growth factor alpha (PDGFRA)
PT polypeptide, useful for screening for a compound useful in influencing
PT PDGFRA-mediated neoplasia in a mammal.
XX
PS Claim 13; SEQ ID NO 22; 302pp; English.
XX
CC The invention relates to a novel isolated variant platelet derived growth
CC factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC for screening for a compound that may influence PDGFRA-mediated neoplasia
CC in a mammal. The current sequence is that of the human PDGFRA cancer-
CC related activating mutant RVIES560-564 cDNA of the invention.
XX
SQ Sequence 6618 BP; 1914 A; 1342 C; 1514 G; 1848 T; 0 U; 0 Other;

Query Match 98.6%; Score 6324.4; DB 12; Length 6618;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 6361; Conservative 0; Mismatches 1; Indels 16; Gaps 2;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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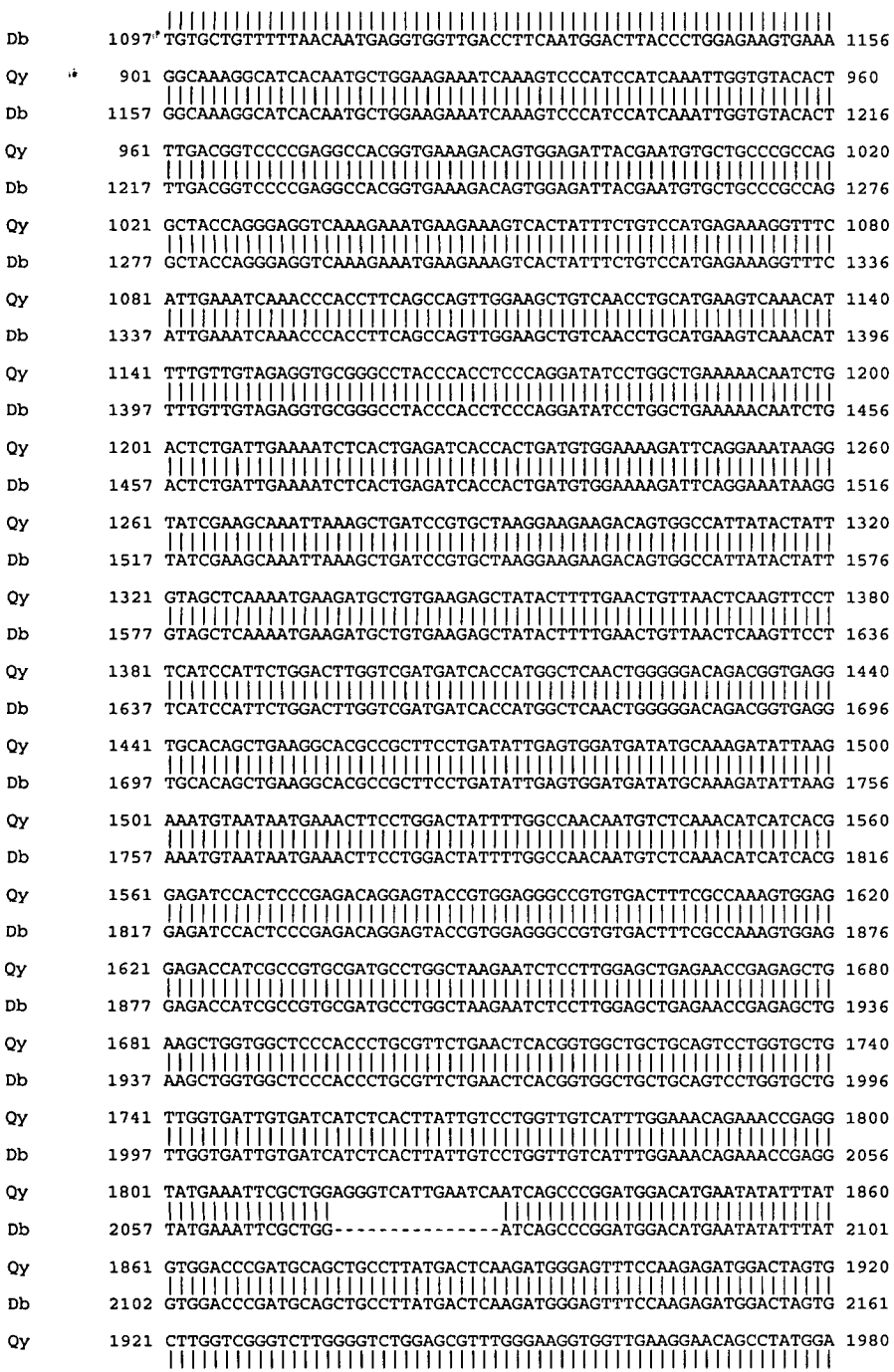
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Db       5221 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5280

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Db       5281 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5340

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db       5341 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5400

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Db       5461 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5520

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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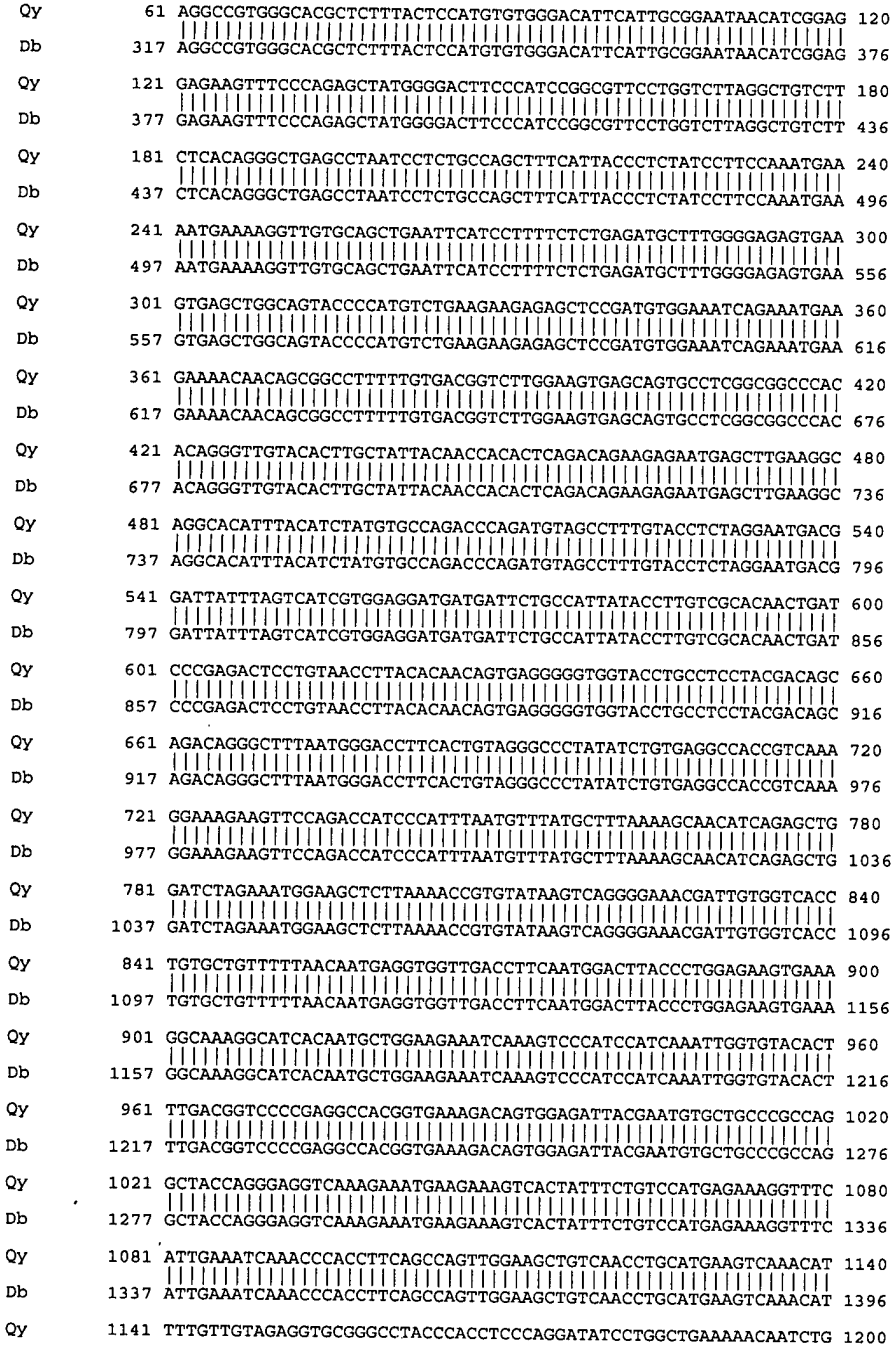
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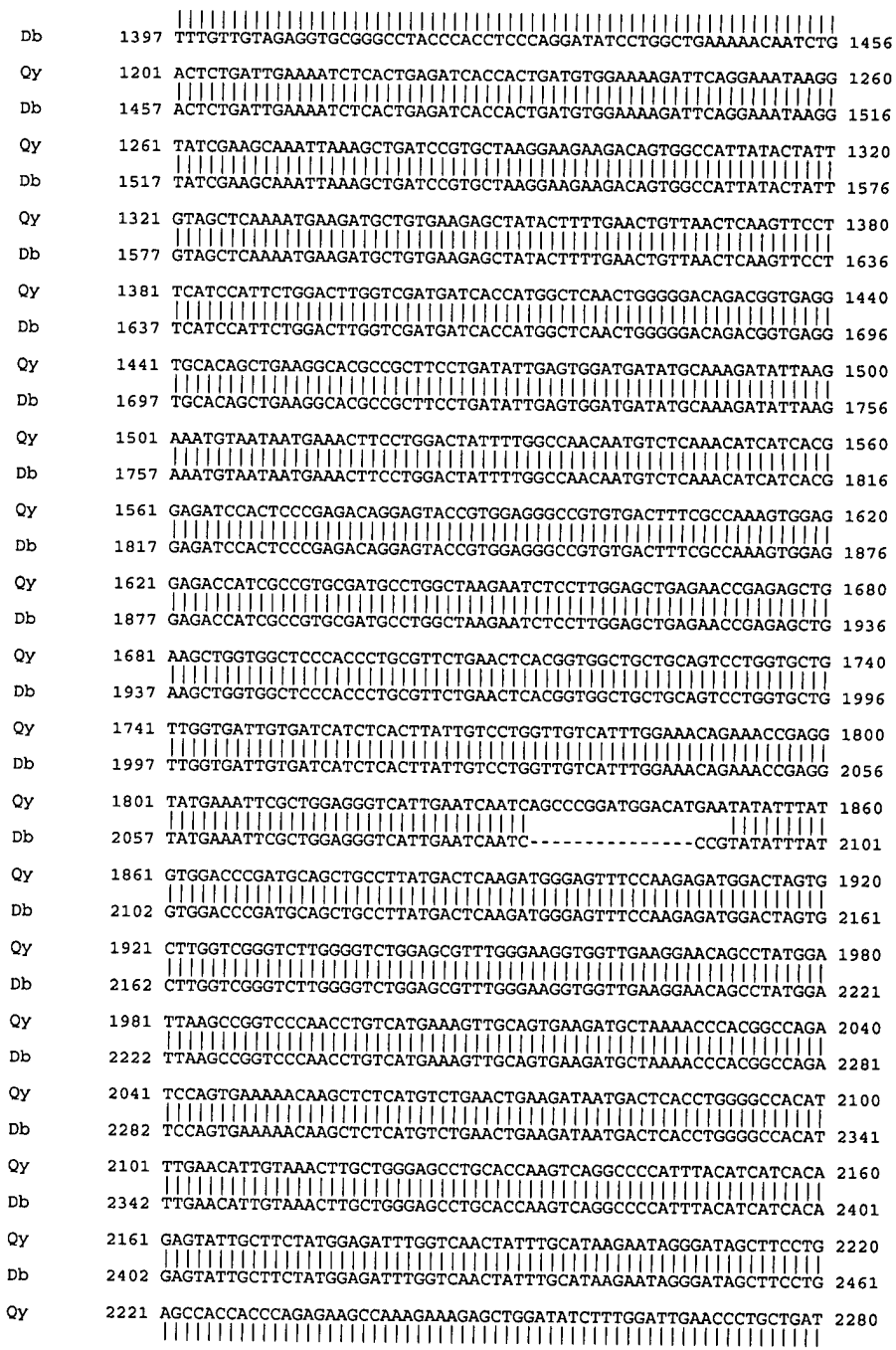
Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6601 GATATATAATTTAAAGTT 6618


RESULT 23
ADM69021
ID   ADM69021 standard; cDNA; 6618 BP.
XX
AC   ADM69021;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human PDGFRA cancer-related activating mutant SPDGHE566-571R cDNA.
XX
KW   platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW   type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3649
FT                   /*tag=  a
FT                   /product= "Human PDGFRA cancer-related activating mutant
FT                   SPDGHE566-571R protein"
FT   misc_difference 2090. .2092
FT                   /*tag=  b
FT                   /note= "Wild-type AGCCCGGATGGACATGAA substituted by CCG"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69022.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 13; SEQ ID NO 11; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant SPDGHE566-571R cDNA of the invention.
XX
SQ   Sequence 6618 BP; 1913 A; 1342 C; 1513 G; 1850 T; 0 U; 0 Other;

  Query Match             98.5%;  Score 6319.6;  DB 12;  Length 6618;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 6358;  Conservative    0;  Mismatches    4;  Indels   16;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316
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Db      2462 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2521

Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2522 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2581

Qy      2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2582 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2641

Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
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Db      2642 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2701

Qy      2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Db      2702 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2761

Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Db      2762 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2821

Qy      2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
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Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
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Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Db      3182 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3241

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Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
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Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
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Db      3362 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3421

Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
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Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
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Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
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Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
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Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5340

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db       5341 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5400

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Db       5461 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5520

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5580

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db       5581 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5640

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6541 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6600

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6601 GATATATAATTTAAAGTT 6618
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RESULT 24
ADM69036
ID ADM69036 standard; DNA; 6633 BP.
XX
AC ADM69036;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human PDGFRA cancer-related activating mutant consensus DNA.
XX
KW platelet derived growth factor receptor alpha; PDGFRA; neoplasia; human;
KW type III receptor tyrosine kinase; RTK; ss; gene; mutant; cancer.
XX

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             395. .3664
FT                   /*tag=  a
FT                   /product= "Human PDGFRA cancer-related activating mutant
FT                   consensus protein"
XX
PN   WO2003105773-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-US018901.
XX
PR   13-JUN-2002; 2002US-0389107P.
PR   08-JAN-2003; 2003US-0438899P.
XX
PA   (UYOR-) UNIV OREGON HEALTH SCI.
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA   (USGO ) US DEPT VETERANS AFFAIRS.
XX
PI   Heinrich MC,  Corless CL,  Fletcher JA,  Demetri GD;
XX
DR   WPI; 2004-082052/08.
DR   P-PSDB; ADM69037.
XX
PT   New isolated variant platelet derived growth factor alpha (PDGFRA)
PT   polypeptide, useful for screening for a compound useful in influencing
PT   PDGFRA-mediated neoplasia in a mammal.
XX
PS   Claim 15; SEQ ID NO 26; 302pp; English.
XX
CC   The invention relates to a novel isolated variant platelet derived growth
CC   factor receptor alpha (PDGFRA) polypeptide. The polypeptide of the
CC   invention is a type III receptor tyrosine kinase (RTK) and may be useful
CC   for screening for a compound that may influence PDGFRA-mediated neoplasia
CC   in a mammal. The current sequence is that of the human PDGFRA cancer-
CC   related activating mutant consensus DNA of the invention.
XX
SQ   Sequence 6633 BP; 1901 A; 1334 C; 1503 G; 1841 T; 0 U; 54 Other;

  Query Match             98.4%;  Score 6310.4;  DB 12;  Length 6633;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 6322;  Conservative    0;  Mismatches   55;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

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Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

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Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
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Db       1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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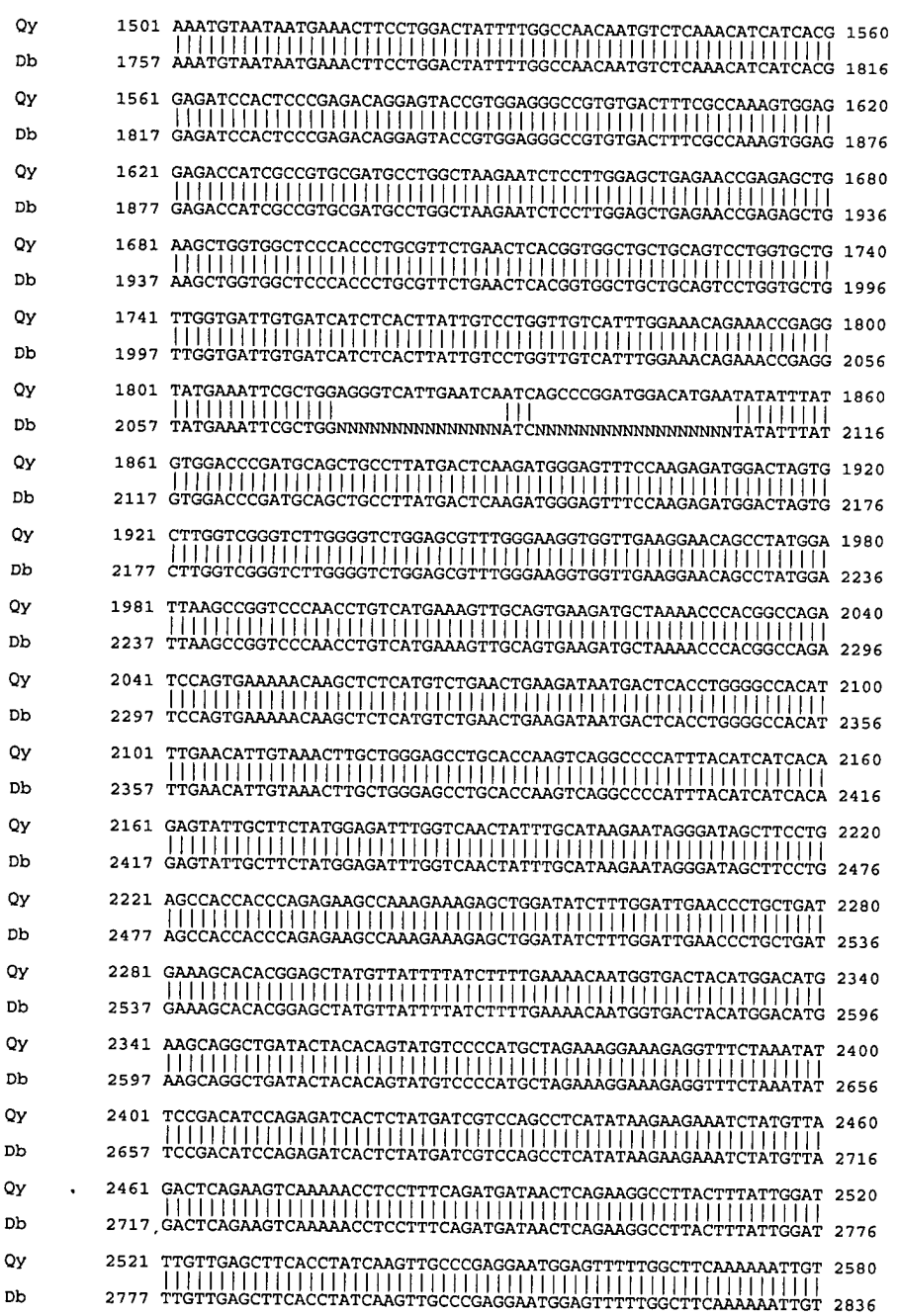
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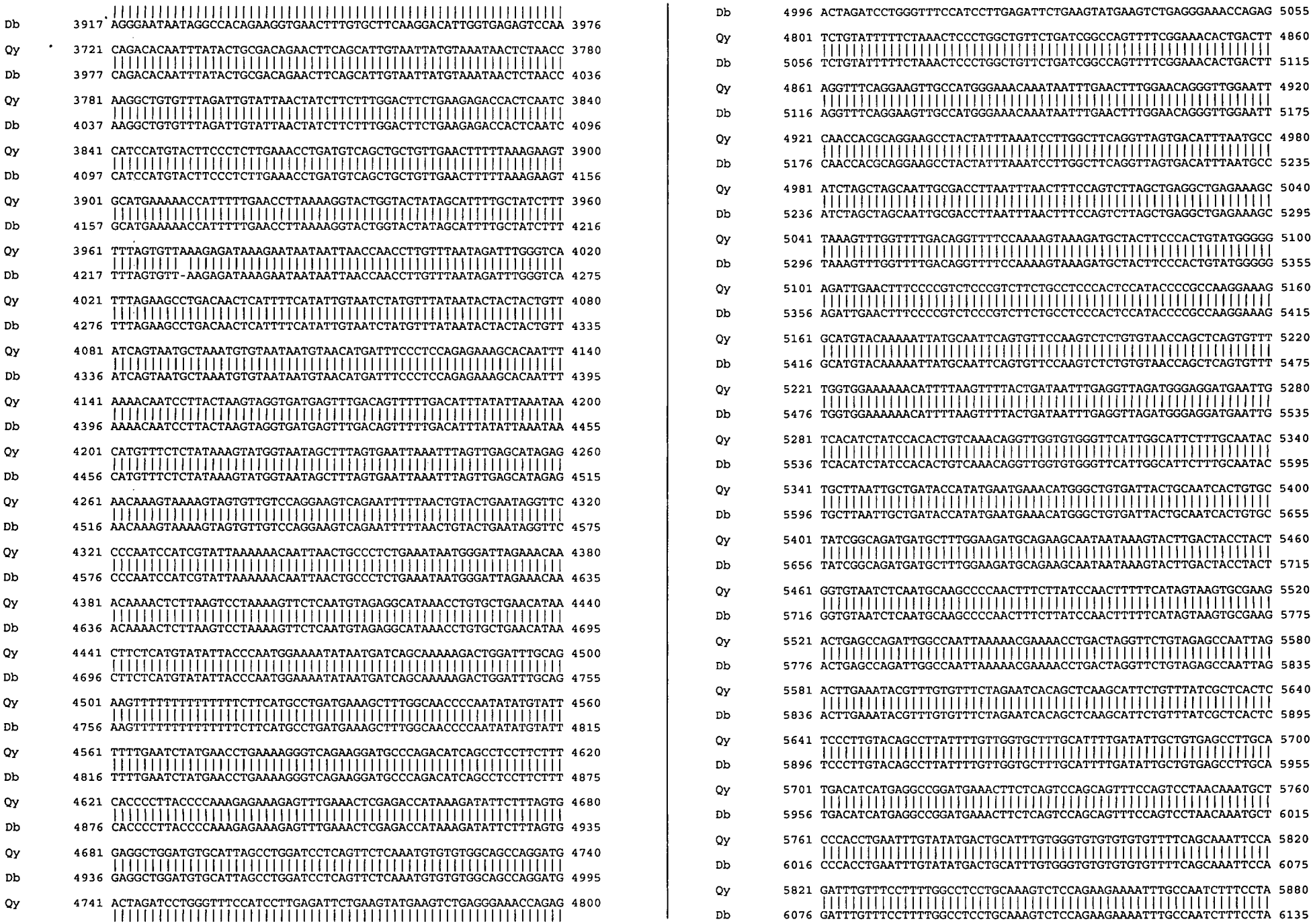
Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
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Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556
Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720


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Db 3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096
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Db 4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156
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Db 4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Db 4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455
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Db 4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635
Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db 4756 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4815
Qy 4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db 4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875
Qy 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db 4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935
Qy 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db 4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db 4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055
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Db 5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115
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Qy 4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Db 5236 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5295
Qy 5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Db 5296 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5355
Qy 5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Db 5356 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5415
Qy 5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Db 5416 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5475
Qy 5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db 5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535
Qy 5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Db 5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595
Qy 5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db 5596 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5655
Qy 5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db 5656 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5715
Qy 5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Db 5716 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5775
Qy 5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Db 5776 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5835
Qy 5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
Db 5836 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5895
Qy 5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Db 5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955
Qy 5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
Db 5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015
Qy 5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Db 6016 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6075
Qy 5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Db 6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135

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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6195

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6315

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6316 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6375

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6376 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6435

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6436 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6495

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6496 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6556 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6615

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 25
ADQ59531
ID ADQ59531 standard; cDNA; 6240 BP.
XX
AC ADQ59531;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer-associated (CA) gene cDNA sequence SEQ ID NO:167.
XX
KW human; cancer-associated gene; cancer-associated protein; cytostatic;
KW gene therapy; vaccine; tyrosine kinase antagonist;
KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004058288-A1.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040082.
XX
PR 17-DEC-2002; 2002US-00322696.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543349/52.
DR P-PSDB; ADQ59532.
XX
PT New cancer-associated nucleic acid for diagnosing, preventing or treating
PT cancer (e.g. lymphoma) or for screening agents that may be used for
PT treating or preventing cancer.
XX
PS Claim 1; SEQ ID NO 167; 143pp; English.
XX
CC The present invention describes human cancer-associated (CA) nucleotide
CC sequences (I). Also described: (1) an expression vector comprising (I);
CC (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC within an open reading frame of a CA sequence; (5) an isolated antibody,
CC or its antigen binding fragment, that binds to the above polypeptide; (6)
CC a hybridoma that produces the monoclonal antibody described above; (7) a
CC pharmaceutical composition comprising the antibody and a pharmaceutical
CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC the above (monoclonal) antibody or polynucleotide that selectively
CC hybridises to any of the polynucleotide sequences mentioned above; (9)
CC methods for diagnosing cancer or for detecting the presence or absence of
CC cancer cells in an individual; (10) a method for inhibiting growth of
CC cancer cells in an individual; (11) a method for delivering a therapeutic
CC agent to cancer cells in an individual; (12) an electronic library
CC comprising the polynucleotide or polypeptide, or their fragments,
CC mentioned above; (13) a method of screening for anticancer activity; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC or the presence of the antibody in a test cell or serum sample; (15) a
CC method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein encoded by the above nucleic acid molecule; and
CC (16) a method for treating cancers. (I) has cytostatic activity, and can
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC and as a G-protein coupled receptor antagonist. The compositions and
CC methods of the present invention can be used for diagnosing, preventing
CC and treating cancer, especially lymphomas. They may also be used in
CC screening for agents that may be used for treating or preventing cancer.
CC The present sequence represents a human CA gene cDNA sequence, which is
CC given in the exemplification of the present invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6240 BP; 1813 A; 1270 C; 1403 G; 1754 T; 0 U; 0 Other;

Query Match 97.1%; Score 6224.2; DB 12; Length 6240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6237; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480
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Qy       619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
Db       481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy       679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
Db       541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy       739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
Db       601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy       799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
Db       661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy       859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db       721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy       919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db       781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy       979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db       841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy      1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db       901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy      1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db       961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy      1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db      1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db      1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db      1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db      1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db      1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db      1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy      1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db      1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db      1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db      1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758

Db      1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy      1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db      1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db      1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db      1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy      1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db      1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy      1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db      1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

Qy      2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db      1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy      2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db      1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy      2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
Db      2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100

Qy      2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db      2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy      2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db      2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy      2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db      2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy      2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db      2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy      2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db      2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

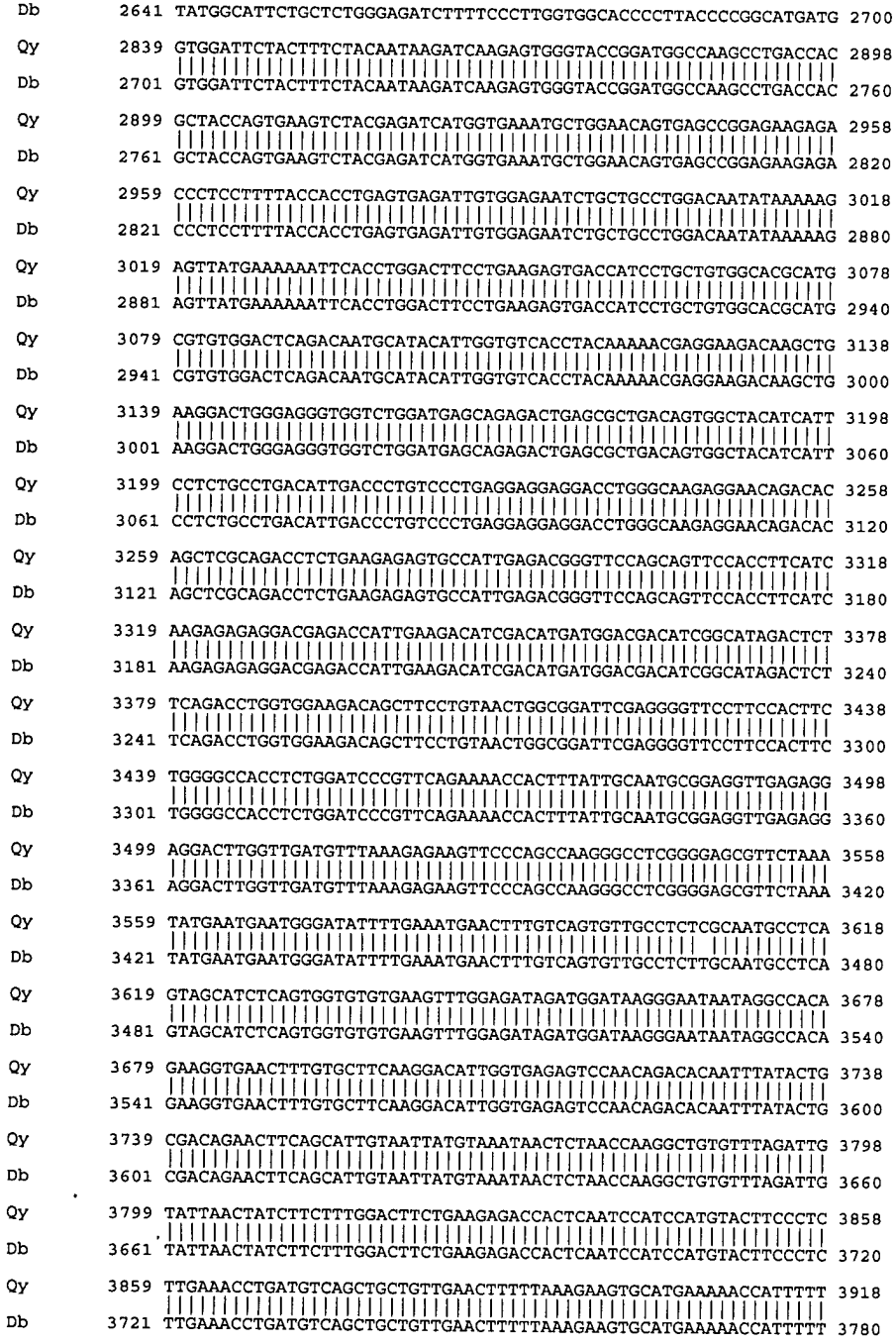
Qy      2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db      2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460

Qy      2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
Db      2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy      2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db      2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580

Qy      2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db      2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy      2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Db 2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy 2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db 2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760
Qy 2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
Db 2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820
Qy 2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
Db 2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880
Qy 3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
Db 2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940
Qy 3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
Db 2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000
Qy 3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
Db 3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060
Qy 3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Qy 3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
Db 3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240
Qy 3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTC 3438
Db 3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTC 3300
Qy 3439 TGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGG 3498
Db 3301 TGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGG 3360
Qy 3499 AGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAA 3558
Db 3361 AGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAA 3420
Qy 3559 TATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTCA 3618
Db 3421 TATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTCA 3480
Qy 3619 GTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACA 3678
Db 3481 GTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACA 3540
Qy 3679 GAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTG 3738
Db 3541 GAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTG 3600
Qy 3739 CGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTG 3798
Db 3601 CGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTG 3660
Qy 3799 TATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTC 3858
Db 3661 TATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTC 3720
Qy 3859 TTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTT 3918
Db 3721 TTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTT 3780
Qy 3919 GAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATA 3978
Db 3781 GAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATA 3840
Qy 3979 AAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACT 4038
Db 3841 AAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACT 3900
Qy 4039 CATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATGT 4098
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Qy 4099 GTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAG 4158
Db 3961 GTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAG 4020
Qy 4159 TAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGT 4218
Db 4021 TAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGT 4080
Qy 4219 ATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTG 4278
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Qy 4279 TTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAA 4338
Db 4141 TTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAA 4200
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Db 4201 AAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCT 4260
Qy 4399 AAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACC 4458
Db 4261 AAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACC 4320
Qy 4459 CAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTC 4518
Db 4321 CAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTC 4379
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Db 4380 TTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACCT 4439
Qy 4579 GAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGA 4638
Db 4440 GAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGA 4499
Qy 4639 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 4698
Db 4500 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 4559
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Db 4560 GCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCC 4619
Qy 4759 ATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACT 4818
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Qy 4819 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 4878
Db 4680 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 4739
Qy 4879 ATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCT 4938
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Qy 4939 ACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCG 4998
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Qy       4999 ACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACA 5058
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Qy       5059 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 5118
Db       4920 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 4979

Qy       5119 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 5178
Db       4980 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 5039

Qy       5179 CAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTT 5238
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Qy       5239 AAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTG 5298
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Qy       5359 ATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTT 5418
Db       5220 ATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTT 5279

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Db       5280 TGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAA 5339

Qy       5479 GCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCA 5538
Db       5340 GCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCA 5399

Qy       5539 ATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTG 5598
Db       5400 ATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTG 5459

Qy       5599 TTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTAT 5658
Db       5460 TTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTAT 5519

Qy       5659 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 5718
Db       5520 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 5579

Qy       5719 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 5778
Db       5580 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 5639

Qy       5779 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 5838
Db       5640 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 5699

Qy       5839 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5898
Db       5700 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5759

Qy       5899 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 5958
Db       5760 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 5819

Qy       5959 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 6018
Db       5820 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 5879

Qy       6019 TAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACT 6078
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Qy       6079 GCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATA 6138
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Qy       6139 ATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAAT 6198
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Qy       6199 AATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAA 6258
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Qy       6259 ACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTT 6318
Db       6120 ACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTT 6179

Qy       6319 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 6378
Db       6180 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 6239

Qy       6379 A 6379
              |
Db       6240 A 6240
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RESULT 26
AAQ27451
ID AAQ27451 standard; DNA; 6075 BP.
XX
AC AAQ27451;
XX
DT 25-MAR-2003 (revised)
DT 09-FEB-1993 (first entry)
XX
DE Type A human platelet-derived growth factor receptor.
XX
KW PDGF; PDGF-R; mesenchyme; tyrosine kinase; ligand binding region; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   129. .3158
FT   /*tag= a
XX
PN WO9213867-A1.
XX
PD 20-AUG-1992.
XX
PF 28-JAN-1992; 92WO-US000730.
XX
PR 31-JAN-1991; 91US-00650793.
XX
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Escobedo JA, Williams LT, Wolf D, Tomlinson JE, Fretto LJ;
PI Giese NA;
XX
DR WPI; 1992-299970/36.
DR P-PSDB; AAR26206.
XX
PT Platelet derived growth factor receptor (PDGF-R) poly:peptide(s) - useful
PT as therapeutic and diagnostic agents e.g. for assaying PDGF activity in
PT sample.
XX
PS Disclosure; Page 90; 109pp; English.
XX
CC The sequence given encodes one allele of type A human platelet- derived
CC growth factor (PDGF) receptor (PDGF-R). This receptor is typically found
CC on cells of mesenchymal origin. It acts while in the form of two
CC transmembrane glycoproteins, each of which is about 180 kD. This receptor
CC has three major regions. The first is a transmembrane region, which spans
CC the membrane once, separating the regions of the receptor exterior to the
CC cell from those interior to the cell. The second region is an
CC extracellular region which contains the domains which bind the PDGF. The

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CC   third region is an intracellular region which posseses a tyrosine kinase
CC   activity. This tyrosine kinase domain is notable in having an insert of
CC   approx. 100 amino acids, as compared with most other receptor tyrosine
CC   kinase domains which are contiguous or have shorter insert sequences.
CC   Fragments of this sequence between 8 and 400 amino acids comprising one
CC   or more PDGF ligand binding region from the extracellular domain may be
CC   used to bind a PDGF ligand. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 6075 BP; 1823 A; 1228 C; 1375 G; 1647 T; 0 U; 2 Other;

  Query Match            64.9%;  Score 4160.8;  DB 2;  Length 6075;
  Best Local Similarity  94.4%;  Pred. No. 0;
  Matches 4534;  Conservative    0;  Mismatches   18;  Indels  253;  Gaps   11;

Qy        10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
             |||||||||||||||||||||  ||||||||| |||||||||||||| |   |||||||
Db         1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy        68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy       128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy       188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy       248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy       308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy       368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy       428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
             |||
Db       418 TGT---------------------------------------------------------- 420

Qy       488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ---------------------------------------------------------- 420

Qy       548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 ---TCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 477

Qy       608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       478 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 537

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       538 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 597

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       598 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 657

Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
             .||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       658 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 717

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       718 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 777

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       778 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 837

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       838 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 897

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       898 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 957

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       958 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1017

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1018 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1077

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1078 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1137

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1138 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1197

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1198 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1257

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1258 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1317

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1318 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1377

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1378 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1437

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1438 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1497

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1498 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1557

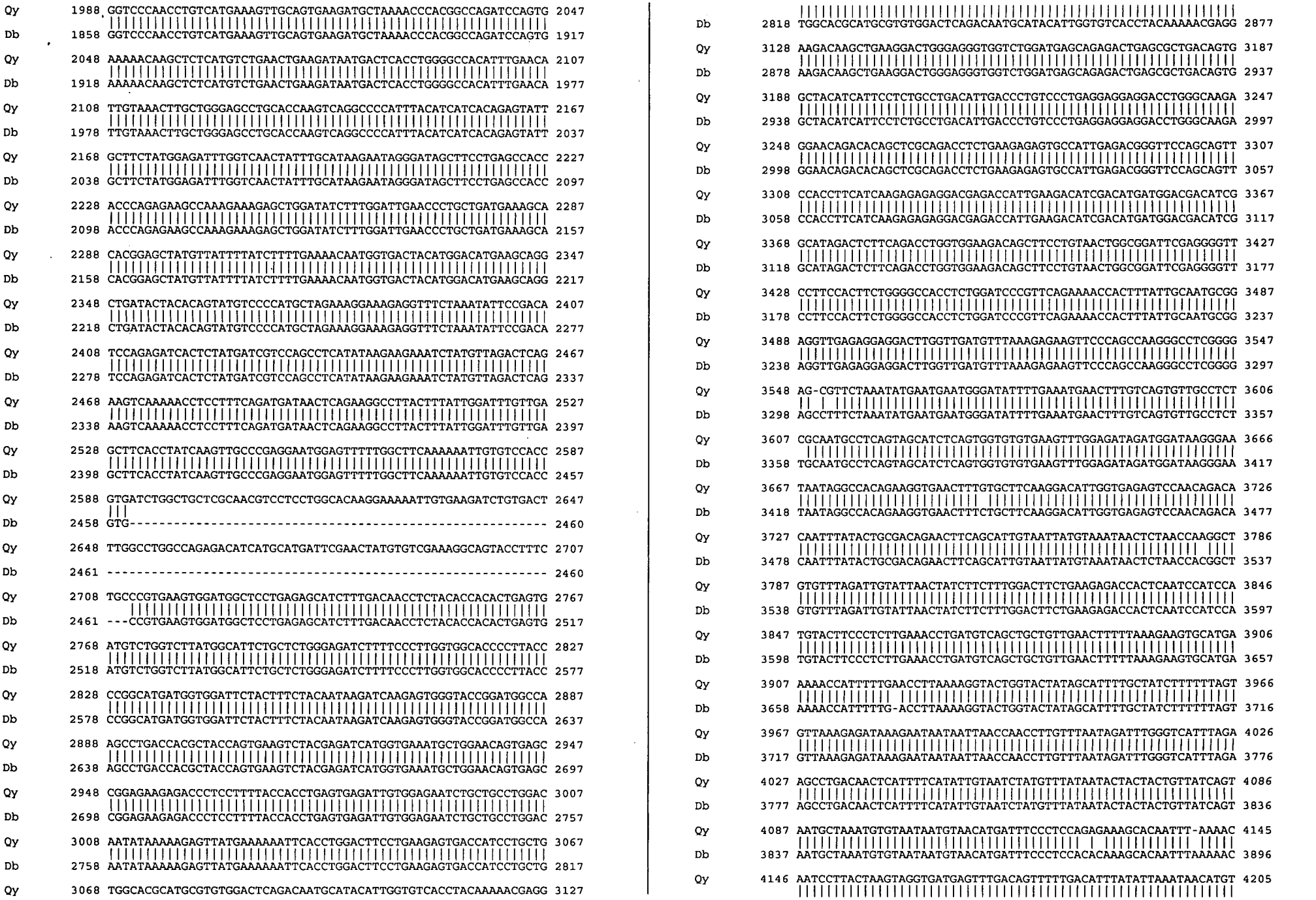
Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1558 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1617

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1618 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1677

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1678 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1737

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1738 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1797

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1798 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1857
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Qy 1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db 1858 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 1917
Qy 2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db 1918 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 1977
Qy 2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db 1978 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2037
Qy 2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db 2038 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2097
Qy 2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
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Qy 2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db 2158 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2217
Qy 2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db 2218 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2277
Qy 2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
Db 2278 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2337
Qy 2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db 2338 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2397
Qy 2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db 2398 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2457
Qy 2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
Db 2458 GTG---------- 2460
Qy 2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
Db 2461 ---------- 2460
Qy 2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
Db 2461 ---CCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2517
Qy 2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
Db 2518 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2577
Qy 2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
Db 2578 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2637
Qy 2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
Db 2638 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2697
Qy 2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
Db 2698 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2757
Qy 3008 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
Db 2758 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 2817
Qy 3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
Db 2818 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 2877
Qy 3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
Db 2878 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 2937
Qy 3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
Db 2938 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 2997
Qy 3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
Db 2998 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3057
Qy 3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
Db 3058 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3117
Qy 3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
Db 3118 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3177
Qy 3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
Db 3178 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3237
Qy 3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
Db 3238 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3297
Qy 3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
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Db 3478 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3537
Qy 3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
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Qy 3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
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Qy 3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
Db 3717 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 3776
Qy 4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
Db 3777 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 3836
Qy 4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
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Qy 4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205

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Db       3897 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 3956

Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3957 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4016

Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4017 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4076

Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4077 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4136

Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4137 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4196

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
             |||||||||||||||||||||||||||||||||  ||| ||||||||||||||||||||
Db       4197 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4256

Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
              || |||||||||||||||| |||||||||||||||||||| |||||||||||||||||||
Db       4257 TTNTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4316

Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
             |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db       4317 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4376

Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4377 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4436

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
             |||||||| |||||||||||| |||||||||||||||||||||||||||||||||  ||
Db       4437 AGGCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGA 4495

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4496 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4555

Qy       4802 CTGTA 4806
             |||||
Db       4556 CTGTA 4560


RESULT 27
AAQ06869
ID   AAQ06869 standard; DNA; 4054 BP.
XX
AC   AAQ06869;
XX
DT   25-MAR-2003  (revised)
DT   07-MAR-1991  (first entry)
XX
DE   Sequence encodes Platelet derived growth factor (PDGF) receptor protein.
XX
KW   Atherosclerosis; fibrotic diseases; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             205. .3471
FT                   /*tag=  a
XX
PN   WO9014425-A.
XX
PD   29-NOV-1990.
XX
PF   22-MAY-1989;   89US-00355018.
XX
PR   22-MAY-1989;   89US-00355018.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Kelly JD,  Murray MJ;
XX
DR   WPI; 1990-375992/50.
DR   P-PSDB; AAR08267.
XX
PT   DNA encoding platelet-derived growth factor - used to transform cells for
PT   culturing to detect PDG agonists and antagonists.
XX
PS   Claim 1; Fig 1; 30pp; English.
XX
CC   Gene product may be expressed from a transformed cell. It has utility in
CC   dection of PDGF agonist and antagonist analogues, binding AA, AB and BB
CC   isoforms. PDGF agonists may be used to enhance wound healing, and
CC   antagonists may be used to block the effects of PDGF eg. in treatment of
CC   atherosclerosis or fibrotic diseases. (Updated on 25-MAR-2003 to correct
CC   PA field.)
XX
SQ   Sequence 4054 BP; 1127 A; 886 C; 1027 G; 1014 T; 0 U; 0 Other;

  Query Match           59.8%;  Score 3837.2;  DB 2;  Length 4054;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3861;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

Qy        244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 429

Qy        364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        430 AACAACAGCGGCCTTTTTGTGACGCTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489

Qy        424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

Qy        544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy        604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729

Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789

Qy        724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 849

Qy        784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 909
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Qy       844 GCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       910 GCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969

Qy       904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       970 AAAGGCATCACAATACTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 1029

Qy       964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089

Qy      1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149

Qy      1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209

Qy      1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269

Qy      1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329

Qy      1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389

Qy      1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1390 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1449

Qy      1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1450 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1509

Qy      1444 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1503
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1510 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1569

Qy      1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629

Qy      1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689

Qy      1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1690 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1749

Qy      1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1750 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1809

Qy      1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1810 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1869

Qy      1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1870 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1929

Qy      1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989
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Qy      1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1990 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 2049

Qy      1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2050 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2109

Qy      2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
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Qy      2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
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Qy      2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
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Qy      2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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Qy      2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
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Qy      2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
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Qy      2644 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2703
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
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Qy      2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
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Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363

Db       3370 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3429

Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423

Db       3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

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Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543

Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603

Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663

Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723

Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783

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Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843

Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

Qy       3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903

Db       3910 CC-TGTACTTCCCTCTTGAAACCTGATGT-AGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3967

Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963

Db       3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989

Db    .  4028 AGTGTTAAAGAGATAAAGAATAATAA 4053


RESULT 28
ADZ61190
ID   ADZ61190 standard; DNA; 6576 BP.
XX
AC   ADZ61190;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Murine Pdgfra gene, SEQ ID 914.
XX
KW   Drug screening; Peroxisome Proliferator-Activated Receptor gamma;
KW   PPAR gamma; gene; ds.
XX
OS   Mus musculus.
XX
PN   US2005084872-A1.
XX
PD   21-APR-2005.
XX
PF   23-JAN-2004; 2004US-00764420.
XX
PR   24-JAN-2003; 2003US-0442797P.
PR   30-MAY-2003; 2003US-0474413P.
XX
PA   (LUMP/) LUM P Y.
PA   (TANY/) TAN Y.
PA   (DAIH/) DAI H.
PA   (MUIS/) MUISE E S.
PA   (BERG/) BERGER J P.
PA   (THOM/) THOMPSON J R.
XX
PI   Lum PY,  Tan Y,  Dai H,  Muise ES,  Berger JP,  Thompson JR;
XX
DR   WPI; 2005-313963/32.
DR   REFSEQ; NM_011058.
XX
PT   Determining whether agent has defined biological activity, by making
PT   comparison e.g. comparing efficacy value, toxicity value and classifier
PT   value of agent to reference values, and using results to determine
PT   whether agent has activity.
XX
PS   Example 2; SEQ ID NO 914; 51pp; English.
XX
CC   The present invention relates to a methods for screening biologically
CC   active agents, such as candidate drugs, to determine whether the agent
CC   possesses a defined biological activity. The methods involve making one
CC   or more comparisons chosen from comparing efficacy value of agent to
CC   reference efficacy value, comparing a toxicity value of the agent to
CC   reference toxicity value, comparing a classifier value of the agent to
CC   reference classifier value, and using the comparison result(s) to
CC   determine whether the agent possesses the defined biological activity.
CC   Also claimed is a population of oligonucleotide probes (I) specific for
CC   measuring the expression levels of members of a classifier population of
CC   genes or a toxicity-related population of genes. (I) are useful for
CC   measuring the expression levels of genes that are useful for identifying
CC   agonists or partial agonists of Peroxisome Proliferator-Activated
CC   Receptor (PPAR) gamma. ADZ61226-ADZ61295 are oligonucleotide probes which
CC   are useful in the method of the invention to measure the expression
CC   pattern of the toxicity-related population of mouse genes ADZ61171-
CC   ADZ61225. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from USPTO at seqdata.uspto.gov/sequence.html?DocID=20050084872.
XX
SQ   Sequence 6576 BP; 1791 A; 1481 C; 1608 G; 1696 T; 0 U; 0 Other;

  Query Match           55.9%;  Score 3585;  DB 14;  Length 6576;
  Best Local Similarity   76.2%;  Pred. No. 0;
  Matches 5013;  Conservative    0;  Mismatches 1305;  Indels  265;  Gaps   38;

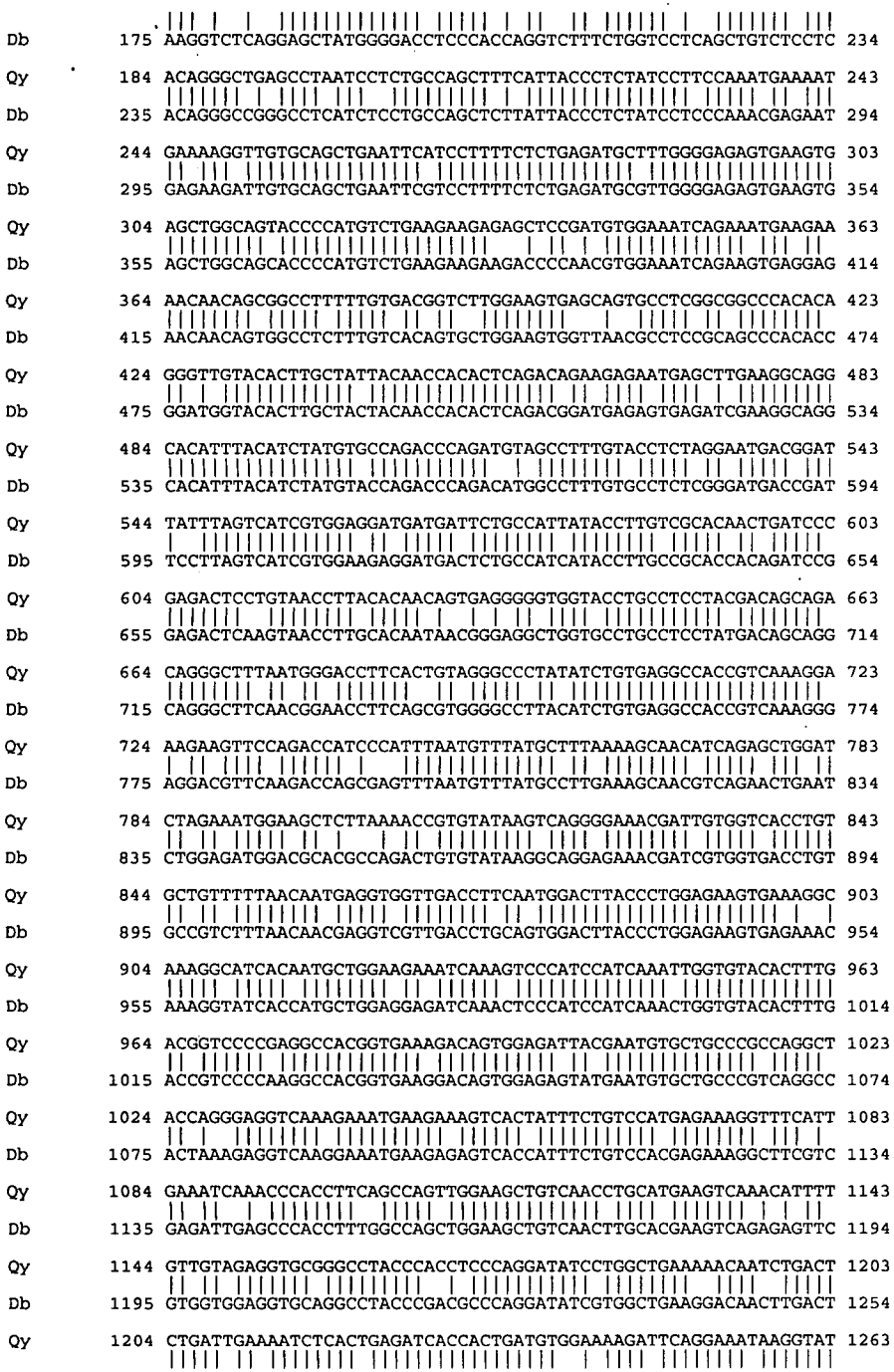
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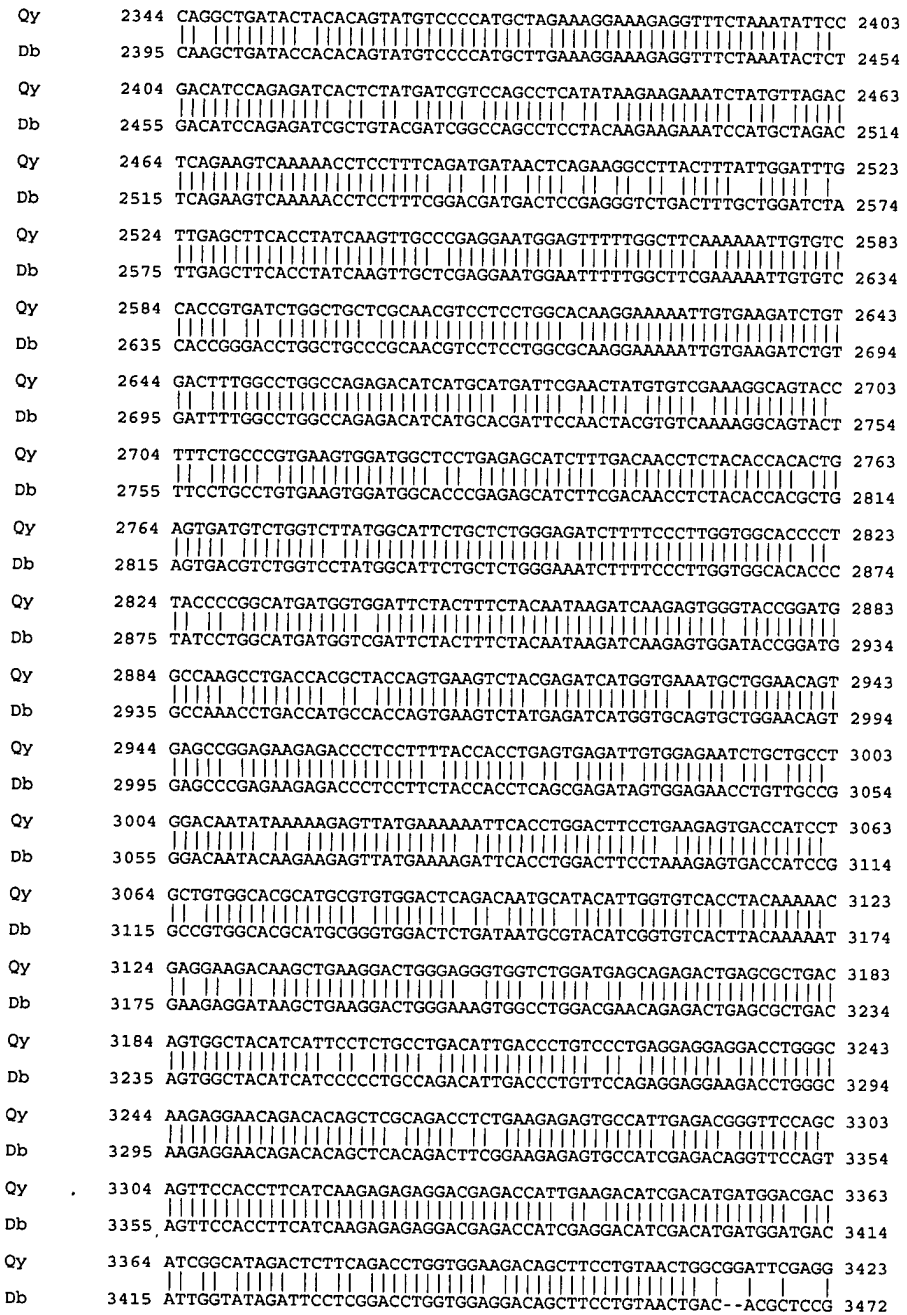
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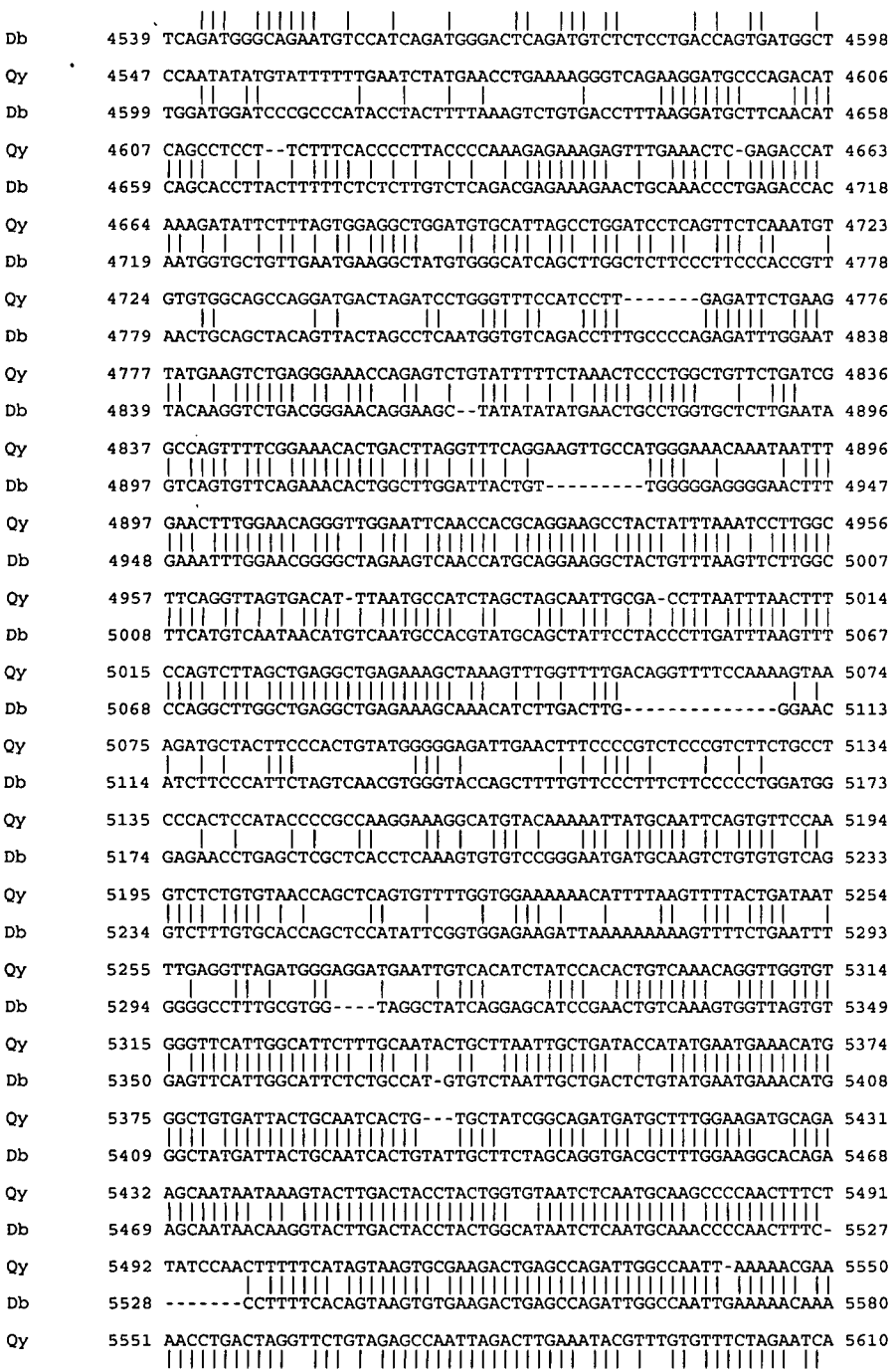
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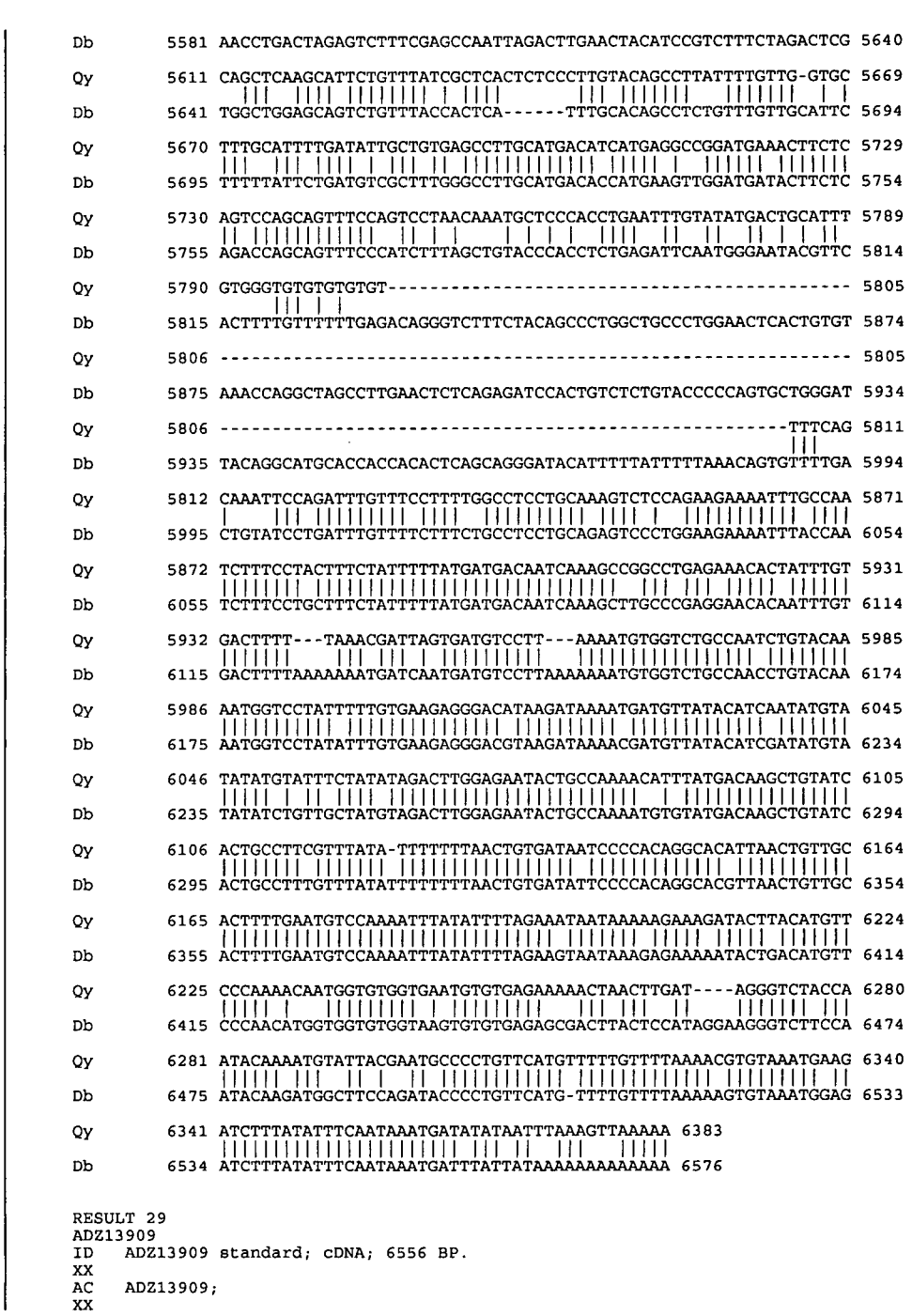
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Qy       124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
```


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Qy 304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
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Qy 2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Db 2995 GAGCCCGAGAAGAGACCCTCCTTCTACCACCTCAGCGAGATAGTGGAGAACCTGTTGCCG 3054
Qy 3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
Db 3055 GGACAATACAAGAAGAGTTATGAAAAGATTCACCTGGACTTCCTAAAGAGTGACCATCCG 3114
Qy 3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
Db 3115 GCCGTGGCACGCATGCGGGTGGACTCTGATAATGCGTACATCGGTGTCACTTACAAAAAT 3174
Qy 3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
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Qy 3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
Db 3235 AGTGGCTACATCATCCCCCTGCCAGACATTGACCCTGTTCCAGAGGAGGAAGACCTGGGC 3294
Qy 3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
Db 3295 AAGAGGAACAGACACAGCTCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGT 3354
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Qy 3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
Db 3415 ATTGGTATAGATTCCTCGGACCTGGTGGAGGACAGCTTCCTGTAACTGAC--ACGCTCCG 3472
Qy 3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
Db 3473 GGTATCATCTTCTCCGGGAGCCTCCTCGGGATAACCTTAAGAAAACCACTTCATTGCAAT 3532
Qy 3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAA--GTTCCCAGCCAAGGGCC 3541
Db 3533 GCAAAAGTTGAGAAGAGGACTTGGGTGATGTGGAGAGAGAAAGTTCCCGAGCCGAGGGCC 3592
Qy 3542 TCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3601
Db 3593 TTGGTAAGCCT-----GTGTGGATGACTGGGATA-CTTGGATTGAACTTTATCCGTGTTG 3646
Qy 3602 CCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3661
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Qy 3662 GGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAC 3721
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Qy 3722 AGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTC-TAACC 3780
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Qy 3781 AAGGCTGTGTTTAGAT-TGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAAT 3839
Db 3827 GAGGATGGGTTTAGATCTGTGTTAACTCTCCTCTCCGGACCTCTGAAGAGACCACTCAGT 3886
Qy 3840 CCATCCATG----TACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAA 3895
Db 3887 CCACCCGTGTGCTTCCTTCCTTCTTGGAATCCGGTACCAGCTGCTGTTGAATTTTCTCAT 3946
Qy 3896 GAAGTGCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTA 3955
Db 3947 GAAGTACATGCAAAACCA-CTTTGAACTTTGGAAGGTACTGGAACCGTTGTGTTTTACTG 4005
Qy 3956 TCTTTTTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTG 4015
Db 4006 TCTTGTAAGTGTTAAAGAGGCAAAAAGATAAAAACTAACCAACCGTGAGTAGTAGGTTTG 4065
Qy 4016 GGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTA 4075
Db 4066 GGTCTTTTAGGCACCCAAGAATTCCTCTGTATCTTGTAATCTGTACTTATAACACTACTA 4125
Qy 4076 CTG-TTATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCA 4134
Db 4126 CTGTTTAACAAGAATGCTAAATATGTAAT--CCTAACATGATTTCTTTACAGAGAAAGCA 4183
Qy 4135 CAATTTAAA-ACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATAT 4193
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Qy 4254 CATAGAGAACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAA 4313
Db 4301 ACTAGAGAGCAGAGTGTAAGTAGTTATCCAGAAAGTCAAACCTTTTTGTTTGTTCTAAG 4360
Qy 4314 TAGGTTCCCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTA 4373
Db 4361 CAGTCTCCCTAATCCAAGGCACTAGGAA--CAGTTAATGACCTCTGAAGTACTGGGATAA 4418
Qy 4374 GAAACAAACAAAACTC--TTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGC 4431
Db 4419 GCAAAGCAGAAACCCCGGTGGTGTCCTAAGTGTTCTCAGTACAAAGGCGTACGCCTGAGC 4478
Qy 4432 TGAACATAACTTCTCA---TGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGA 4488
Db 4479 CCAGTGTGACTCCTCACGCTGTGTGCGACCTTTTGGAAGAGACTCATTCACAAAAAGGAC 4538
Qy 4489 CTGGATTTGCAGAAGTTTTTTTTTTTTTTCTTC--ATGCCTGATGAAAGCTTTGGCAACC 4546





RESULT 29
ADZ13909
ID ADZ13909 standard; cDNA; 6556 BP.
XX
AC ADZ13909;
XX

DT 16-JUN-2005 (first entry)
XX
DE Murine cancer-associated cDNA #157.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ss.
XX
OS Mus sp.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
DR P-PSDB; ADZ13910.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1429; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents murine cancer-associated cDNA of the
CC invention.
XX
SQ Sequence 6556 BP; 1777 A; 1478 C; 1608 G; 1693 T; 0 U; 0 Other;

Query Match 55.8%; Score 3581.2; DB 14; Length 6556;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 5020; Conservative 0; Mismatches 1278; Indels 282; Gaps 39;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Db         39 CCATTACTGTTGGAGCTTGAGGGAGAGAAACAAACGGAGGA-GCTGCGGGGAAGGACTGG 97

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              | ||   ||||   || || |||||  || | |||  ||| ||||  | | |||| | ||
Db         98 AAGCTTGGGGCTTACTTTTCACTCCGGGTATCGGATTTTCTTTGCAAATTGACATAGAAG 157

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Db        158 GAGAAGGTCTCAGGAGCTATGGGGACCTCCCACCAGGTCTTTCTGGTCCTCAGCTGTCTC 217

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        278 AATGAGAAGATTGTGCAGCTGAATTCGTCCTTTTCTCTGAGATGCGTTGGGGAGAGTGAA 337

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||  |||||||||||||||||||||    | ||  | ||||||||||||| |||
Db        338 GTGAGCTGGCAGCACCCCATGTCTGAAGAAGACGACCCCAACGTGGAAATCAGAAGTGAG 397

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              || ||||||||  |||||  |||||  || ||  ||||||||    |  |||||  || ||||||
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Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              || || | |||||||||||| |||||||||||||||||| || |||| |||| | ||||||
Db        458 ACCGGATGGTACACTTGCTACTACAACCACACTCAGACGGATGAGAGTGAGATCGAAGGC 517

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              |||||||||||||||||||| ||||||||||  | ||||||| |||||  || |||||
Db        518 AGGCACATTTACATCTATGTACCAGACCCAGACATGGCCTTTGTGCCTCTCGGGATGACC 577

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||  |||||||||||||| || ||||| |||||||| |||||||| |||||  || |||
Db        578 GATTCCTTAGTCATCGTGGAAGAGGATGACTCTGCCATCATACCTTGCCGCACCACAGAT 637

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              || |||||||  |||||||| |||||  |  | | || |||| |||||||||  ||||||
Db        638 CCGGAGACTCAAGTAACCTTGCACAATAACGGGAGGCTGGTGCCTGCCTCCTATGACAGC 697

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              || |||||||| || || |||||||  || |||||  || ||||||||||||||||||||||
Db        698 AGGCAGGGCTTCAACGGAACCTTCAGCGTGGGGCCTTACATCTGTGAGGCCACCGTCAAA 757

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              || | || |||| |||||| |   |||||||||||||| || |||||||| |||||  |||
Db        758 GGGAGGACGTTCAAGACCAGCGAGTTTAATGTTTATGCCTTGAAAGCAACGTCAGAACTG 817

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              |||| || ||||| || |   | || |||||||| |||| |||||||| ||||| |||
Db        818 AATCTGGAGATGGACGCACGCCAGACTGTGTATAAGGCAGGAGAAACGATCGTGGTGACC 877

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||| || |||||||| ||||| |||||||| || |||||||||||||||||||||| |
Db        878 TGTGCCGTCTTTAACAACGAGGTCGTTGACCTGCAGTGGACTTACCCTGGAGAAGTGAGA 937

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Db        938 AACAAAGGTATCACCATGCTGGAGGAGATCAAACTCCCATCCATCAAACTGGTGTACACT 997

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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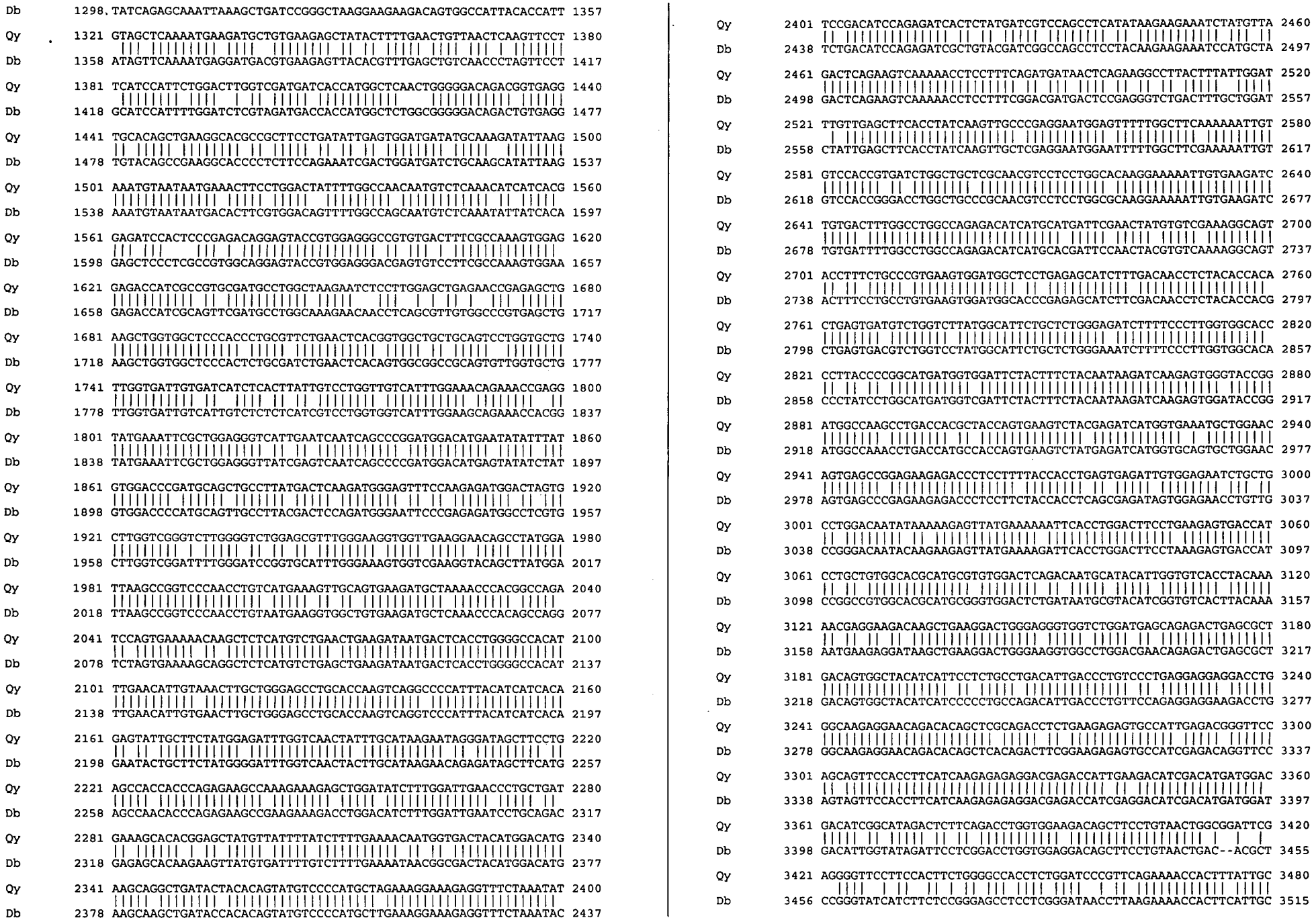
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              || || |  |||||||| |||||||||| |||||| |||||||||||  |||||||| |||
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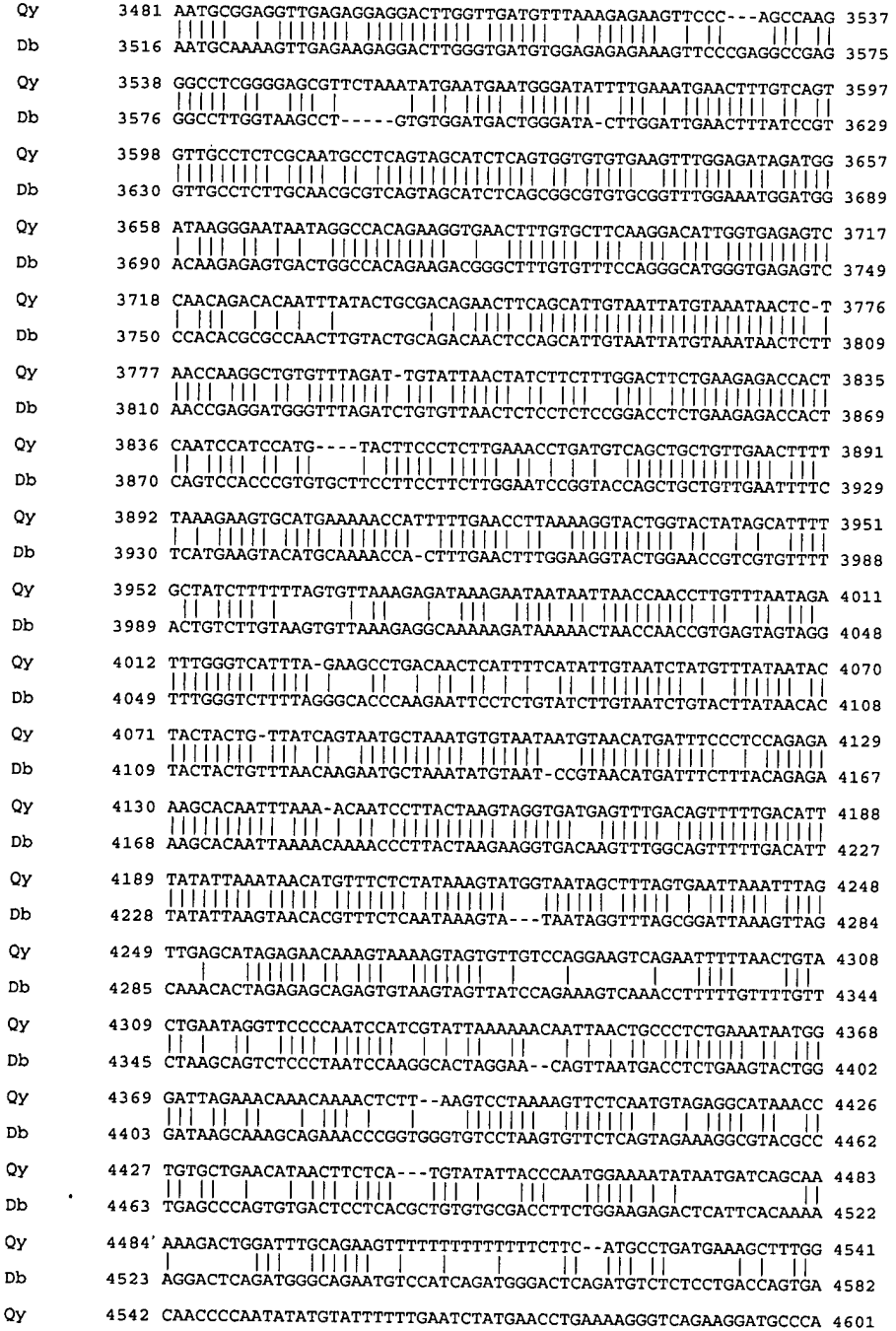
Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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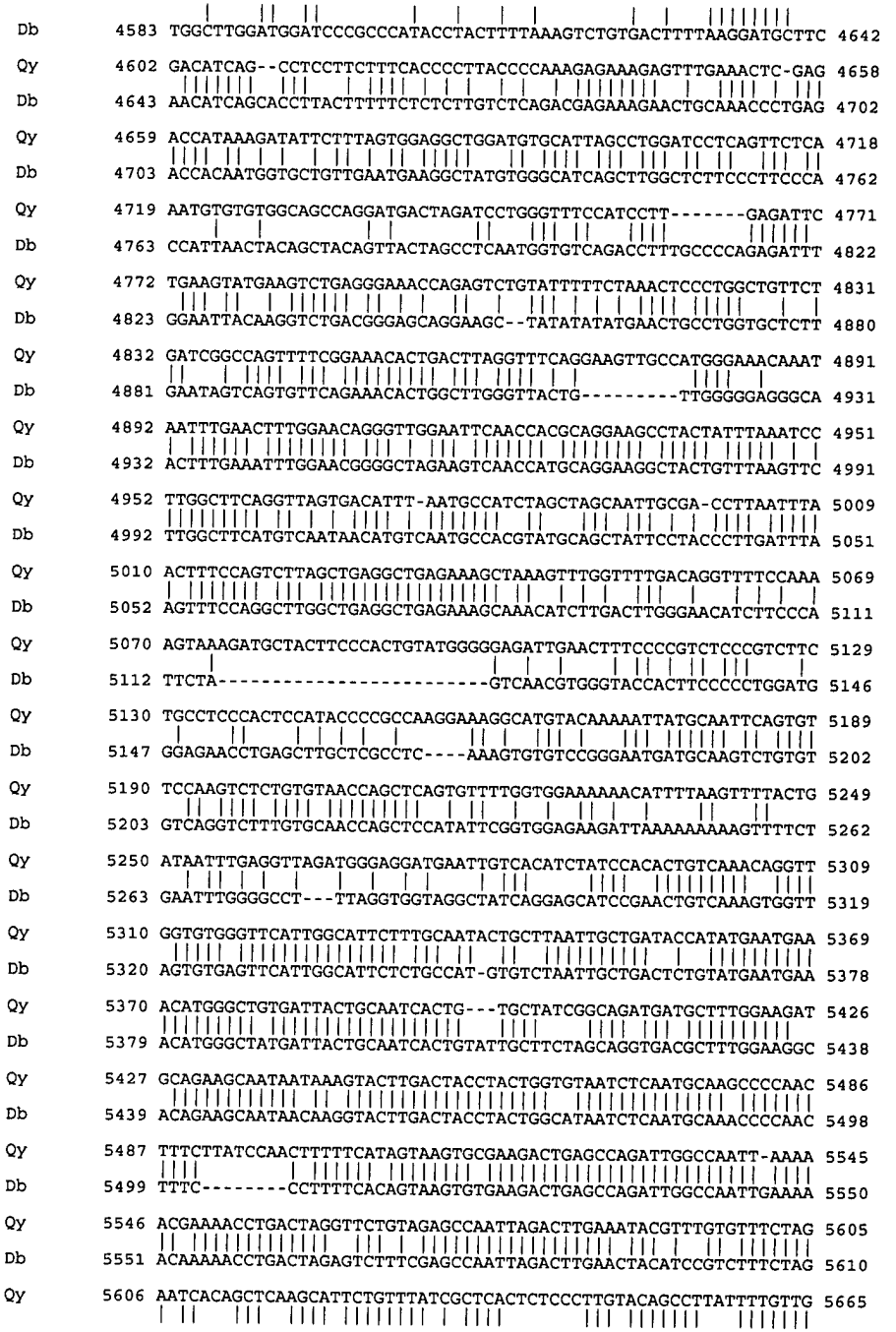
Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              || || || ||||||| |||||||||  | |||||||||| ||||||||  |||| ||
Db       1178 TTCGTGGTGGAGGTGCAGGCCTACCCGACGCCCAGGATATCGTGGCTGAAGGACAACTTG 1237

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              |||||||| || |||||||| |||||||||||||||  | |||| |||||||| ||||
Db       1238 ACTCTGATAGAGAATCTCACCGAGATCACCACTGATGTACAGAAGAGTCAGGAAACAAGG 1297

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
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Db       5611 ACTCGTGGCTGGAGCAGTCTGTTTACCACTCA------TTTGCACAGCCTCTGTTTGTTG 5664

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Db       5665 CTTCTTTTTATTCTGATGTCGCTTTGGGCCTTGCATGACACCATGAAGTTGGATGATACT 5724

Qy       5726 TCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGC 5785

Db       5725 TCTCAGACCAGCAGTTTCCCATCTTTAGCTGTACCCACCTCTGAGATTCAATGGGAATAC 5784

Qy       5786 ATTTGTGGGTGTGTGT---------------------------------------------- 5801

Db       5785 GTTCACTTTTGTTTTTTGAGACAGGGTCTTTCTACGCAGCCCTGGCTGCCCTGGAACTCA 5844

Qy       5802 ------------------------------------------------------------ 5801

Db       5845 CTGTGTAAACCAGGCTAGCCTTGAACTCTCAGAGATCCACTGTCTCTGTACCCCCAGTGC 5904

Qy       5802 ------------------------------------------------------GTG 5804

Db       5905 TGGGATTACAGGCATGCACCACCACACTCAGCAGGGATACATTTTTATTTTTAAACAGTG 5964

Qy       5805 TTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAAT 5864

Db       5965 TTTTGACTGTATCCTGATTTGTTTTCTTTCTGGCCTCCTGCAGAGTCCCTGGAAGAAAAT 6024

Qy       5865 TTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACAC 5924

Db       6025 TTACCAATCTTTCCTGCTTTCTATTTTTATGATGACAATCAAAGCTTGCCCGAGGAACAC 6084

Qy       5925 TATTTGTGACTTTT---TAAACGATTAGTGATGTCCTT---AAAATGTGGTCTGCCAATC 5978

Db       6085 AATTTGTGACTTTTAAAAAAATGATCAATGATGTCCTTAAAAAAATGTGGTCTGCCAACC 6144

Qy       5979 TGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCA 6038

Db       6145 TGTACAAAATGGTCCTATATTTGTGAAGAGGGACGTAAGATAAAACGATGTTATACATCG 6204

Qy       6039 ATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAG 6098

Db       6205 ATATGTATATATCTGTTGCTATGTAGACTTGGAGAATACTGCCAAAATGTGTATGACAAG 6264

Qy       6099 CTGTATCACTGCCTTCGTTTATA-TTTTTTTAACTGTGATAATCCCCACAGGCACATTAA 6157

Db       6265 CTGTATCACTGCCTTTGTTTATATTTTTTTTAACTGTGATATTCCCCACAGGCACGTTAA 6324

Qy       6158 CTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTT 6217

Db       6325 CTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAGTAATAAAGAGAAAAATACTG 6384

Qy       6218 ACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGAT----AGGG 6273

Db       6385 ACATGTTCCCAACATGGTGGTGTGGTAAGTGTGTGAGAGCGACTTACTCCATAGGAAGGG 6444

Qy       6274 TCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTA 6333

Db       6445 TCTTCCAATACAAGATGGCTTCCAGATACCCCTGTTCATG-TTTTGTTTTAAAAAGTGTA 6503

Qy       6334 AATGAAGATCTTTATATTTCAATAAATGATATATAATTTA 6373

Db       6504 AATGGAGATCTTTATATTTCAATAAATGATTTATTATATA 6543
```

RESULT 30
ADQ59528
ID ADQ59528 standard; cDNA; 6499 BP.
XX
AC ADQ59528;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer-associated (CA) gene cDNA sequence SEQ ID NO:164.
XX
KW human; cancer-associated gene; cancer-associated protein; cytostatic;
KW gene therapy; vaccine; tyrosine kinase antagonist;
KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004058288-A1.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040082.
XX
PR 17-DEC-2002; 2002US-00322696.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543349/52.
DR P-PSDB; ADQ59529.
XX
PT New cancer-associated nucleic acid for diagnosing, preventing or treating
PT cancer (e.g. lymphoma) or for screening agents that may be used for
PT treating or preventing cancer.
XX
PS Disclosure; SEQ ID NO 164; 143pp; English.
XX
CC The present invention describes human cancer-associated (CA) nucleotide
CC sequences (I). Also described: (1) an expression vector comprising (I);
CC (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC within an open reading frame of a CA sequence; (5) an isolated antibody,
CC or its antigen binding fragment, that binds to the above polypeptide; (6)
CC a hybridoma that produces the monoclonal antibody described above; (7) a
CC pharmaceutical composition comprising the antibody and a pharmaceutical
CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC the above (monoclonal) antibody or polynucleotide that selectively
CC hybridises to any of the polynucleotide sequences mentioned above; (9)
CC methods for diagnosing cancer or for detecting the presence or absence of
CC cancer cells in an individual; (10) a method for inhibiting growth of
CC cancer cells in an individual; (11) a method for delivering a therapeutic
CC agent to cancer cells in an individual; (12) an electronic library
CC comprising the polynucleotide or polypeptide, or their fragments,
CC mentioned above; (13) a method of screening for anticancer activity; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC or the presence of the antibody in a test cell or serum sample; (15) a
CC method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein encoded by the above nucleic acid molecule; and
CC (16) a method for treating cancers. (I) has cytostatic activity, and can
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC and as a G-protein coupled receptor antagonist. The compositions and
CC methods of the present invention can be used for diagnosing, preventing
CC and treating cancer, especially lymphomas. They may also be used in
CC screening for agents that may be used for treating or preventing cancer.
CC The present sequence represents a human CA gene cDNA sequence, which is
CC given in the exemplification of the present invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6499 BP; 1756 A; 1469 C; 1599 G; 1675 T; 0 U; 0 Other;

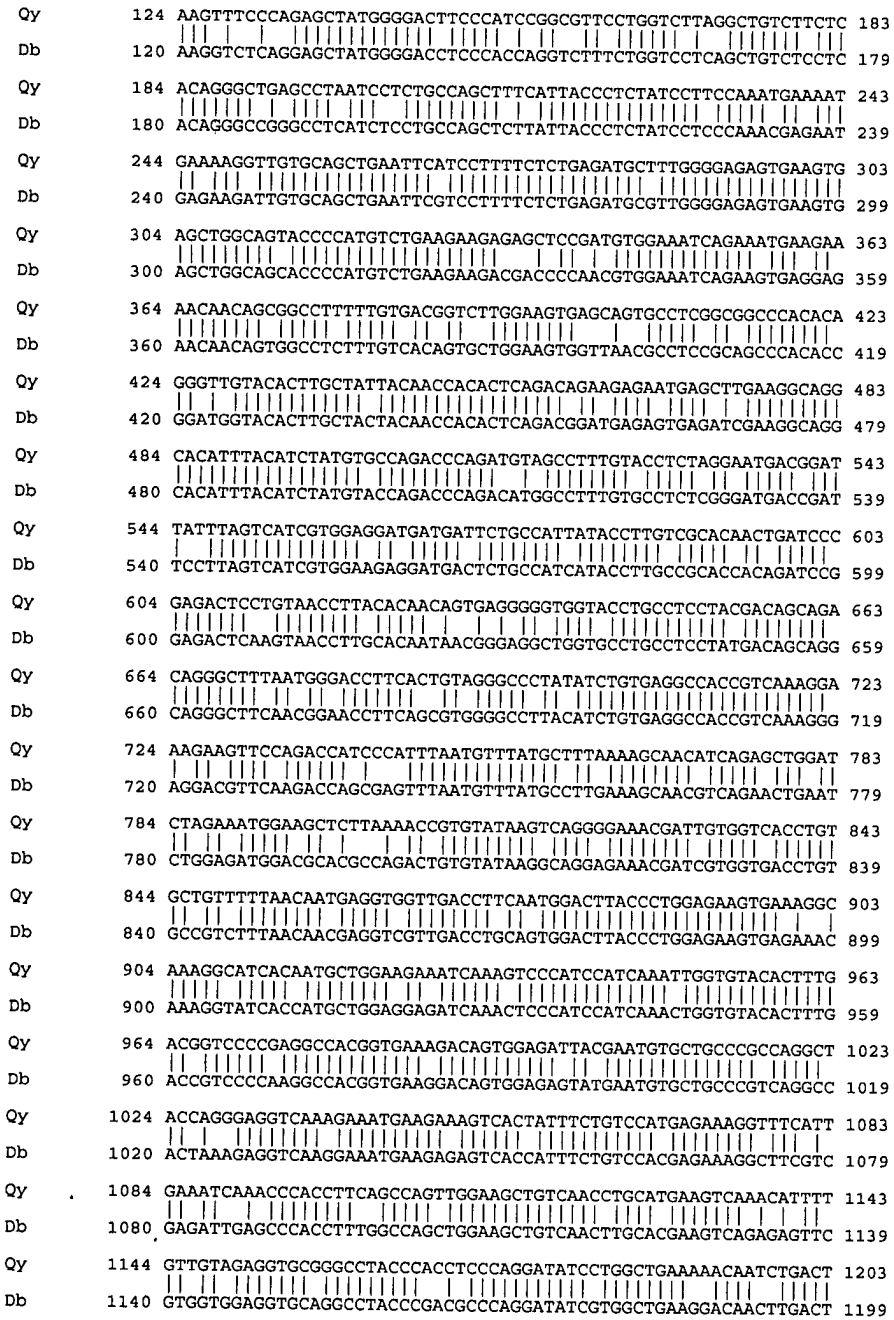
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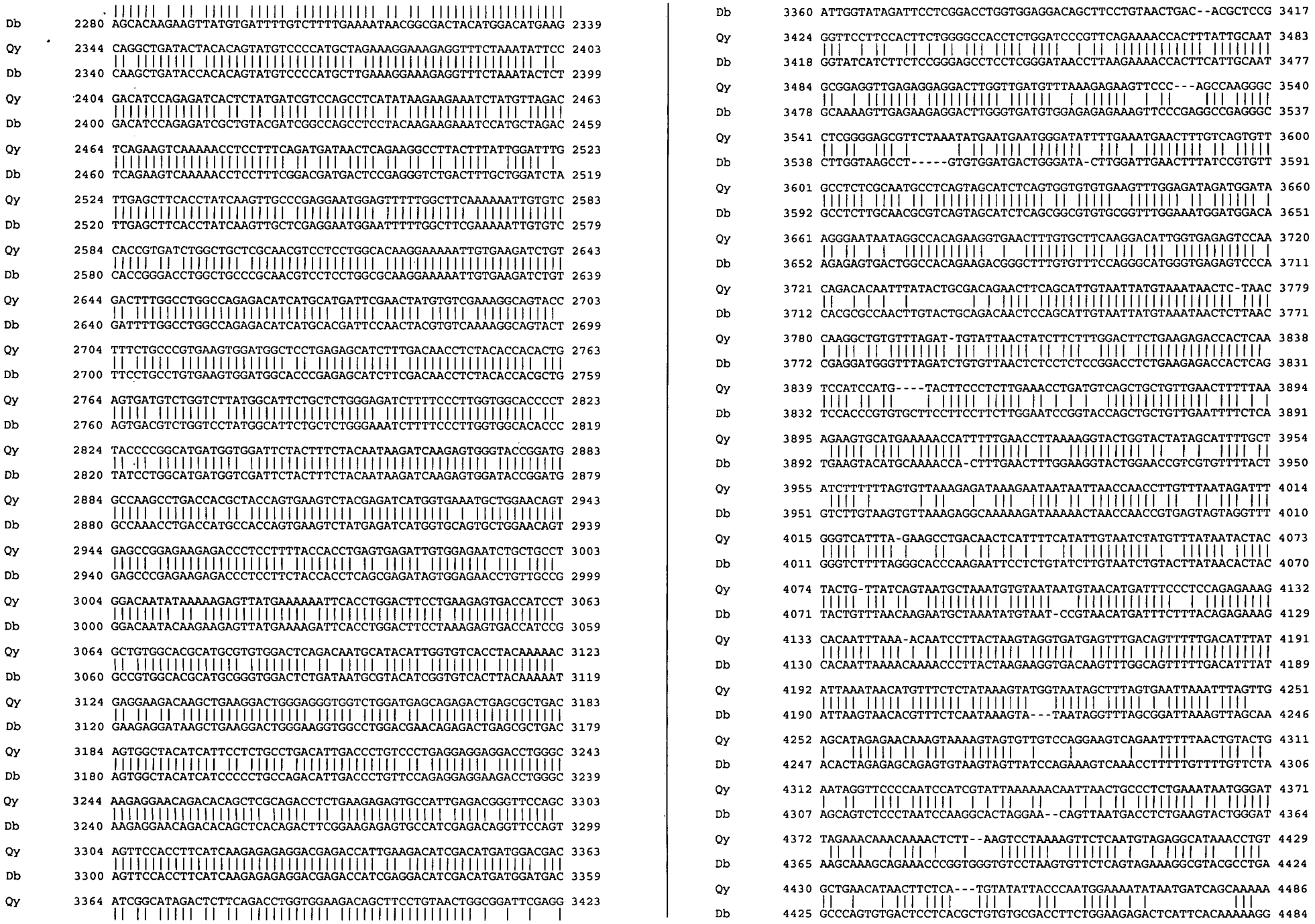
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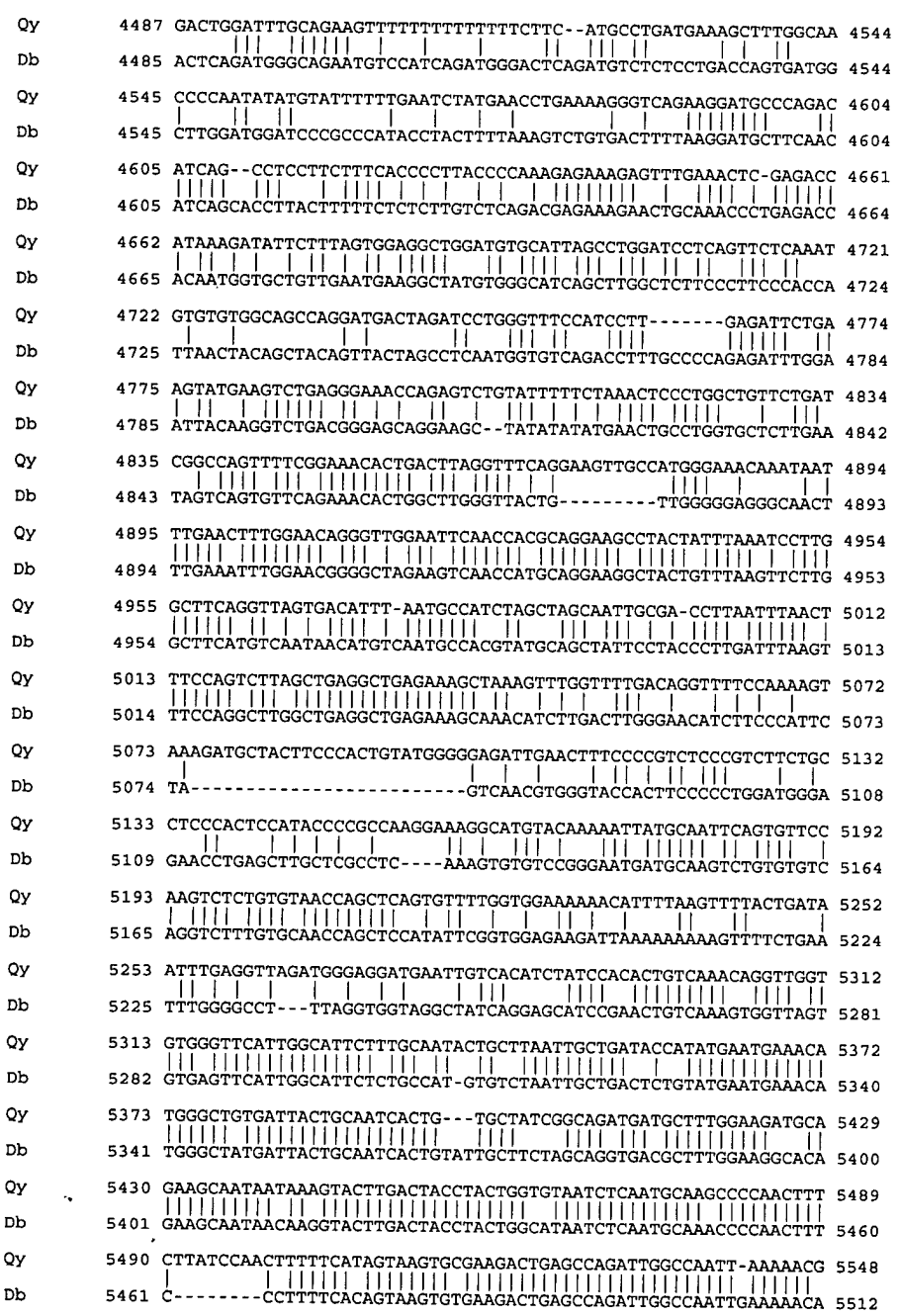
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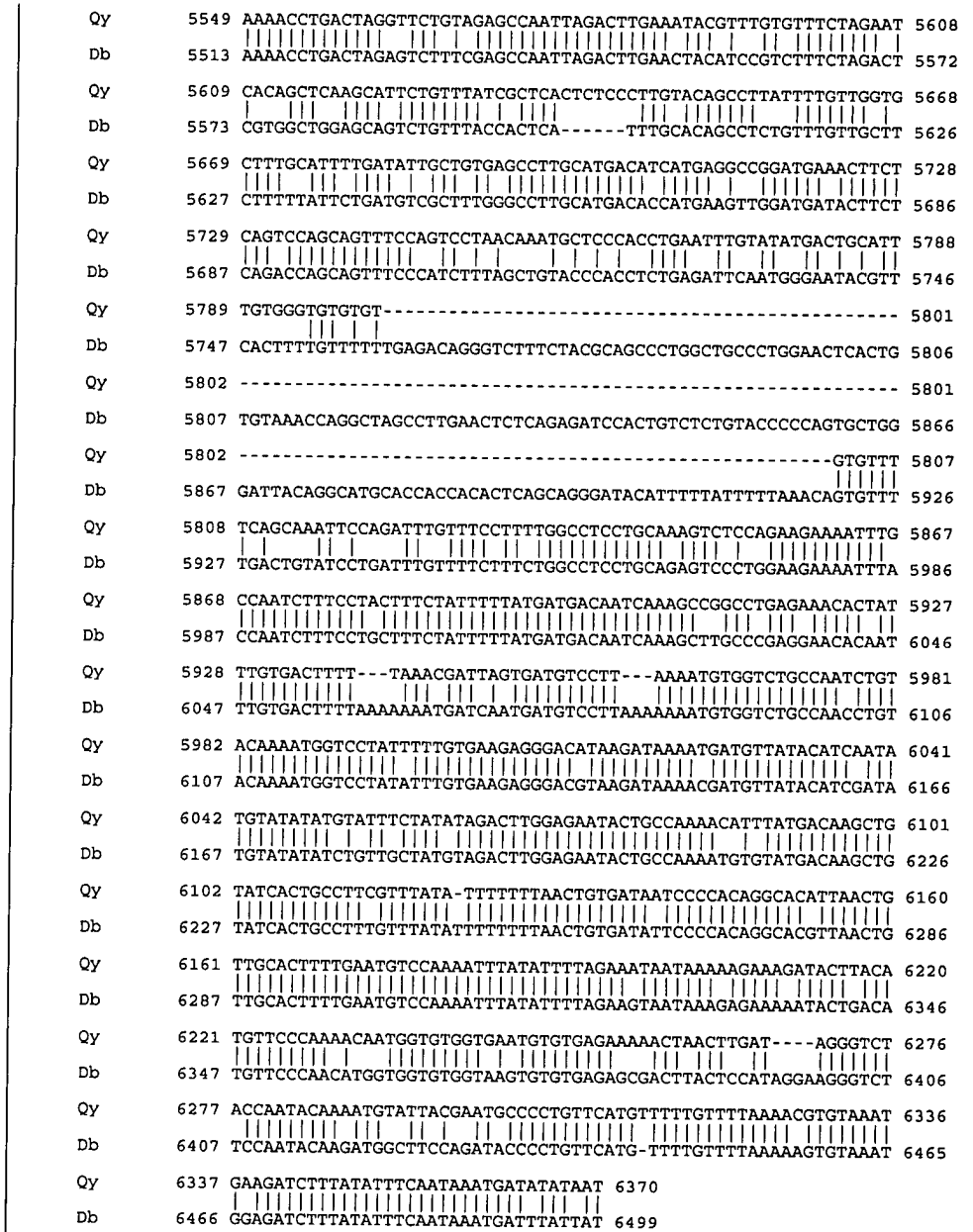
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Qy 184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
Db 180 ACAGGGCCGGGCCTCATCTCCTGCCAGCTCTTATTACCCTCTATCCTCCCAAACGAGAAT 239
Qy 244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
Db 240 GAGAAGATTGTGCAGCTGAATTCGTCCTTTTCTCTGAGATGCGTTGGGGAGAGTGAAGTG 299
Qy 304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
Db 300 AGCTGGCAGCACCCCATGTCTGAAGAAGACGACCCCAACGTGGAAATCAGAAGTGAGGAG 359
Qy 364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
Db 360 AACAACAGTGGCCTCTTTGTCACAGTGCTGGAAGTGGTTAACGCCTCCGCAGCCCACACC 419
Qy 424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
Db 420 GGATGGTACACTTGCTACTACAACCACACTCAGACGGATGAGAGTGAGATCGAAGGCAGG 479
Qy 484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
Db 480 CACATTTACATCTATGTACCAGACCCAGACATGGCCTTTGTGCCTCTCGGGATGACCGAT 539
Qy 544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
Db 540 TCCTTAGTCATCGTGGAAGAGGATGACTCTGCCATCATACCTTGCCGCACCACAGATCCG 599
Qy 604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
Db 600 GAGACTCAAGTAACCTTGCACAATAACGGGAGGCTGGTGCCTGCCTCCTATGACAGCAGG 659
Qy 664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
Db 660 CAGGGCTTCAACGGAACCTTCAGCGTGGGGCCTTACATCTGTGAGGCCACCGTCAAAGGG 719
Qy 724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
Db 720 AGGACGTTCAAGACCAGCGAGTTTAATGTTTATGCCTTGAAAGCAACGTCAGAACTGAAT 779
Qy 784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
Db 780 CTGGAGATGGACGCACGCCAGACTGTGTATAAGGCAGGAGAAACGATCGTGGTGACCTGT 839
Qy 844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
Db 840 GCCGTCTTTAACAACGAGGTCGTTGACCTGCAGTGGACTTACCCTGGAGAAGTGAGAAAC 899
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Db 900 AAAGGTATCACCATGCTGGAGGAGATCAAACTCCCATCCATCAAACTGGTGTACACTTTG 959
Qy 964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
Db 960 ACCGTCCCCAAGGCCACGGTGAAGGACAGTGGAGAGTATGAATGTGCTGCCCGTCAGGCC 1019
Qy 1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db 1020 ACTAAAGAGGTCAAGGAAATGAAGAGAGTCACCATTTCTGTCCACGAGAAAGGCTTCGTC 1079
Qy 1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db 1080 GAGATTGAGCCCACCTTTGGCCAGCTGGAAGCTGTCAACTTGCACGAAGTCAGAGAGTTC 1139
Qy 1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db 1140 GTGGTGGAGGTGCAGGCCTACCCGACGCCCAGGATATCGTGGCTGAAGGACAACTTGACT 1199
Qy 1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
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Qy 1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db 1260 CAGAGCAAATTAAAGCTGATCCGGGCTAAGGAAGAAGACAGTGGCCATTACACCATTATA 1319
Qy 1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
Db 1320 GTTCAAAATGAGGATGACGTGAAGAGTTACACGTTTGAGCTGTCAACCCTAGTTCCTGCA 1379
Qy 1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
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Qy 1444 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1503
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Qy 1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
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Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
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Qy 1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
Db 1620 ACCATCGCAGTTCGATGCCTGGCAAAGAACAACCTCAGCGTTGTGGCCCGTGAGCTGAAG 1679
Qy 1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
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Qy 1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
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Qy 1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
Db 1800 GAAATTCGCTGGAGGGTTATCGAGTCAATCAGCCCCGATGGACATGAGTATATCTATGTG 1859
Qy 1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
Db 1860 GACCCCATGCAGTTGCCTTACGACTCCAGATGGGAATTCCCGAGAGATGGCCTCGTGCTT 1919
Qy 1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
Db 1920 GGTCGGATTTTGGGATCCGGTGCATTTGGGAAAGTGGTCGAAGGTACAGCTTATGGATTA 1979
Qy 1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
Db 1980 AGCCGGTCCCAACCTGTAATGAAGGTGGCTGTGAAGATGCTCAAACCCACAGCCAGGTCT 2039
Qy 2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
Db 2040 AGTGAAAAGCAGGCTCTCATGTCTGAGCTGAAGATAATGACTCACCTGGGGCCACATTTG 2099
Qy 2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
Db 2100 AACATTGTGAACTTGCTGGGAGCCTGCACCAAGTCAGGTCCCATTTACATCATCACAGAA 2159
Qy 2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
Db 2160 TACTGCTTCTATGGGGATTTGGTCAACTACTTGCATAAGAACAGAGATAGCTTCATGAGC 2219
Qy 2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
Db 2220 CAACACCCAGAGAAGCCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGCAGACGAG 2279
Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343







RESULT 31
ABS57780
ID ABS57780 standard; cDNA; 3270 BP.
XX

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AC   ABS57780;
XX
DT   13-FEB-2003  (first entry)
XX
DE   cDNA encoding human platelet derived growth factor receptor alpha.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3270
FT                   /*tag=  c
FT                   /product= "PDGFR"
FT                   /note= "Platelet derived growth factor receptor"
FT   misc_feature    1. .1471
FT                   /*tag=  f
FT                   /note= "Encodes the extracellular domain of mature PDGFR"
FT   sig_peptide     1. .72
FT                   /*tag=  b
FT                   /note= "Signal peptide sequence number 2"
FT   sig_peptide     1. .60
FT                   /*tag=  a
FT                   /note= "Signal peptide sequence number 1"
FT   mat_peptide     61. .3267
FT                   /*tag=  d
FT                   /label= Mature_PDGFR
FT                   /note= "Mature peptide sequence number 1"
FT   mat_peptide     73. .3267
FT                   /*tag=  e
FT                   /label= Mature_PDGFR
FT                   /note= "Mature peptide sequence number 2"
FT   misc_feature    1472. .1546
FT                   /*tag=  g
FT                   /note= "Encodes the transmembrane domain of mature PDGFR"
FT   misc_feature    1547. .3166
FT                   /*tag=  h
FT                   /note= "Encodes the intracellular domain of mature PDGFR"
FT   misc_signal     1669. .1982
FT                   /*tag=  i
FT                   /note= "Encodes segment 1 of the split tyrosine kinase
FT                   region"
FT   misc_signal     2279. .2700
FT                   /*tag=  j
FT                   /note= "Encodes segment 2 of the split tyrosine kinase
FT                   domain"
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   P-PSDB; ABG72449.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Example 1; Page 34-38; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC   human platelet derived growth factor receptor (PDGFR) alpha
XX
SQ   Sequence 3270 BP; 916 A; 730 C; 822 G; 802 T; 0 U; 0 Other;

  Query Match             51.0%;  Score 3270;  DB 10;  Length 3270;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3270;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720
Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db        721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780
Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840
Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900
Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960
Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020
Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140
Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200
Qy       1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260
Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320
Qy       1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380
Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440
Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560
Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680
Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740
Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db       1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860
Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920
Qy       2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980
Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040
Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220
Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280
Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340
Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400
Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db       2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460
Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db       2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580
Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760
Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820
Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880
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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    .  2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
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Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||||||||
Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270
```

```
RESULT 32
ADV42434
ID   ADV42434 standard; cDNA; 3270 BP.
XX
AC   ADV42434;
XX
DT   10-MAR-2005  (first entry)
XX
DE   Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 62.
XX
KW   microarray; psychoneuroendocrinimmune; chronic fatigue;
KW   non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW   cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004108899-A2.
XX
PD   16-DEC-2004.
XX
PF   04-JUN-2004; 2004WO-US017686.
XX
PR   04-JUN-2003; 2003US-0475915P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nicholson A,  Vernon SD;
XX
DR   WPI; 2005-031682/03.
XX
PT   New microarray comprising probes for genes involved in
PT   psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT   condition associated with PNI activity, e.g., inflammatory or infectious
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 62; 254pp; English.
XX
CC   The invention relates to a new microarray which comprises probes for
CC   genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC   microarray is useful in diagnosing a condition associated with PNI
CC   activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC   cancer and infection. The present sequence represents a
CC   psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC   specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC   SEQ ID NO 1829 are provided.
XX
SQ   Sequence 3270 BP; 916 A; 730 C; 822 G; 802 T; 0 U; 0 Other;

  Query Match           51.0%;  Score 3270;  DB 14;  Length 3270;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3270;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
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Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
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Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
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Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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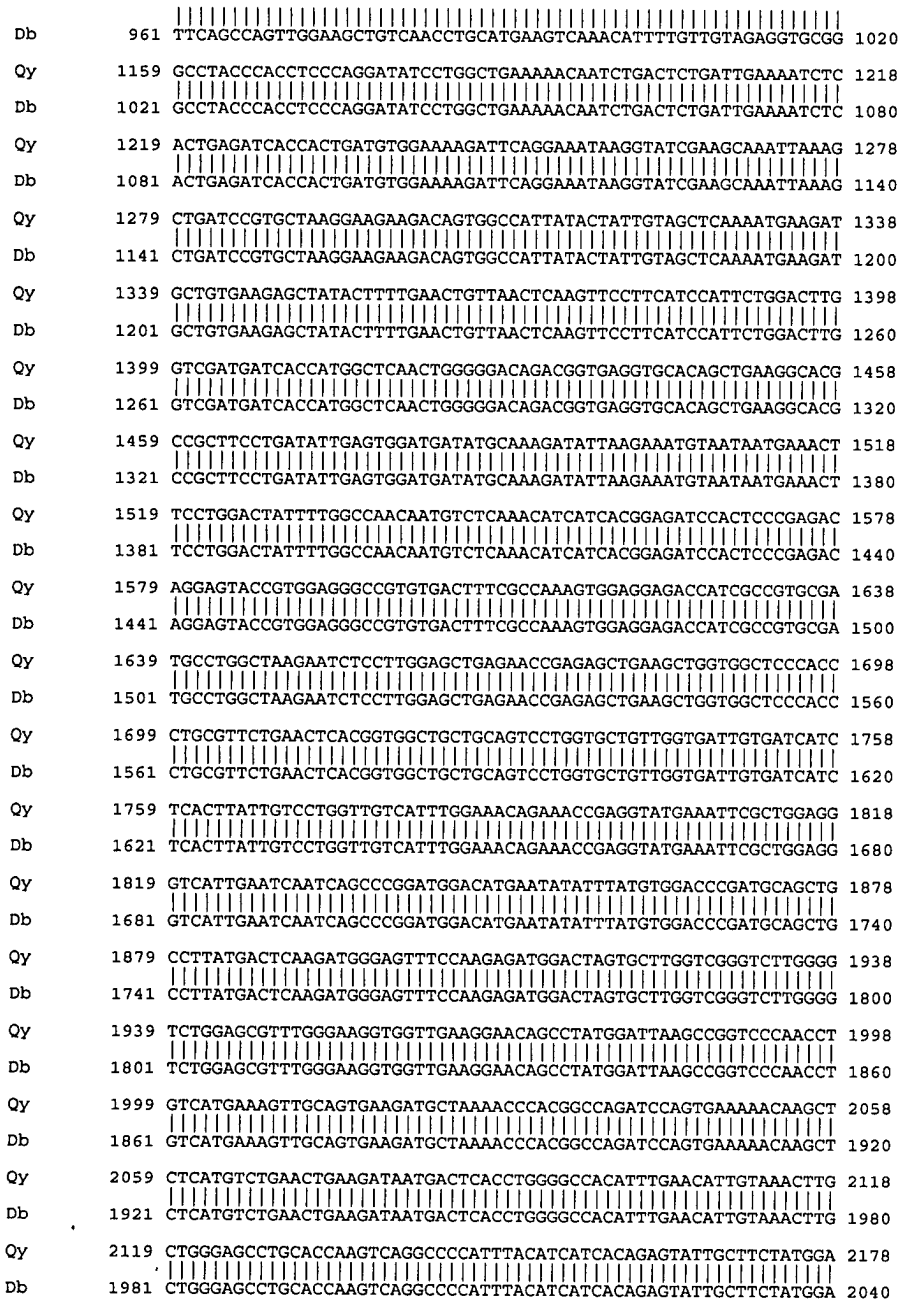
Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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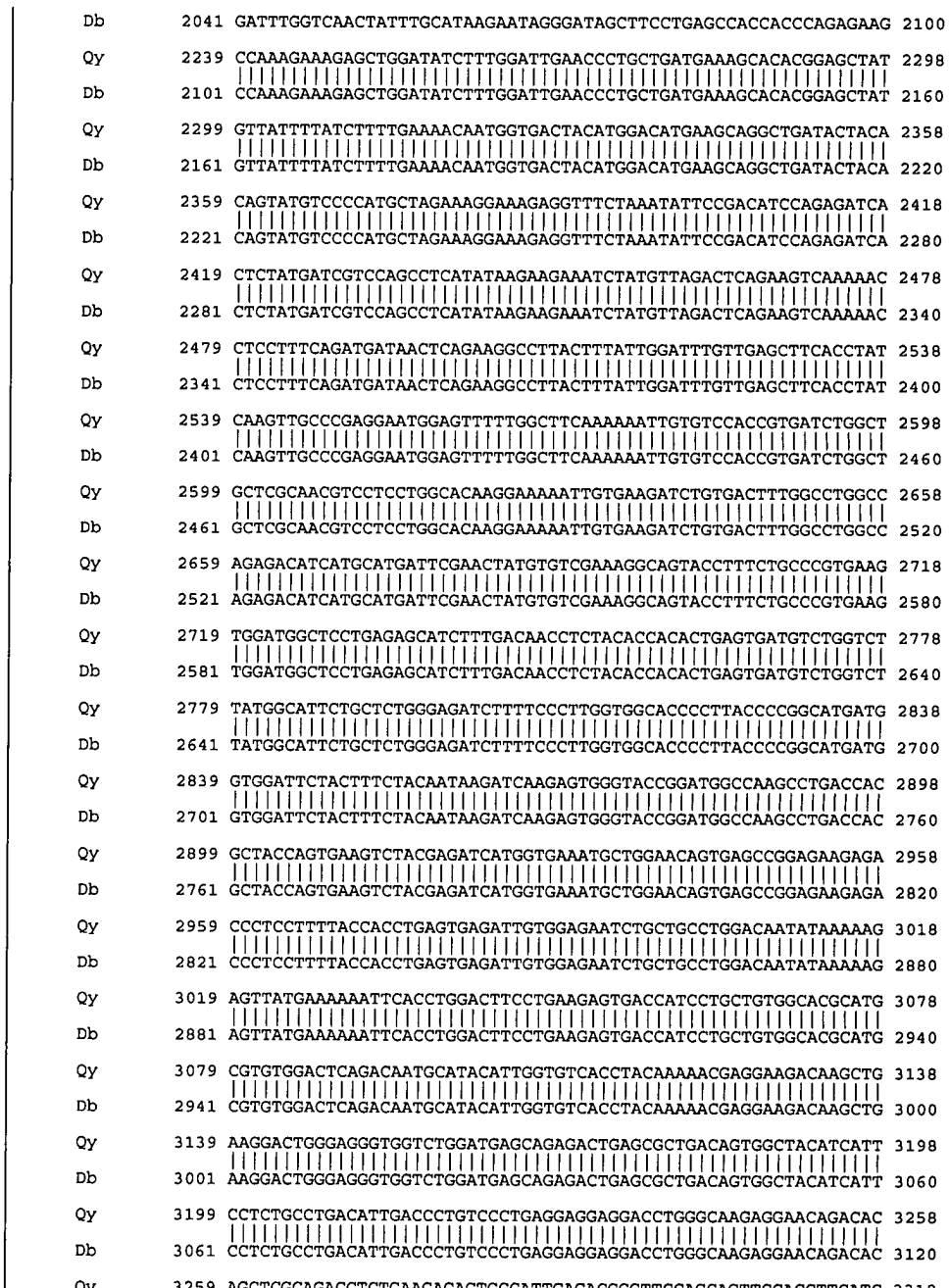
Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
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Db 961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020
Qy 1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db 1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
Qy 1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db 1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140
Qy 1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db 1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200
Qy 1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db 1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260
Qy 1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db 1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320
Qy 1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
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Qy 1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db 1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440
Qy 1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db 1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
Qy 1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db 1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560
Qy 1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db 1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
Qy 1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db 1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680
Qy 1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db 1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740
Qy 1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db 1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800
Qy 1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db 1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860
Qy 1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db 1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920
Qy 2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db 1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980
Qy 2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db 1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040
Qy 2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238


Db 2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100
Qy 2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db 2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
Qy 2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db 2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220
Qy 2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db 2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280
Qy 2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db 2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340
Qy 2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db 2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400
Qy 2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db 2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460
Qy 2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
Db 2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520
Qy 2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
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Qy 2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db 2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
Qy 2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db 2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy 2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db 2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760
Qy 2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
Db 2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820
Qy 2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
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Qy 3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
Db 2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940
Qy 3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
Db 2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000
Qy 3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
Db 3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060
Qy 3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
Db 3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120
Qy 3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
Db 3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

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Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
             ||||||||||||||||||||||||||||||
Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270


RESULT 33
ABS57784
ID   ABS57784 standard; cDNA; 3270 BP.
XX
AC   ABS57784;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha V859M mutant DNA.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW   ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3270
FT                   /*tag=  c
FT                   /product= "PDGFR mutant"
FT                   /note= "Platelet derived growth factor receptor"
FT   misc_feature    1. .1471
FT                   /*tag=  f
FT                   /note= "Encodes the extracellular domain of mature PDGFR"
FT   sig_peptide     1. .72
FT                   /*tag=  b
FT                   /note= "Signal peptide sequence number 2"
FT   sig_peptide     1. .60
FT                   /*tag=  a
FT                   /note= "Signal peptide sequence number 1"
FT   mat_peptide     61. .3267
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FT                   /label= Mature_PDGFR_mutant
FT                   /note= "Mature peptide sequence number 1"
FT   mat_peptide     73. .3267
FT                   /*tag=  e
FT                   /label= Mature_PDGFR
FT                   /note= "Mature peptide sequence number 2"
FT   misc_feature    1472. .1546
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FT                   /note= "Encodes the transmembrane domain of mature PDGFR"
FT   misc_feature    1547. .3166
FT                   /*tag=  h
FT                   /note= "Encodes the intracellular domain of mature PDGFR"
FT   misc_signal     1669. .1982
FT                   /*tag=  i
FT                   /note= "Encodes segment 1 of the split tyrosine kinase
FT                   region"
FT   misc_signal     2279. .2700
FT                   /*tag=  j
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FT   mutation        replace(2575,G)
FT                   /*tag=  k
XX
PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   P-PSDB; ABG72453.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 14; Page 61-64; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC   human platelet derived growth factor receptor (PDGFR) alpha mutant V859M
XX
SQ   Sequence 3270 BP; 917 A; 730 C; 821 G; 802 T; 0 U; 0 Other;

  Query Match             51.0%;  Score 3268.4;  DB 10;  Length 3270;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3269;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
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Db      421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480
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Db      481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540
Qy      679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
Db      541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600
Qy      739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
Db      601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660
Qy      799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
Db      661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720
Qy      859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db      721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780
Qy      919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db      781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840
Qy      979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db      841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900
Qy     1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db      901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960
Qy     1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db      961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020
Qy     1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db     1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
Qy     1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db     1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140
Qy     1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db     1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200
Qy     1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db     1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260
Qy     1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db     1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320
Qy     1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db     1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380
Qy     1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db     1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440
Qy     1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db     1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
Qy     1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db     1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560
Qy     1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db     1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
Qy     1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db     1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680
Qy     1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db     1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740
Qy     1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db     1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800
Qy     1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
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Qy     1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
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Qy     2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db     1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040
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Qy     2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db     2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
Qy     2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db     2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220
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Qy     2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db     2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340
Qy     2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db     2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400
Qy     2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Qy     2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db     2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCATGAAG 2580
Qy     2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db     2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
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Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
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Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
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Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
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Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
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Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
             ||||||||||||||||||||||||||||||
Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270


RESULT 34
ABS57781
ID   ABS57781 standard; cDNA; 3270 BP.
XX
AC   ABS57781;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human platelet derived growth factor receptor alpha E587K mutant DNA.
XX
KW   Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW   hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW   cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW   phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW   cell migration; extracellular matrix synthesis; secretion;
KW   cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW   liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW   keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW   ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3270
FT                   /*tag=  c
FT                   /product= "PDGFR mutant"
FT                   /note= "Platelet derived growth factor receptor"
FT   misc_feature    1. .1471
FT                   /*tag=  f
FT                   /note= "Encodes the extracellular domain of mature PDGFR"
FT   sig_peptide     1. .72
FT                   /*tag=  b
FT                   /note= "Signal peptide sequence number 2"
FT   sig_peptide     1. .60
FT                   /*tag=  a
FT                   /note= "Signal peptide sequence number 1"
FT   mat_peptide     61. .3267
FT                   /*tag=  d
FT                   /label= Mature_PDGFR_mutant
FT                   /note= "Mature peptide sequence number 1"
FT   mat_peptide     73. .3267
FT                   /*tag=  e
FT                   /label= Mature_PDGFR_mutant
FT                   /note= "Mature peptide sequence number 2"
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FT   misc_feature    1547. .3166
FT                   /*tag=  h
FT                   /note= "Encodes the intracellular domain of mature PDGFR"
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FT                   /*tag=  i
FT                   /note= "Encodes segment 1 of the split tyrosine kinase
FT                   region"
FT   mutation        replace(1759,G)
FT                   /*tag=  j
FT   misc_signal     2279. .2700
FT                   /*tag=  k
FT                   /note= "Encodes segment 2 of the split tyrosine kinase
FT                   domain"
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PN   US2002111304-A1.
XX
PD   15-AUG-2002.
XX
PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   P-PSDB; ABG72450.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 14; Page 41-45; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC   human platelet derived growth factor receptor (PDGFR) alpha mutant E587K
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XX
SQ Sequence 3270 BP; 917 A; 730 C; 821 G; 802 T; 0 U; 0 Other;

Query Match 51.0%; Score 3268.4; DB 10; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3269; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
Db         1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy       199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
Db        61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy       259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
Db       121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy       319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
Db       181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy       379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
Db       241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy       439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
Db       301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy       499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
Db       361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy       559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
Db       421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy       619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
Db       481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy       679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
Db       541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy       739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
Db       601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy       799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
Db       661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy       859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db       721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy       919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db       781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy       979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db       841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy      1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db       901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy      1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db       961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy      1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy      1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy      1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db       1741 CCTTATGACTCAAGATGGAAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy      1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy      1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

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Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy      2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy      2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
Db       2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100
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Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
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Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
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Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
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Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
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Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
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Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Db       2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
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Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
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Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
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Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
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Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
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Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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RESULT 35
ABS57783
ID ABS57783 standard; cDNA; 3270 BP.
XX
AC ABS57783;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human platelet derived growth factor receptor alpha D818N mutant DNA.
XX
KW Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW ss; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT		domain"
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PN US2002111304-A1.
XX

PD 15-AUG-2002.
XX
PF 25-MAY-2001; 2001US-00866510.
XX
PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.
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PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
XX
PI Kazlauskas A, Ikuno Y;
XX
DR WPI; 2003-066697/06.
DR P-PSDB; ABG72452.
XX
PT New polypeptide for treating or preventing diseases associated with an
PT abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT or -beta.
XX
PS Claim 14; Page 54-58; 127pp; English.
XX
CC The invention describes a polypeptide comprising a portion of the
CC receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC treating or preventing diseases and conditions associated with an
CC abnormal PDGF level or response, such as cell proliferation, cell
CC migration, extracellular matrix synthesis and secretion or cell
CC contraction. Exemplary diseases or disorders include cell proliferative
CC diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC scleroderma, keloids, hypertrophic scars, skin wound healing or
CC proliferative vitreoretinopathy). The method may be used in identifying
CC compounds for treating or preventing the development of diseases
CC involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC human platelet derived growth factor receptor (PDGFR) alpha mutant D818N
XX
SQ Sequence 3270 BP; 917 A; 730 C; 821 G; 802 T; 0 U; 0 Other;

Query Match 51.0%; Score 3268.4; DB 10; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3269; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270
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RESULT 36
ABS57782
ID ABS57782 standard; cDNA; 3270 BP.
XX
AC ABS57782;
XX
DT 13-FEB-2003 (first entry)
XX
DE Human platelet derived growth factor receptor alpha T665M mutant DNA.
XX
KW Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW ss; mutant.
XX
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OS Synthetic.
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FT   misc_feature    1. .1471
FT                   /*tag=  f
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PD   15-AUG-2002.
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PF   25-MAY-2001; 2001US-00866510.
XX
PR   01-DEC-2000; 2000US-0250747P.
PR   07-MAY-2001; 2001US-0289103P.
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   P-PSDB; ABG72451.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Claim 14; Page 48-51; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC   human platelet derived growth factor receptor (PDGFR) alpha mutant T665M
XX
SQ   Sequence 3270 BP; 916 A; 728 C; 823 G; 803 T; 0 U; 0 Other;

  Query Match           50.9%;  Score 3266.8;  DB 10;  Length 3270;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3268;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
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Qy       199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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Qy       259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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Qy       439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
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Qy       499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
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Qy       559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
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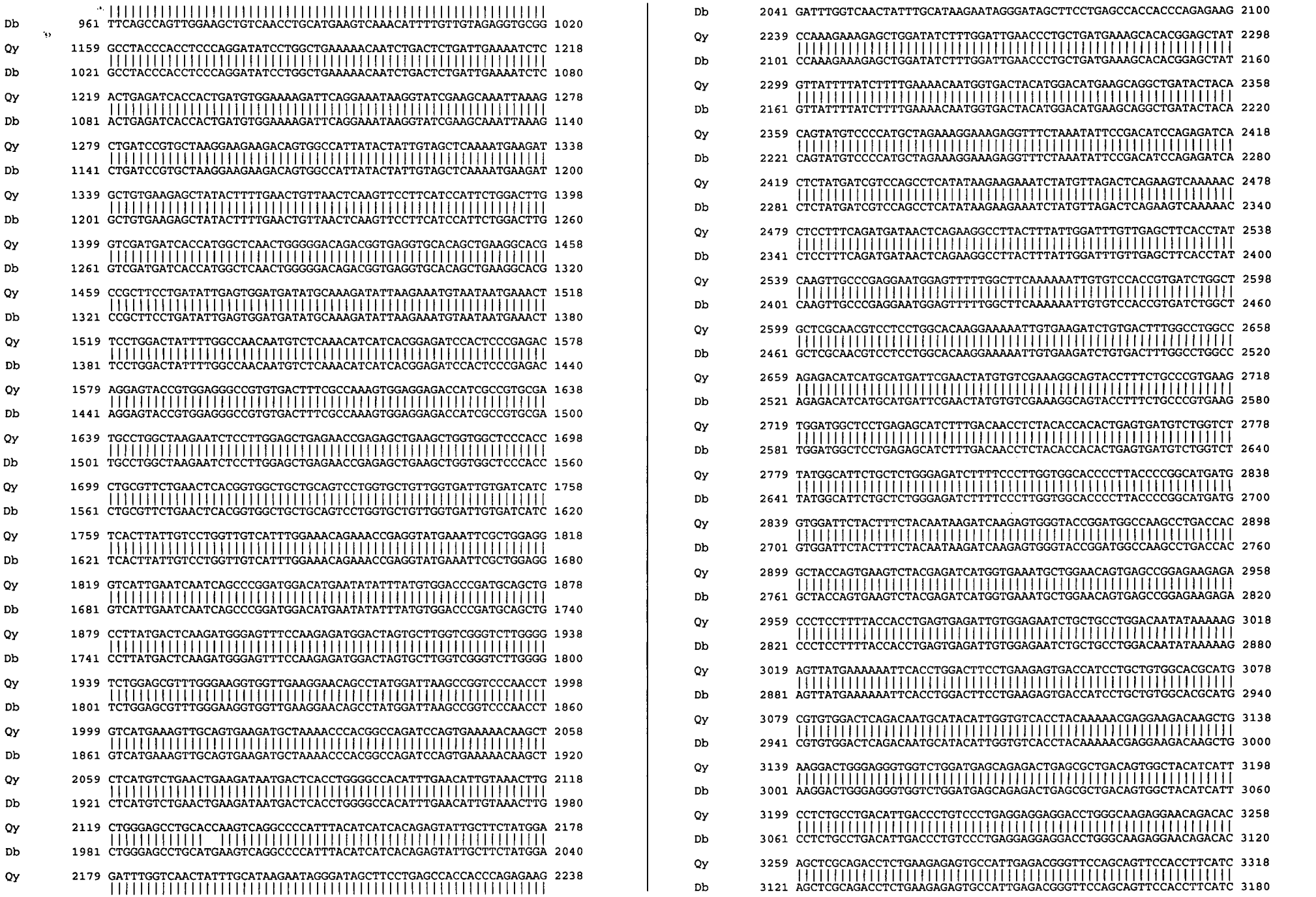
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Qy       919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
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RESULT 37
ADZ60757
ID ADZ60757 standard; DNA; 6264 BP.
XX
AC ADZ60757;
XX
DT 30-JUN-2005 (first entry)
XX
DE Rat Pdgfra gene, SEQ ID 481.
XX
KW Drug screening; Peroxisome Proliferator-Activated Receptor gamma;
KW PPAR gamma; gene; ds.
XX
OS Rattus norvegicus.
XX
PN US2005084872-A1.
XX
PD 21-APR-2005.
XX
PF 23-JAN-2004; 2004US-00764420.
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PR 24-JAN-2003; 2003US-0442797P.
PR 30-MAY-2003; 2003US-0474413P.
XX
PA (LUMP/) LUM P Y.
PA (TANY/) TAN Y.
PA (DAIH/) DAI H.
PA (MUIS/) MUISE E S.
PA (BERG/) BERGER J P.
PA (THOM/) THOMPSON J R.
XX
PI Lum PY, Tan Y, Dai H, Muise ES, Berger JP, Thompson JR;
XX
DR WPI; 2005-313963/32.
DR GENBANK; M63837.
XX
PT Determining whether agent has defined biological activity, by making
PT comparison e.g. comparing efficacy value, toxicity value and classifier
PT value of agent to reference values, and using results to determine
PT whether agent has activity.
XX
PS Example 2; SEQ ID NO 481; 51pp; English.
XX
CC The present invention relates to a methods for screening biologically
CC active agents, such as candidate drugs, to determine whether the agent
CC possesses a defined biological activity. The methods involve making one
CC or more comparisons chosen from comparing efficacy value of agent to
CC reference efficacy value, comparing a toxicity value of the agent to
CC reference toxicity value, comparing a classifier value of the agent to
CC reference classifier value, and using the comparison result(s) to
CC determine whether the agent possesses the defined biological activity.
CC Also claimed is a population of oligonucleotide probes (I) specific for
CC measuring the expression levels of members of a classifier population of
CC genes or a toxicity-related population of genes. (I) are useful for
CC measuring the expression levels of genes that are useful for identifying
CC agonists or partial agonists of Peroxisome Proliferator-Activated
CC Receptor (PPAR) gamma. ADZ60827-ADZ61170 are oligonucleotide probes which
CC are useful in the method of the invention to measure the expression
CC pattern of the toxicity-related population of rat genes ADZ60495-
CC ADZ60826. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20050084872.
XX

SQ Sequence 6264 BP; 1633 A; 1453 C; 1600 G; 1578 T; 0 U; 0 Other;

  Query Match   50.8%; Score 3260.6; DB 14; Length 6264;
  Best Local Similarity 74.9%; Pred. No. 0;
  Matches 4766; Conservative   0; Mismatches 1269; Indels 324; Gaps   42;

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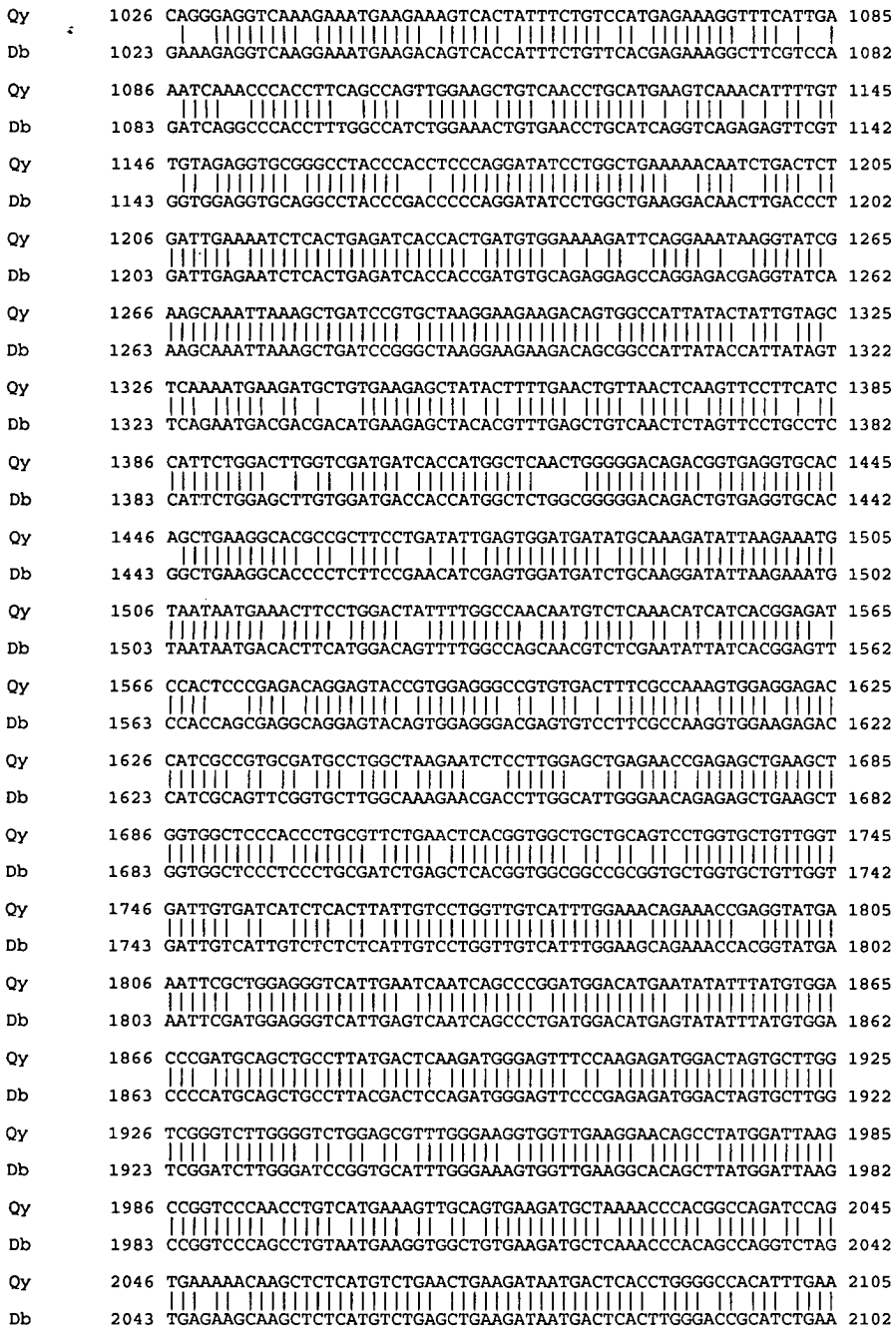
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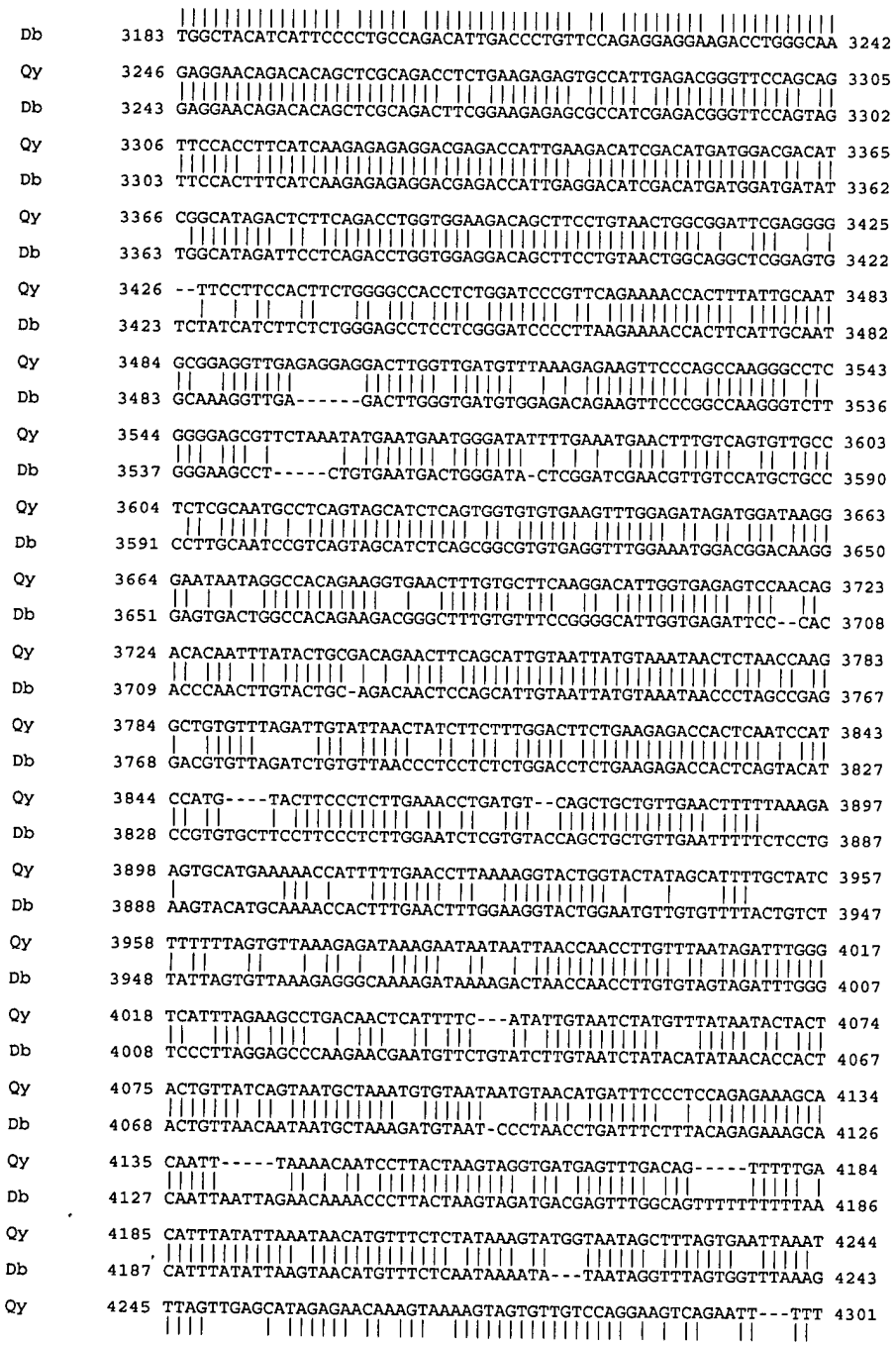
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Db        903 AGGCATCACCATGCTGGAGGAGATCAAACTCCCGTCCATCAAACTGGTGTACACGCTGAC 962

Qy        966 GGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTAC 1025
              ||||||  ||||||||||||  ||||||||||||||  ||||||||||||||||||||  ||
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Qy 1086 AATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGT 1145
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Db 2823 CCCTGGCATGATGGTTGATTCTACTTTCTACAATAAGATCAAGAGCGGATACAGGATGGC 2882
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RESULT 38
ADZ13911
ID ADZ13911 standard; DNA; 89210 BP.
XX
AC ADZ13911;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated genomic DNA #124.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1431; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.
XX
SQ Sequence 89210 BP; 25119 A; 19368 C; 19676 G; 25047 T; 0 U; 0 Other;

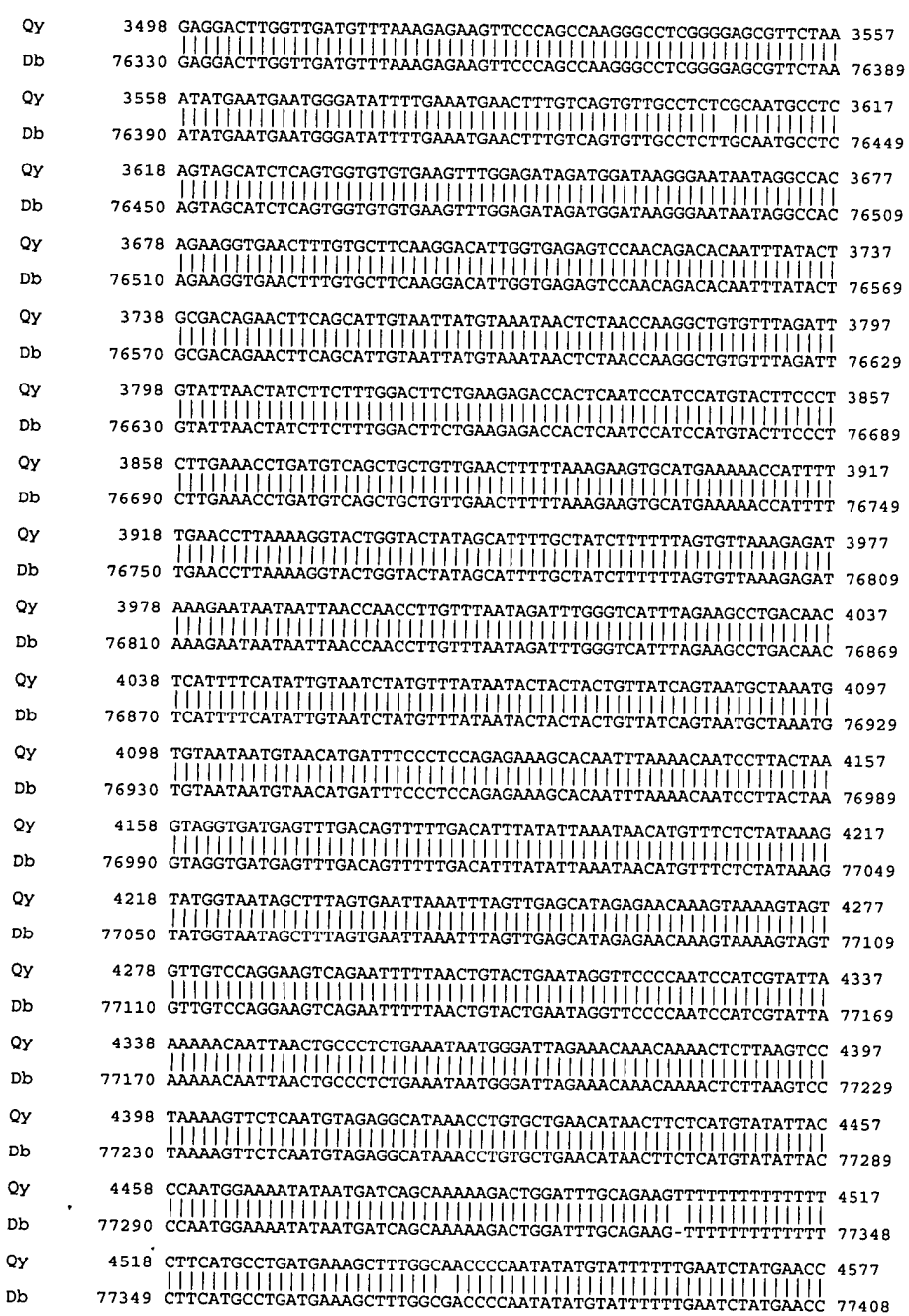
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  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3122;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

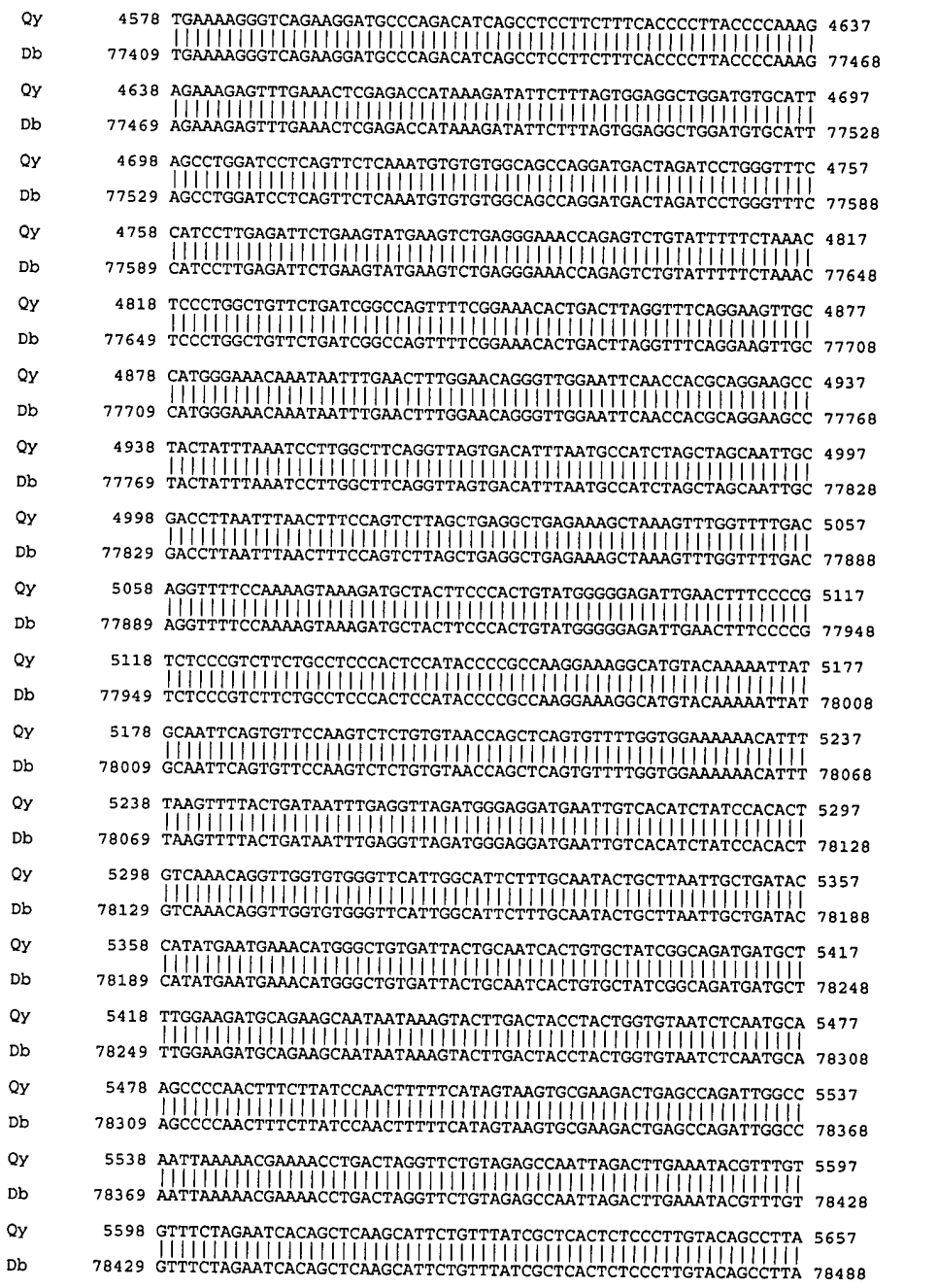
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Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
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Db      76210 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 76269

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Db 76390 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 76449
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Db 76690 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 76749
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Qy 4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
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Qy 4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
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Db 77589 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 77648
Qy 4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
Db 77649 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 77708
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Db 77709 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 77768
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Qy 5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717

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Db      78489 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 78548

Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
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Db      78549 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 78608

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
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Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
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Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
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Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
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Db      78789 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 78848

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78849 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 78908

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78909 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 78968

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
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Db      78969 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 79028

Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79029 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 79088

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
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Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       6378 TAAAAAAA 6385
              || |  ||
Db      79209 TATACTAA 79216
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RESULT 39
ADQ59530
ID   ADQ59530 standard; DNA; 59475 BP.
XX
AC   ADQ59530;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human cancer-associated (CA) gene sequence SEQ ID NO:166.
XX
KW   human; cancer-associated gene; cancer-associated protein; cytostatic;
KW   gene therapy; vaccine; tyrosine kinase antagonist;
KW   G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004058288-A1.
XX
PD   15-JUL-2004.
XX
PF   15-DEC-2003; 2003WO-US040082.
XX
PR   17-DEC-2002; 2002US-00322696.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-543349/52.
DR   P-PSDB; ADQ59532.
XX
PT   New cancer-associated nucleic acid for diagnosing, preventing or treating
PT   cancer (e.g. lymphoma) or for screening agents that may be used for
PT   treating or preventing cancer.
XX
PS   Claim 16; SEQ ID NO 166; 143pp; English.
XX
CC   The present invention describes human cancer-associated (CA) nucleotide
CC   sequences (I). Also described: (1) an expression vector comprising (I);
CC   (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC   for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC   within an open reading frame of a CA sequence; (5) an isolated antibody,
CC   or its antigen binding fragment, that binds to the above polypeptide; (6)
CC   a hybridoma that produces the monoclonal antibody described above; (7) a
CC   pharmaceutical composition comprising the antibody and a pharmaceutical
CC   excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC   the above (monoclonal) antibody or polynucleotide that selectively
CC   hybridises to any of the polynucleotide sequences mentioned above; (9)
CC   methods for diagnosing cancer or for detecting the presence or absence of
CC   cancer cells in an individual; (10) a method for inhibiting growth of
CC   cancer cells in an individual; (11) a method for delivering a therapeutic
CC   agent to cancer cells in an individual; (12) an electronic library
CC   comprising the polynucleotide or polypeptide, or their fragments,
CC   mentioned above; (13) a method of screening for anticancer activity; (14)
CC   methods for detecting cancer associated with expression of a polypeptide
CC   or the presence of the antibody in a test cell or serum sample; (15) a
CC   method for screening for a bioactive agent capable of modulating the
CC   activity of a CA protein encoded by the above nucleic acid molecule; and
CC   (16) a method for treating cancers. (I) has cytostatic activity, and can
CC   be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC   and as a G-protein coupled receptor antagonist. The compositions and
CC   methods of the present invention can be used for diagnosing, preventing
CC   and treating cancer, especially lymphomas. They may also be used in
CC   screening for agents that may be used for treating or preventing cancer.
CC   The present sequence represents a human CA gene sequence, which is given
CC   in the exemplification of the present invention. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 59475 BP; 16910 A; 12069 C; 12177 G; 17176 T; 0 U; 1143 Other;

  Query Match           48.4%;  Score 3106.4;  DB 12;  Length 59475;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3121;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

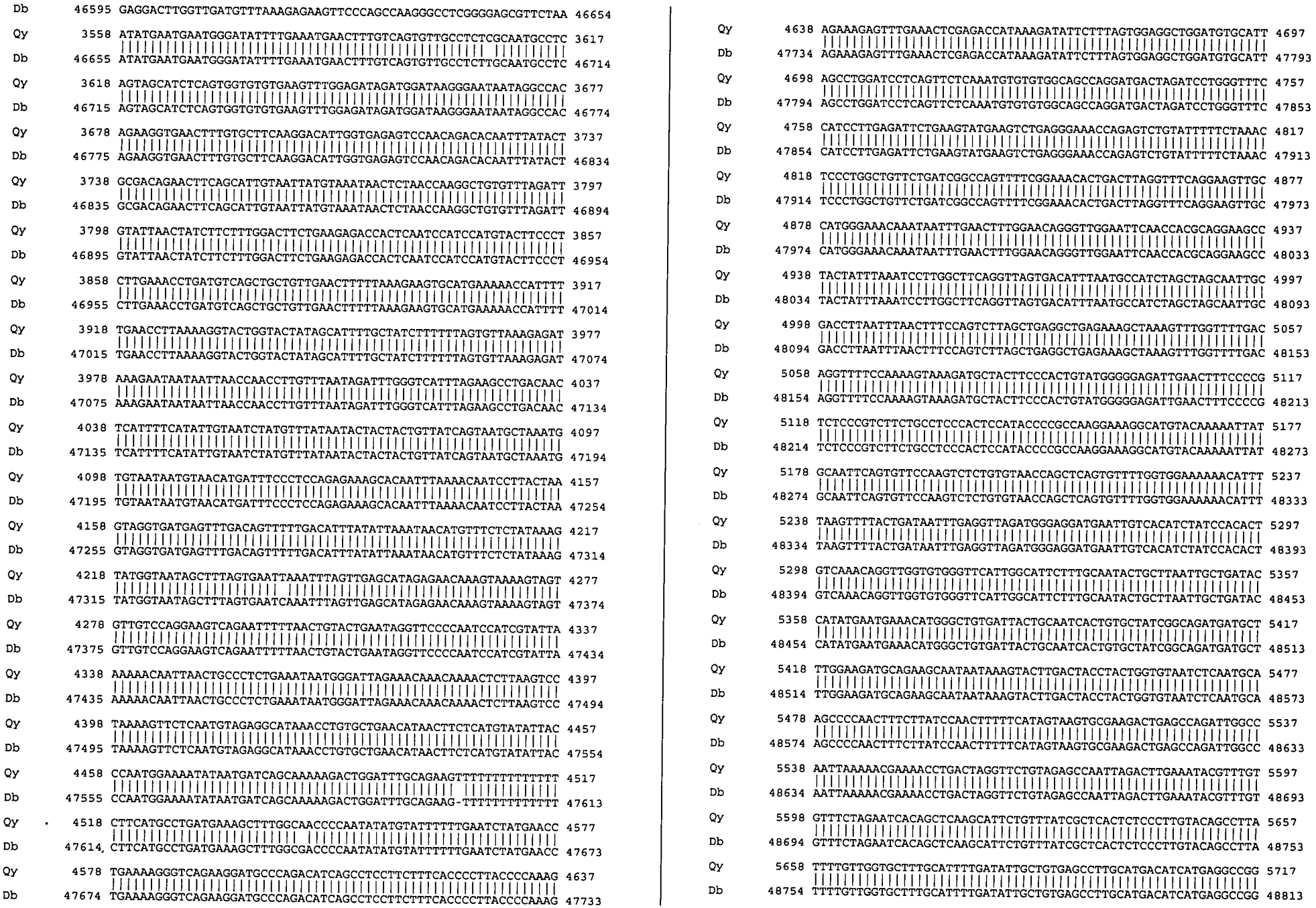
Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
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Db      46355 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 46414

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46415 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 46474

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
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Db      46475 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 46534

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
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Db      46535 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 46594

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
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Db 46595 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 46654
Qy 3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
Db 46655 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 46714
Qy 3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
Db 46715 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 46774
Qy 3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
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Qy 4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
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Db 47435 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 47494
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Qy 4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
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Qy 4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
Db 47854 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 47913
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Qy 5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
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Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
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Db      48814 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 48873

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
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Db      48874 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 48933

Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48994 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 49053

Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49054 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 49113

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49114 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 49173

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49174 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 49233

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49234 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 49293

Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49294 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 49353

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49354 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 49413

Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49414 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 49473

Qy       6378 TAAAAAAA 6385
             || |  ||
Db      49474 TATACTAA 49481
```

RESULT 40
ADV44174
ID ADV44174 standard; cDNA; 3270 BP.
XX
AC ADV44174;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1802.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 8; SEQ ID NO 1802; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 3270 BP; 879 A; 796 C; 866 G; 729 T; 0 U; 0 Other;

Query Match 39.9%; Score 2561.2; DB 14; Length 3270;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2827; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

```
Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||| ||||| | ||  || ||||| |  ||||||| |||||||||| | ||||
Db          1 ATGGGGACCTCCCACCAGGTCTTTCTGGTCCTCAGCTGTCTCCTCACAGGGCCGGGCCTC 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              |||  ||||||||| | |||||||||||||| ||||| || ||||| ||| ||||||||
Db         61 ATCTCCTGCCAGCTCTTATTACCCTCTATCCTCCCAAACGAGAATGAGAAGATTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              |||||||| |||||||||||||||||| ||||||||||||||||||||||||| |||||
Db        121 CTGAATTCGTCCTTTTCTCTGAGATGCGTTGGGGAGAGTGAAGTGAGCTGGCAGCACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              |||||||||||||   | || | |||||||||||||| ||| || |||||||| |||||
Db        181 ATGTCTGAAGAAGACGACCCCAACGTGGAAATCAGAAGTGAGGAGAACAACAGTGGCCTC 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||| || ||  ||||||||   | ||||| || |||||||| || | ||||||||||
Db        241 TTTGTCACAGTGCTGGAAGTGGTTAACGCCTCCGCAGCCCACACCGGATGGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              || |||||||||||||||| || |||| |||| | ||||||||||||||||||||||||
Db        301 TACTACAACCACACTCAGACGGATGAGAGTGAGATCGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              || |||||||||||  | |||||||| ||||| || ||||| |||| ||||||||||||
Db        361 GTACCAGACCCAGACATGGCCTTTGTGCCTCTCGGGATGACCGATTCCTTAGTCATCGTG 420

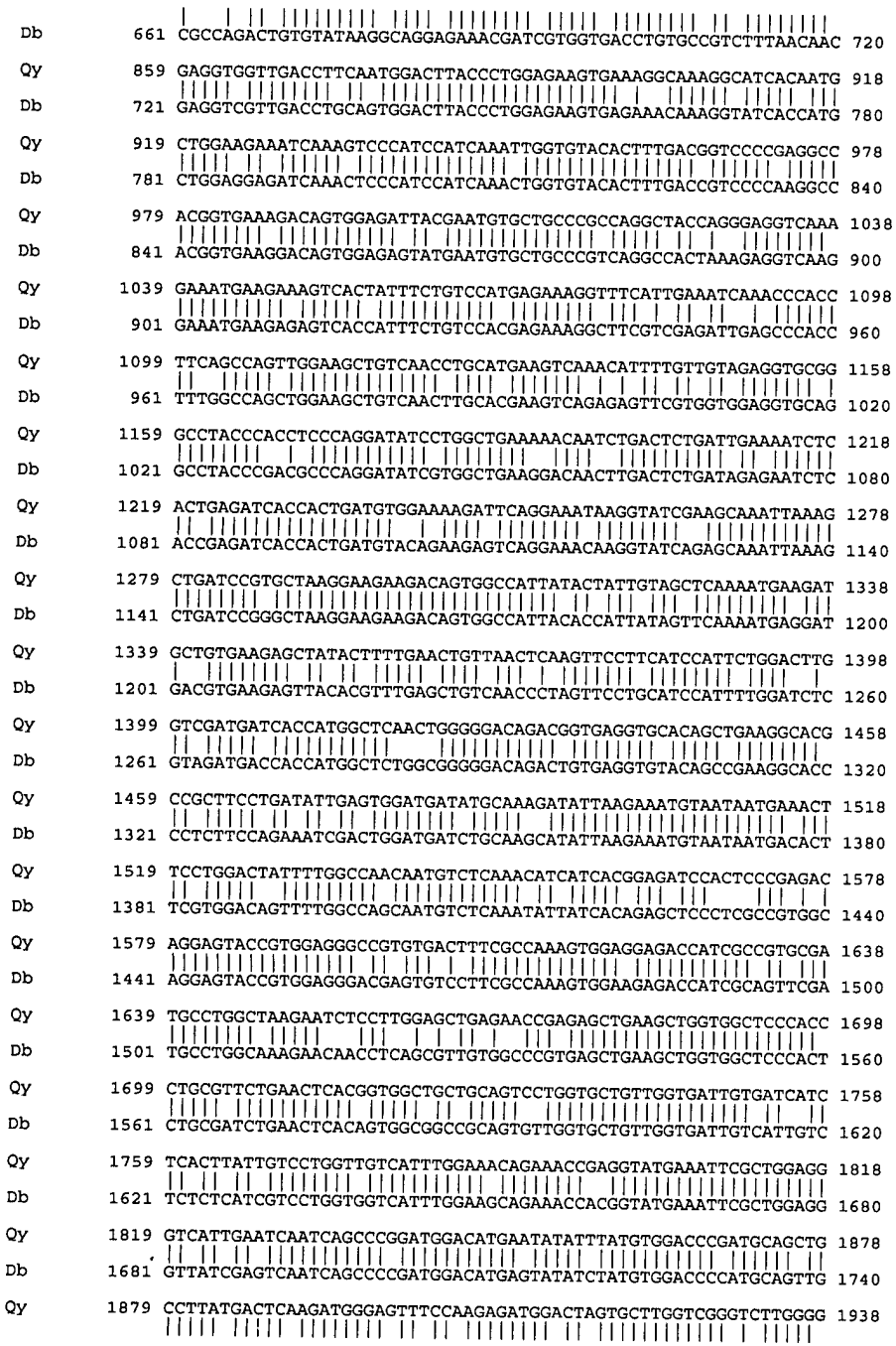
Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              || || ||||| |||||||| |||||||| ||||| || ||||| |||||||  ||||||
Db        421 GAAGAGGATGACTCTGCCATCATACCTTGCCGCACCACAGATCCGGAGACTCAAGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              || ||||| |  | | || |||| |||||||||| |||||||| |||||||| || ||
Db        481 TTGCACAATAACGGGAGGCTGGTGCCTGCCTCCTATGACAGCAGGCAGGGCTTCAACGGA 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              |||||||  || ||||| || |||||||||||||||||||||| | || |||| |||||
Db        541 ACCTTCAGCGTGGGGCCTTACATCTGTGAGGCCACCGTCAAAGGGAGGACGTTCAAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
              | |  |||||||||||||| || |||||||| ||||| ||| |||| || ||||| ||
Db        601 AGCGAGTTTAATGTTTATGCCTTGAAAGCAACGTCAGAACTGAATCTGGAGATGGACGCA 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
```


Db 661 CGCCAGACTGTGTATAAGGCAGGAGAAACGATCGTGGTGACCTGTGCCGTCTTTAACAAC 720
Qy 859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db 721 GAGGTCGTTGACCTGCAGTGGACTTACCCTGGAGAAGTGAGAAACAAAGGTATCACCATG 780
Qy 919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db 781 CTGGAGGAGATCAAACTCCCATCCATCAAACTGGTGTACACTTTGACCGTCCCCAAGGCC 840
Qy 979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db 841 ACGGTGAAGGACAGTGGAGAGTATGAATGTGCTGCCCGTCAGGCCACTAAAGAGGTCAAG 900
Qy 1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db 901 GAAATGAAGAGAGTCACCATTTCTGTCCACGAGAAAGGCTTCGTCGAGATTGAGCCCACC 960
Qy 1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db 961 TTTGGCCAGCTGGAAGCTGTCAACTTGCACGAAGTCAGAGAGTTCGTGGTGGAGGTGCAG 1020
Qy 1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db 1021 GCCTACCCGACGCCCAGGATATCGTGGCTGAAGGACAACTTGACTCTGATAGAGAATCTC 1080
Qy 1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db 1081 ACCGAGATCACCACTGATGTACAGAAGAGTCAGGAAACAAGGTATCAGAGCAAATTAAAG 1140
Qy 1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db 1141 CTGATCCGGGCTAAGGAAGAAGACAGTGGCCATTACACCATTATAGTTCAAAATGAGGAT 1200
Qy 1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db 1201 GACGTGAAGAGTTACACGTTTGAGCTGTCAACCCTAGTTCCTGCATCCATTTTGGATCTC 1260
Qy 1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db 1261 GTAGATGACCACCATGGCTCTGGCGGGGGACAGACTGTGAGGTGTACAGCCGAAGGCACC 1320
Qy 1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db 1321 CCTCTTCCAGAAATCGACTGGATGATCTGCAAGCATATTAAGAAATGTAATAATGACACT 1380
Qy 1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db 1381 TCGTGGACAGTTTTGGCCAGCAATGTCTCAAATATTATCACAGAGCTCCCTCGCCGTGGC 1440
Qy 1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db 1441 AGGAGTACCGTGGAGGGACGAGTGTCCTTCGCCAAAGTGGAAGAGACCATCGCAGTTCGA 1500
Qy 1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db 1501 TGCCTGGCAAAGAACAACCTCAGCGTTGTGGCCCGTGAGCTGAAGCTGGTGGCTCCCACT 1560
Qy 1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db 1561 CTGCGATCTGAACTCACAGTGGCGGCCGCAGTGTTGGTGCTGTTGGTGATTGTCATTGTC 1620
Qy 1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db 1621 TCTCTCATCGTCCTGGTGGTCATTTGGAAGCAGAAACCACGGTATGAAATTCGCTGGAGG 1680
Qy 1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db 1681 GTTATCGAGTCAATCAGCCCCGATGGACATGAGTATATCTATGTGGACCCCATGCAGTTG 1740
Qy 1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db 1741 CCTTACGACTCCAGATGGGAATTCCCGAGAGATGGCCTCGTGCTTGGTCGGATTTTGGGA 1800
Qy 1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db 1801 TCCGGTGCATTTGGGAAAGTGGTCGAAGGTACAGCTTATGGATTAAGCCGGTCCCAACCT 1860
Qy 1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db 1861 GTAATGAAGGTGGCTGTGAAGATGCTCAAACCCACAGCCAGGTCTAGTGAAAAGCAGGCT 1920
Qy 2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db 1921 CTCATGTCTGAGCTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTGAACTTG 1980
Qy 2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db 1981 CTGGGAGCCTGCACCAAGTCAGGTCCCATTTACATCATCACAGAATACTGCTTCTATGGG 2040
Qy 2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
Db 2041 GATTTGGTCAACTACTTGCATAAGAACAGAGATAGCTTCATGAGCCAACACCCAGAGAAG 2100
Qy 2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db 2101 CCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGCAGACGAGAGCACAAGAAGTTAT 2160
Qy 2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db 2161 GTGATTTTGTCTTTTGAAAATAACGGCGACTACATGGACATGAAGCAAGCTGATACCACA 2220
Qy 2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db 2221 CAGTATGTCCCCATGCTTGAAAGGAAAGAGGTTTCTAAATACTCTGACATCCAGAGATCG 2280
Qy 2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db 2281 CTGTACGATCGGCCAGCCTCCTACAAGAAGAAATCCATGCTAGACTCAGAAGTCAAAAAC 2340
Qy 2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db 2341 CTCCTTTCGGACGATGACTCCGAGGGTCTGACTTTGCTGGATCTATTGAGCTTCACCTAT 2400
Qy 2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db 2401 CAAGTTGCTCGAGGAATGGAATTTTTGGCTTCGAAAAATTGTGTCCACCGGGACCTGGCT 2460
Qy 2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
Db 2461 GCCCGCAACGTCCTCCTGGCGCAAGGAAAAATTGTGAAGATCTGTGATTTTGGCCTGGCC 2520
Qy 2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db 2521 AGAGACATCATGCACGATTCCAACTACGTGTCAAAAGGCAGTACTTTCCTGCCTGTGAAG 2580
Qy 2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db 2581 TGGATGGCACCCGAGAGCATCTTCGACAACCTCTACACCACGCTGAGTGACGTCTGGTCC 2640
Qy 2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db 2641 TATGGCATTCTGCTCTGGGAAATCTTTTCCCTTGGTGGCACACCCTATCCTGGCATGATG 2700
Qy 2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db 2701 GTCGATTCTACTTTCTACAATAAGATCAAGAGTGGATACCGGATGGCCAAACCTGACCAT 2760
Qy 2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
Db 2761 GCCACCAGTGAAGTCTATGAGATCATGGTGCAGTGCTGGAACAGTGAGCCCGAGAAGAGA 2820
Qy 2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
Db 2821 CCCTCCTTCTACCACCTCAGCGAGATAGTGGAGAACCTGTTGCCGGGACAATACAAGAAG 2880

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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             |||||||||| |||||||||||||||| ||||||||||||| || ||||||||||||
Db       2881 AGTTATGAAAAGATTCACCTGGACTTCCTAAAGAGTGACCATCCGGCCGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
             || |||||||| || ||||| ||||| |||||||| |||||||| || || || ||||||
Db       2941 CGGGTGGACTCTGATAATGCGTACATCGGTGTCACTTACAAAAATGAAGAGGATAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
             |||||||||| ||||| ||||| || ||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAAGGTGGCCTGGACGAACAGAGACTGAGCGCTGACAGTGGCTACATCATC 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
             || ||||| |||||||||||||| || |||||||| ||||||||||||||||||||||||
Db       3061 CCCCTGCCAGACATTGACCCTGTTCCAGAGGAGGAAGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
             ||||| ||||| || |||||||||||||| ||||| |||||||| ||||||||||||||||
Db       3121 AGCTCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             |||||||||||||||||||| || |||||||||||||||| ||||| || ||||| ||
Db       3181 AAGAGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATTCC 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
             || |||||||||| ||||||||||||||||
Db       3241 TCGGACCTGGTGGAGGACAGCTTCCTGTAA 3270
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RESULT 41
AAC77955
ID AAC77955 standard; cDNA; 1842 BP.
XX
AC AAC77955;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated gene sequence SEQ ID NO:349.
XX
KW Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
XX
OS Homo sapiens.
XX
PN WO200055350-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005882.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587533/55.
DR P-PSDB; AAB43746.
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer.
XX
PS Claim 1; Page 898-899; 2352pp; English.
XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given in
CC AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerary; immunomodulator;
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 1842 BP; 540 A; 349 C; 360 G; 591 T; 0 U; 2 Other;

Query Match 28.6%; Score 1836.4; DB 3; Length 1842;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1837; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy       4549 AATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCA 4608
             |||||:|||||||||||||  ||:||||||||||||||||||||||||||||||||||||
Db          1 AATATWTGTATTTTTTGATCCTWTGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCA 60

Qy       4609 GCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGA 4668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGA 120

Qy       4669 TATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTG 4728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTG 180

Qy       4729 GCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGA 4788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGA 240

Qy       4789 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 4848
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 300

Qy       4849 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 4908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 360

Qy       4909 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 4968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 420

Qy       4969 ACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGA 5028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGA 480

Qy       5029 GGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCC 5088
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCC 540

Qy       5089 ACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCC 5148
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCC 600

Qy       5149 CGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACC 5208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACC 660

Qy       5209 AGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGG 5268
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Db        661 AGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGG 720

Qy       5269 GAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCAT 5328

Db        721 GAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCAT 780

Qy       5329 TCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTG 5388

Db        781 TCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTG 840

Qy       5389 CAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACT 5448

Db        841 CAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACT 900

Qy       5449 TGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATA 5508

Db        901 TGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATA 960

Qy       5509 GTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGT 5568

Db        961 GTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGT 1020

Qy       5569 AGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTT 5628

Db       1021 AGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTT 1080

Qy       5629 TATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCT 5688

Db       1081 TATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCT 1140

Qy       5689 GTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTC 5748

Db       1141 GTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTC 1200

Qy       5749 CTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 5808

Db       1201 CTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 1260

Qy       5809 CAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGC 5868

Db       1261 CAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGC 1320

Qy       5869 CAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATT 5928

Db       1321 CAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATT 1380

Qy       5929 TGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAAT 5988

Db       1381 TGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAAT 1440

Qy       5989 GGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATAT 6048

Db       1441 GGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATAT 1500

Qy       6049 ATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACT 6108

Db       1501 ATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACT 1560

Qy       6109 GCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTT 6168

Db       1561 GCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTT 1620

Qy       6169 TTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCA 6228

Db       1621 TTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCA 1680

Qy       6229 AAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAA 6288

Db       1681 AAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAA 1740

Qy       6289 TGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTAT 6348

Db       1741 TGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTAT 1800

Qy       6349 ATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAA 6390

Db       1801 ATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAGA 1842
```

RESULT 42
ABS57785
ID ABS57785 standard; cDNA; 1767 BP.
XX
AC ABS57785;
XX
DT 13-FEB-2003 (first entry)
XX
DE Truncated Human platelet derived growth factor receptor alpha DNA.
XX
KW Human; platelet derived growth factor receptor alpha; PDGFRalpha;
KW hepatotropic; dermatological; nephrotropic; vulnerary; ophthalmological;
KW cytostatic; gene therapy; vaccine; phosphoinositide-Kinase-Inhibitor-3;
KW phospholipase-Inhibitor-C; receptor tyrosine kinase; cell proliferation;
KW cell migration; extracellular matrix synthesis; secretion;
KW cell contraction; cancer; psoriasis; fibrotic diseases; atherosclerosis;
KW liver cirrhosis; pulmonary fibrosis; kidney fibrosis; scleroderma;
KW keloid; hypertrophic scar; wound; proliferative vitreoretinopathy; gene;
KW ss; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1767
FT		/*tag= c
FT		/product= "PDGFR mutant"
FT		/note= "Platelet derived growth factor receptor mutant"
FT		/partial
FT		/note= "No stop codon given"
FT	misc_feature	1. .1471
FT		/*tag= f
FT		/note= "Encodes the extracellular domain of mature PDGFR"
FT	sig_peptide	1. .72
FT		/*tag= b
FT		/note= "Signal peptide sequence number 2"
FT	sig_peptide	1. .60
FT		/*tag= a
FT		/note= "Signal peptide sequence number 1"
FT	mat_peptide	61. .1767
FT		/*tag= d
FT		/label= Mature_PDGFR_mutant
FT		/note= "Mature peptide sequence number 1"
FT	mat_peptide	73. .1767
FT		/*tag= e
FT		/label= Mature_PDGFR
FT		/note= "Mature peptide sequence number 2"
FT	misc_feature	1472. .1546
FT		/*tag= g
FT		/note= "Encodes the transmembrane domain of mature PDGFR"
FT	misc_feature	1547. .3166
FT		/*tag= h
FT		/note= "Encodes the intracellular domain of mature PDGFR"
FT	misc_signal	1669. .1767
FT		/*tag= i
FT		/note= "Encodes a truncated segment 1 of the split
FT		tyrosine kinase region"

XX
PN US2002111304-A1.
XX
PD 15-AUG-2002.
XX
PF 25-MAY-2001; 2001US-00866510.
XX
PR 01-DEC-2000; 2000US-0250747P.
PR 07-MAY-2001; 2001US-0289103P.

```
XX
PA   (KAZL/) KAZLAUSKAS A.
PA   (IKUN/) IKUNO Y.
XX
PI   Kazlauskas A,  Ikuno Y;
XX
DR   WPI; 2003-066697/06.
DR   P-PSDB; ABG72454.
XX
PT   New polypeptide for treating or preventing diseases associated with an
PT   abnormal platelet-derived growth factor (PDGF) level, e.g. cell
PT   proliferative or fibrotic diseases, comprises a portion of a PDGF-alpha
PT   or -beta.
XX
PS   Example 1; Page 67-69; 127pp; English.
XX
CC   The invention describes a polypeptide comprising a portion of the
CC   receptor tyrosine kinase platelet-derived growth factor alpha receptor
CC   (PDGFalphaR). The polypeptide and the polynucleotide are useful in
CC   treating or preventing diseases and conditions associated with an
CC   abnormal PDGF level or response, such as cell proliferation, cell
CC   migration, extracellular matrix synthesis and secretion or cell
CC   contraction. Exemplary diseases or disorders include cell proliferative
CC   diseases (e.g. cancer, psoriasis) or fibrotic diseases (e.g.
CC   atherosclerosis, liver cirrhosis, pulmonary fibrosis, kidney fibrosis,
CC   scleroderma, keloids, hypertrophic scars, skin wound healing or
CC   proliferative vitreoretinopathy). The method may be used in identifying
CC   compounds for treating or preventing the development of diseases
CC   involving cell contraction, e.g. fibrotic diseases. This sequence encodes
CC   human platelet derived growth factor receptor (PDGFR) alpha truncation
CC   mutant
XX
SQ   Sequence 1767 BP; 492 A; 393 C; 442 G; 440 T; 0 U; 0 Other;

  Query Match          27.6%;  Score 1767;  DB 10;  Length 1767;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-312;
  Matches 1767;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy       1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy       1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
```

```
Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCA 1905
             ||||||||||||||||||||||||||||
Db       1741 CCTTATGACTCAAGATGGGAGTTTCCA 1767
```

RESULT 43
ADJ93556
ID ADJ93556 standard; cDNA; 2427 BP.
XX
AC ADJ93556;
XX
DT 06-MAY-2004 (first entry)
XX
DE NM_030917-PDGFR-alpha fusion protein splice variant #3 coding sequence.
XX
KW ss; gene; NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase;
KW chromosome 4; translocation; hyperproliferation; cancer; atherosclerosis;
KW graft coronary vascular disease; transplantation; restenosis;
KW angioplasty; stent replacement; epidermal hyperproliferation;
KW tissue remodeling; repair; psoriasis; multiple sclerosis;
KW rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .2427
FT /*tag= a
FT /product= "NM_030917-PDGFR-alpha fusion protein splice
FT variant"
FT /transl_except= pos:901. .906, aa:Gln Leu Pro Tyr Asp
XX
PN WO2004015082-A2.
XX
PD 19-FEB-2004.
XX
PF 08-AUG-2003; 2003WO-US024992.
XX
PR 09-AUG-2002; 2002US-0402330P.
PR 16-JAN-2003; 2003US-0440491P.
XX
PA (THER-) THERAVANCE INC.
XX
PI Briesewitz R, Griffin JH;
XX
DR WPI; 2004-180662/17.
DR P-PSDB; ADJ93552.
XX
PT New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT conditions associated with the fusion polypeptide, and for identifying
PT agents for treating associated hyperproliferative disease conditions,
PT e.g. cancer or psoriasis.
XX
PS Claim 13; SEQ ID NO 8; 95pp; English.
XX
CC This sequence encodes an NM_030917-PDGFR-alpha fusion protein splice
CC variant. The fusion polypeptide of the invention comprises a C-terminal
CC tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC constitutively activated kinase activity, and is present in other than
CC its naturally occurring environment. The N- and C-terminal domains are
CC from chromosome 4 encoded proteins, and the fusion protein is not a
CC product of a translocation event. The fusion polypeptide or the
CC polynucleotide encoding it, are useful for determining whether a host
CC suffers from a disease condition, e.g. a hyperproliferative disease
CC condition. An agent that inhibits the activity or expression of the
CC fusion polypeptide is useful for treating a hyperproliferative disease
CC condition, such as cancer, atherosclerosis, graft coronary vascular
CC disease after transplantation, restenosis after angioplasty or stent
CC replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC or inflammatory bowel disease. The polynucleotides are also useful as
CC probes and primers in hybridization applications, or in the
CC identification of homologues, expression regulatory factors or expression
CC patterns in biological specimens.
XX
SQ Sequence 2427 BP; 726 A; 506 C; 626 G; 569 T; 0 U; 0 Other;

Query Match 23.7%; Score 1522.8; DB 12; Length 2427;
Best Local Similarity 99.9%; Pred. No. 6e-268;
Matches 1524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 961

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1021

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1081

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1141

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1201

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1261

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1321

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1381

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1441

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1501

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1561

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1621

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1681

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1741

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1742 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1801

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1861

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1921

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 1981

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2041

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2101

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2161

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2221

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2281

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2282 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2341

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2401

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||
Db       2402 ACCTGGTGGAAGACAGCTTCCTGTAA 2427


RESULT 44
ADJ93555
ID   ADJ93555 standard; cDNA; 2472 BP.
XX
AC   ADJ93555;
XX
DT   06-MAY-2004  (first entry)
XX
DE   NM_030917-PDGFR-alpha fusion protein splice variant #2 coding sequence.
XX
KW   ss; gene; NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase;
KW   chromosome 4; translocation; hyperproliferation; cancer; atherosclerosis;
KW   graft coronary vascular disease; transplantation; restenosis;
KW   angioplasty; stent replacement; epidermal hyperproliferation;
KW   tissue remodeling; repair; psoriasis; multiple sclerosis;
KW   rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2472
FT                   /*tag= a
FT                   /product= "NM_030917-PDGFR-alpha fusion protein splice
FT                   variant"
FT                   /transl_except= pos:946. .951, aa:Gln Leu Pro Tyr Asp
XX
PN   WO2004015082-A2.
XX
PD   19-FEB-2004.
XX
PF   08-AUG-2003; 2003WO-US024992.
XX
PR   09-AUG-2002; 2002US-0402330P.
PR   16-JAN-2003; 2003US-0440491P.
XX
PA   (THER-) THERAVANCE INC.
XX
PI   Briesewitz R,  Griffin JH;
XX
DR   WPI; 2004-180662/17.
DR   P-PSDB; ADJ93551.
XX
PT   New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT   conditions associated with the fusion polypeptide, and for identifying
PT   agents for treating associated hyperproliferative disease conditions,
PT   e.g. cancer or psoriasis.
XX
PS   Claim 13; SEQ ID NO 7; 95pp; English.
XX
CC   This sequence encodes an NM_030917-PDGFR-alpha fusion protein splice
CC   variant. The fusion polypeptide of the invention comprises a C-terminal
CC   tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC   constitutively activated kinase activity, and is present in other than
CC   its naturally occurring environment. The N- and C-terminal domains are
CC   from chromosome 4 encoded proteins, and the fusion protein is not a
CC   product of a translocation event. The fusion polypeptide or the
CC   polynucleotide encoding it, are useful for determining whether a host
CC   suffers from a disease condition, e.g. a hyperproliferative disease
CC   condition. An agent that inhibits the activity or expression of the
CC   fusion polypeptide is useful for treating a hyperproliferative disease
CC   condition, such as cancer, atherosclerosis, graft coronary vascular
CC   disease after transplantation, restenosis after angioplasty or stent
CC   replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC   psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC   or inflammatory bowel disease. The polynucleotides are also useful as
CC   probes and primers in hybridization applications, or in the
CC   identification of homologues, expression regulatory factors or expression
CC   patterns in biological specimens.
XX
SQ   Sequence 2472 BP; 737 A; 516 C; 641 G; 578 T; 0 U; 0 Other;

  Query Match           23.7%;  Score 1522.8;  DB 12;  Length 2472;
  Best Local Similarity  99.9%;  Pred. No. 6.1e-268;
  Matches 1524;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1006

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1066

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1126

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1186

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1246

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1247 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1306
```

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Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1366

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1426

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1486

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1546

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1547 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1606

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1607 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1666

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1726

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1786

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1846

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1906

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1966

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1967 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2026

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2086

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2146

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2206

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2266

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2267 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2326

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2327 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2386

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2446

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
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Db       2447 ACCTGGTGGAAGACAGCTTCCTGTAA 2472
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RESULT 45
ADJ93554
ID ADJ93554 standard; cDNA; 2496 BP.
XX
AC ADJ93554;
XX
DT 06-MAY-2004 (first entry)
XX
DE Coding sequence for NM_030917-PDGFR-alpha fusion protein splice variant.
XX
KW ss; gene; NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase;
KW chromosome 4; translocation; hyperproliferation; cancer; atherosclerosis;
KW graft coronary vascular disease; transplantation; restenosis;
KW angioplasty; stent replacement; epidermal hyperproliferation;
KW tissue remodeling; repair; psoriasis; multiple sclerosis;
KW rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .2496
FT   /*tag= a
FT   /product= "NM_030917-PDGFR-alpha fusion protein splice
FT   variant"
FT   /transl_except= pos:970. .975, aa:Gln Leu Pro Tyr Asp
XX
PN WO2004015082-A2.
XX
PD 19-FEB-2004.
XX
PF 08-AUG-2003; 2003WO-US024992.
XX
PR 09-AUG-2002; 2002US-0402330P.
PR 16-JAN-2003; 2003US-0440491P.
XX
PA (THER-) THERAVANCE INC.
XX
PI Briesewitz R, Griffin JH;
XX
DR WPI; 2004-180662/17.
DR P-PSDB; ADJ93550.
XX
PT New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT conditions associated with the fusion polypeptide, and for identifying
PT agents for treating associated hyperproliferative disease conditions,
PT e.g. cancer or psoriasis.
XX
PS Claim 13; SEQ ID NO 6; 95pp; English.
XX
CC This sequence encodes an NM_030917-PDGFR-alpha fusion protein splice
CC variant. The fusion polypeptide of the invention comprises a C-terminal
CC tyrosine kinase domain and an N-terminal domain. The fusion protein has a
CC constitutively activated kinase activity, and is present in other than
CC its naturally occurring environment. The N- and C-terminal domains are
CC from chromosome 4 encoded proteins, and the fusion protein is not a
CC product of a translocation event. The fusion polypeptide or the
CC polynucleotide encoding it, are useful for determining whether a host
CC suffers from a disease condition, e.g. a hyperproliferative disease
CC condition. An agent that inhibits the activity or expression of the
CC fusion polypeptide is useful for treating a hyperproliferative disease
CC condition, such as cancer, atherosclerosis, graft coronary vascular
CC disease after transplantation, restenosis after angioplasty or stent
CC replacement, epidermal hyperproliferation, tissue remodeling and repair,
CC psoriasis, multiple sclerosis, rheumatoid arthritis, diabetes mellitus,
CC or inflammatory bowel disease. The polynucleotides are also useful as

```
CC   probes and primers in hybridization applications, or in the
CC   identification of homologues, expression regulatory factors or expression
CC   patterns in biological specimens.
XX
SQ   Sequence 2496 BP; 748 A; 519 C; 643 G; 586 T; 0 U; 0 Other;

  Query Match            23.7%;  Score 1522.8;  DB 12;  Length 2496;
  Best Local Similarity  99.9%;  Pred. No. 6.1e-268;
  Matches 1524;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
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Db        971 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1030

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1090

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1150

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1151 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1210

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1270

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1330

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1390

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1391 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1450

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1451 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1510

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1511 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1570

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1571 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1630

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1631 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1690

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1691 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1750

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1751 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1810

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1811 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1870

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1871 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1930

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1931 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1990

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1991 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2050

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2051 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2110

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2111 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2170

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2171 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2230

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2231 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2290

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2291 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2350

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2351 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2410

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2411 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2470

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||||
Db       2471 ACCTGGTGGAAGACAGCTTCCTGTAA 2496


RESULT 46
ADJ93553
ID   ADJ93553 standard; cDNA; 2541 BP.
XX
AC   ADJ93553;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Coding sequence for NM_030917-PDGFR-alpha fusion protein.
XX
KW   ss; gene; NM_030917; PDGFR-alpha; fusion protein; tyrosine kinase;
KW   chromosome 4; translocation; hyperproliferation; cancer; atherosclerosis;
KW   graft coronary vascular disease; transplantation; restenosis;
KW   angioplasty; stent replacement; epidermal hyperproliferation;
KW   tissue remodeling; repair; psoriasis; multiple sclerosis;
KW   rheumatoid arthritis; diabetes mellitus; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2541
FT                   /*tag= a
FT                   /product= "NM_030917-PDGFR-alpha fusion protein"
FT                   /transl_except= pos:1015. .1020, aa:Gln Leu Pro Tyr Asp
XX
PN   WO2004015082-A2.
XX
PD   19-FEB-2004.
XX
PF   08-AUG-2003; 2003WO-US024992.
XX
```

PR 09-AUG-2002; 2002US-0402330P.
PR 16-JAN-2003; 2003US-0440491P.
XX
PA (THER-) THERAVANCE INC.
XX
PI Briesewitz R, Griffin JH;
XX
DR WPI; 2004-180662/17.
DR P-PSDB; ADJ93549.
XX
PT New tyrosine kinase fusion polypeptide, useful for diagnosing disease
PT conditions associated with the fusion polypeptide, and for identifying
PT agents for treating associated hyperproliferative disease conditions,
PT e.g. cancer or psoriasis.
XX
PS Claim 13; Page 61-63; 95pp; English.
XX
CC This sequence encodes an NM_030917-PDGFR-alpha fusion protein. The fusion
CC polypeptide of the invention comprises a C-terminal tyrosine kinase
CC domain and an N-terminal domain. The fusion protein has a constitutively
CC activated kinase activity, and is present in other than its naturally
CC occurring environment. The N- and C-terminal domains are from chromosome
CC 4 encoded proteins, and the fusion protein is not a product of a
CC translocation event. The fusion polypeptide or the polynucleotide
CC encoding it, are useful for determining whether a host suffers from a
CC disease condition, e.g. a hyperproliferative disease condition. An agent
CC that inhibits the activity or expression of the fusion polypeptide is
CC useful for treating a hyperproliferative disease condition, such as
CC cancer, atherosclerosis, graft coronary vascular disease after
CC transplantation, restenosis after angioplasty or stent replacement,
CC epidermal hyperproliferation, tissue remodeling and repair, psoriasis,
CC multiple sclerosis, rheumatoid arthritis, diabetes mellitus, or
CC inflammatory bowel disease. The polynucleotides are also useful as probes
CC and primers in hybridization applications, or in the identification of
CC homologues, expression regulatory factors or expression patterns in
CC biological specimens.
XX
SQ Sequence 2541 BP; 759 A; 529 C; 658 G; 595 T; 0 U; 0 Other;

Query Match 23.7%; Score 1522.8; DB 12; Length 2541;
Best Local Similarity 99.9%; Pred. No. 6.1e-268;
Matches 1524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy    1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1016 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1075

Qy    1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1076 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1135

Qy    2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1136 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1195

Qy    2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1196 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1255

Qy    2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1256 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1315

Qy    2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1316 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1375

Qy    2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1376 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1435

Qy    2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1436 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1495

Qy    2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1496 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1555

Qy    2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1556 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1615

Qy    2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1616 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1675

Qy    2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1676 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1735

Qy    2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1736 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1795

Qy    2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1796 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1855

Qy    2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1856 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1915

Qy    2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1916 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1975

Qy    2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1976 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2035

Qy    2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2036 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2095

Qy    2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2096 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2155

Qy    3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2156 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2215

Qy    3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2216 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2275

Qy    3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2276 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2335

Qy    3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2336 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2395

Qy    3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2396 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2455

Qy    3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2456 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2515

Qy    3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
           |||||||||||||||||||||||||
Db    2516 ACCTGGTGGAAGACAGCTTCCTGTAA 2541
```

RESULT 47
ADQ59527
ID ADQ59527 standard; DNA; 65952 BP.
XX
AC ADQ59527;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer-associated (CA) gene sequence SEQ ID NO:163.
XX
KW human; cancer-associated gene; cancer-associated protein; cytostatic;
KW gene therapy; vaccine; tyrosine kinase antagonist;
KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004058288-A1.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040082.
XX
PR 17-DEC-2002; 2002US-00322696.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-543349/52.
DR P-PSDB; ADQ59529.
XX
PT New cancer-associated nucleic acid for diagnosing, preventing or treating
PT cancer (e.g. lymphoma) or for screening agents that may be used for
PT treating or preventing cancer.
XX
PS Disclosure; SEQ ID NO 163; 143pp; English.
XX
CC The present invention describes human cancer-associated (CA) nucleotide
CC sequences (I). Also described: (1) an expression vector comprising (I);
CC (2) a host cell comprising (I) or the expression vector; (3) a microarray
CC for detecting a CA nucleic acid; (4) an isolated polypeptide encoded
CC within an open reading frame of a CA sequence; (5) an isolated antibody,
CC or its antigen binding fragment, that binds to the above polypeptide; (6)
CC a hybridoma that produces the monoclonal antibody described above; (7) a
CC pharmaceutical composition comprising the antibody and a pharmaceutical
CC excipient; (8) a kit for detecting or diagnosing cancer cells, comprising
CC the above (monoclonal) antibody or polynucleotide that selectively
CC hybridises to any of the polynucleotide sequences mentioned above; (9)
CC methods for diagnosing cancer or for detecting the presence or absence of
CC cancer cells in an individual; (10) a method for inhibiting growth of
CC cancer cells in an individual; (11) a method for delivering a therapeutic
CC agent to cancer cells in an individual; (12) an electronic library
CC comprising the polynucleotide or polypeptide, or their fragments,
CC mentioned above; (13) a method of screening for anticancer activity; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC or the presence of the antibody in a test cell or serum sample; (15) a
CC method for screening for a bioactive agent capable of modulating the
CC activity of a CA protein encoded by the above nucleic acid molecule; and
CC (16) a method for treating cancers. (I) has cytostatic activity, and can
CC be used in gene therapy, in vaccines, as a tyrosine kinase antagonist,
CC and as a G-protein coupled receptor antagonist. The compositions and
CC methods of the present invention can be used for diagnosing, preventing
CC and treating cancer, especially lymphomas. They may also be used in
CC screening for agents that may be used for treating or preventing cancer.
CC The present sequence represents a human CA gene sequence, which is given
CC in the exemplification of the present invention. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65952 BP; 16337 A; 14592 C; 15492 G; 18357 T; 0 U; 1174 Other;

Query Match 17.1%; Score 1094.6; DB 12; Length 65952;
Best Local Similarity 67.3%; Pred. No. 1.4e-189;
Matches 2241; Conservative 0; Mismatches 809; Indels 281; Gaps 38;

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Qy      3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
             |||||| ||||| || ||||||||||||||| ||||| |||||||| ||||||||||||||
Db     52707 CAGCTCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCAT 52766

Qy      3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
             |||||||||||||||||||||| || |||||||||||||||| ||||| || ||||| ||
Db     52767 CAAGAGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATTC 52826

Qy      3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
              || |||||||||| |||||||||||||||||| |  |  |   ||||  | ||  ||
Db     52827 CTCGGACCTGGTGGAGGACAGCTTCCTGTAACTGAC--ACGCTCCGGGTATCATCTTCTC 52884

Qy      3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
             | || ||| |||| ||||  | || |||||||||||| ||||||||||  | |||||||
Db     52885 CGGGAGCCTCCTCGGGATAACCTTAAGAAAACCACTTCATTGCAATGCAAAAGTTGAGAA 52944

Qy      3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCC---AGCCAAGGGCCTCGGGGAGCGTTC 3554
             |||||||||| ||||||  | ||||||  | ||    ||| |||||||  ||  ||| |
Db     52945 GAGGACTTGGGTGATGTGGAGAGAGAAAGTTCCCGAGGCCGAGGGCCTTGGTAAGCCT-- 53002

Qy      3555 TAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGC 3614
                | || |||| |||||||  ||| | |||||||| || |||||||||| |||| ||
Db     53003 ---GTGTGGATGACTGGGATA-CTTGGATTGAACTTTATCCGTGTTGCCTCTTGCAACGC 53058

Qy      3615 CTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGC 3674
             |||||||||||||||| || |||||  ||||||| || |||||| ||| || | |  |||
Db     53059 GTCAGTAGCATCTCAGCGGCGTGTGCGGTTTGGAAATGGATGGACAAGAGAGTGACTGGC 53118

Qy      3675 CACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTAT 3734
             |||||||  |  ||||||| ||| ||| ||| |||||||||| |||  | | |  |
Db     53119 CACAGAAGACGGGCTTTGTGTTTCCAGGGCATGGGTGAGAGTCCCACACGCGCCAACTTG 53178

Qy      3735 ACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTC-TAACCAAGGCTGTGTTTA 3793
                | | |||| |||||||||||||||||||||||||| ||||| ||| || |||||
Db     53179 TACTGCAGACAACTCCAGCATTGTAATTATGTAAATAACTCTTAACCGAGGATGGGTTTA 53238

Qy      3794 GAT-TGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATG---- 3848
             ||| ||| |||||| || |||  |||| |||||||||||||||| |||| || ||
Db     53239 GATCTGTGTTAACTCTCCTCTCCGGACCTCTGAAGAGACCACTCAGTCCACCCGTGTGCT 53298

Qy      3849 TACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAA 3908
             | ||||| ||||| || | |  |||||||||||||| ||| | |  ||||| |||| ||
Db     53299 TCCTTCCTTCTTGGAATCCGGTACCAGCTGCTGTTGAATTTTCTCATGAAGTACATGCAA 53358

Qy      3909 AACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGT 3968
             |||||  ||||||| ||  |||||||||| ||  | |  |||| || |||| |      |
Db     53359 AACCA-CTTTGAACTTTGGAAGGTACTGGAACCGTCGTGTTTTACTGTCTTGTAAGTGTT 53417

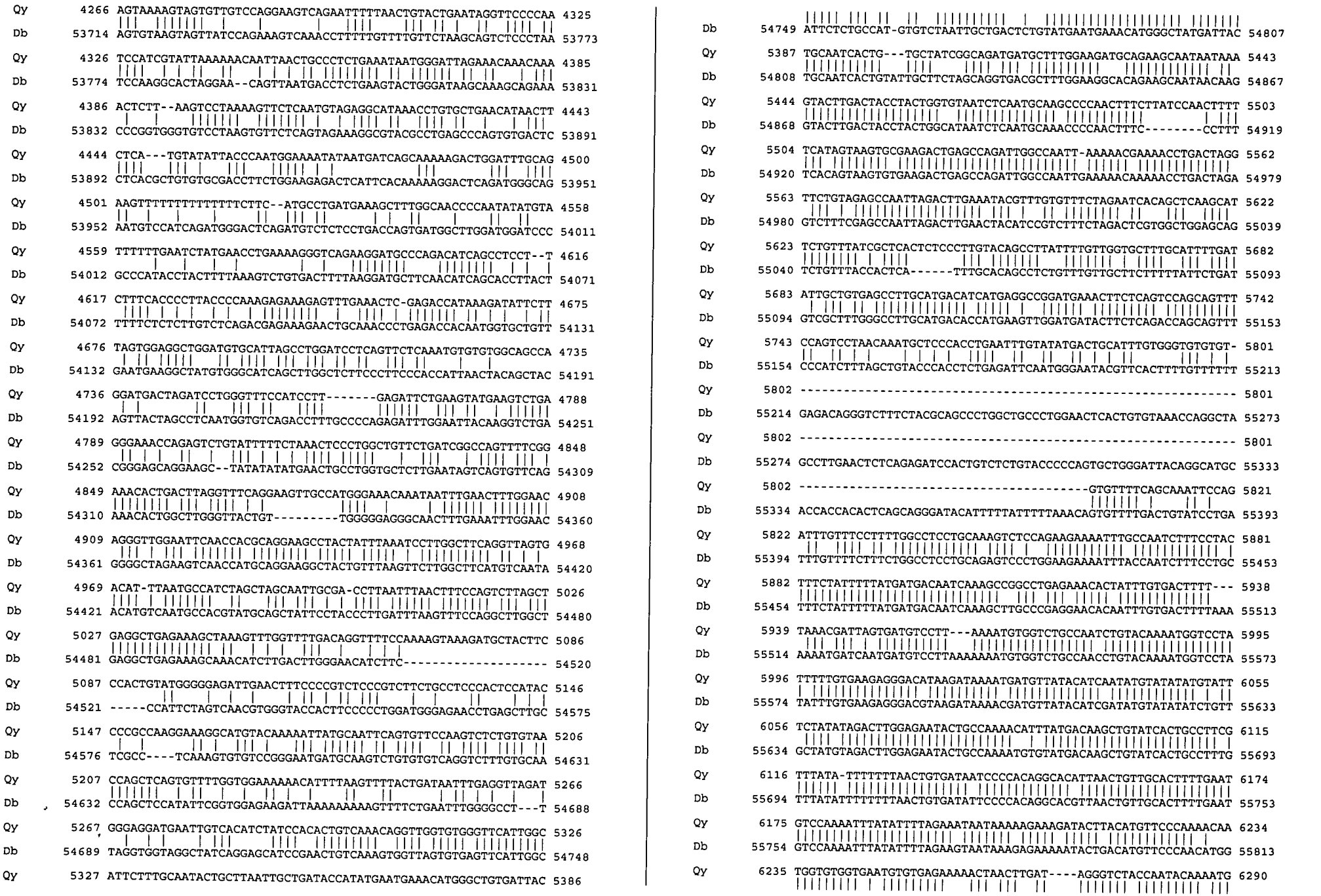
Qy      3969 TAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTA-GAA 4027
              ||   |  |||  |||| || |||||||||  ||  || ||| ||||||||  |||| |
Db     53418 AAAGAGGCAAAAAGATAAAAACTAACCAACCGTGAGTAGTAGGTTTGGGTCTTTTAGGGC 53477

Qy      4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTG-TTATCAGT 4086
             ||  | || || | |  || |||||||| |  |||||| ||||||||| ||| ||
Db     53478 ACCCAAGAATTCCTCTGTATCTTGTAATCTGTACTTATAACACTACTACTGTTTAACAAG 53537

Qy      4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAA-AC 4145
             |||||||||| ||||||   |||||||||||||  | |||||||||||||||| ||| |
Db     53538 AATGCTAAATATGTAAT-CCGTAACATGATTTCTTTACAGAGAAAGCACAATTAAAACAA 53596

Qy      4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
             || |||||||||| ||||||  |||||| |||||||||||||||||||||| ||||| ||
Db     53597 AACCCTTACTAAGAAGGTGACAAGTTTGGCAGTTTTTGACATTTATATTAAGTAACACGT 53656

Qy      4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
             ||||| ||||||||   |||||| ||||| | |||||| ||||   |   |||||| ||
Db     53657 TTCTCAATAAAGTA---TAATAGGTTTAGCGGATTAAAGTTAGCAAACACTAGAGAGCAG 53713
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Db      55814 TGGTGTGGTAAGTGTGTGAGAGCGACTTACTCCATAGGAAGGGTCTTCCAATACAAGATG 55873

Qy       6291 TATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATAT 6350
              ||  |  || |||||||||||| |||||||||||| |||||||| ||||||||||||
Db      55874 GCTTCCAGATACCCCTGTTCATG-TTTTGTTTTAAAAAGTGTAAATGGAGATCTTTATAT 55932

Qy       6351 TTCAATAAATGATATATAATTTAAAGTTAAA 6381
              |||||||||||||  ||| || ||    | ||
Db      55933 TTCAATAAATGATTTATTATATATGACTTAA 55963
```

RESULT 48
ADZ13908

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ID   ADZ13908 standard; DNA; 66009 BP.
XX
AC   ADZ13908;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Murine cancer-associated genomic DNA #125.
XX
KW   Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW   cytostatic; gene; ds.
XX
OS   Mus sp.
XX
PN   WO2005031001-A2.
XX
PD   07-APR-2005.
XX
PF   23-SEP-2004; 2004WO-US031617.
XX
PR   23-SEP-2003; 2003US-00669920.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2005-273395/28.
XX
PT   Nucleic acid array useful for detecting cancer associated nucleic acid,
PT   comprises two or more nucleic acid probes.
XX
PS   Disclosure; SEQ ID NO 1428; 198pp; English.
XX
CC   The invention relates to a nucleic acid array for detecting a cancer
CC   associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC   The invention also relates to a peptide array comprising two or more
CC   isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC   that binds to a polypeptide, an isolated antibody or its fragment which
CC   binds to a polypeptide, which is prepared by immunizing a host animal
CC   with a composition comprising the polypeptide or its antigen binding
CC   fragment and collecting cells from the host expressing antibodies against
CC   the antigen or its antigen binding fragment, a composition comprising the
CC   antibody and a carrier, a method of screening for anticancer activity, a
CC   method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC   method of treating cancer and a method of inhibiting expression of a CA
CC   nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC   nucleic acids. The antibody is useful for detecting the presence or
CC   absence of cancer cells in an individual which involves contacting cells
CC   from the individual with the antibody and detecting a complex of a CA
CC   protein from the cancer cells and the antibody, where the detection of
CC   the complex correlates with the presence of cancer cells in the
CC   individual. The composition is useful for inhibiting growth of cancer
CC   cells in an individual or for delivering a therapeutic agent to cancer
CC   cells in an individual. The invention is also useful for diagnosing
CC   cancer, for treating cancer and for inhibiting expression of a CA gene in
CC   a cell. This sequence represents murine cancer-associated genomic DNA of
CC   the invention.
XX
SQ   Sequence 66009 BP; 16350 A; 14600 C; 15508 G; 18377 T; 0 U; 1174 Other;

  Query Match             17.1%;  Score 1094.6;  DB 14;  Length 66009;
  Best Local Similarity   67.3%;  Pred. No. 1.4e-189;
  Matches 2241;  Conservative    0;  Mismatches  809;  Indels  281;  Gaps   38;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
              |||||| ||||| || |||||||||||||| ||||| |||||||| ||||||||||||||
Db      52748 CAGCTCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCAT 52807

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
              |||||||||||||||||||| || |||||||||||||||| ||||| || ||||| ||
Db      52808 CAAGAGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATTC 52867

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
              || |||||||||| |||||||||||||||||| |  |  |  ||||  | ||  ||
Db      52868 CTCGGACCTGGTGGAGGACAGCTTCCTGTAACTGAC--ACGCTCCGGGTATCATCTTCTC 52925

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
              | || ||| |||| ||||  | || |||||||||||| ||||||||||  | |||||||
Db      52926 CGGGAGCCTCCTCGGGATAACCTTAAGAAAACCACTTCATTGCAATGCAAAAGTTGAGAA 52985

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCC---AGCCAAGGGCCTCGGGGAGCGTTC 3554
              |||||||||| ||||||  | ||||||  | ||    ||| |||||||  ||  ||| |
Db      52986 GAGGACTTGGGTGATGTGGAGAGAGAAAGTTCCCGAGGCCGAGGGCCTTGGTAAGCCT-- 53043

Qy       3555 TAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGC 3614
                | || |||| ||||||| ||| | ||||||||| || |||||||||||| |||| ||
Db      53044 ---GTGTGGATGACTGGGATA-CTTGGATTGAACTTTATCCGTGTTGCCTCTTGCAACGC 53099

Qy       3615 CTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGC 3674
              |||||||||||||| || |||||  ||||||| || ||||||  ||| || | |  |||
Db      53100 GTCAGTAGCATCTCAGCGGCGTGTGCGGTTTGGAAATGGATGGACAAGAGAGTGACTGGC 53159

Qy       3675 CACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTAT 3734
              ||||||||  |  ||||||| ||| ||| ||| |||||||||||| |||  | | |  |
Db      53160 CACAGAAGACGGGCTTTGTGTTTCCAGGGCATGGGTGAGAGTCCCACACGCGCCAACTTG 53219

Qy       3735 ACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTC-TAACCAAGGCTGTGTTTA 3793
                | | |||| |||||||||||||||||||||||||||| ||||| ||| || |||||
Db      53220 TACTGCAGACAACTCCAGCATTGTAATTATGTAAATAACTCTTAACCGAGGATGGGTTTA 53279

Qy       3794 GAT-TGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATG---- 3848
              ||| ||| |||||| || |||  |||| ||||||||||||||||| |||| || ||
Db      53280 GATCTGTGTTAACTCTCCTCTCCGGACCTCTGAAGAGACCACTCAGTCCACCCGTGTGCT 53339

Qy       3849 TACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAA 3908
              | ||||| ||||| || | | |  |||||||||||||| ||| | | |||||  |||| ||
Db      53340 TCCTTCCTTCTTGGAATCCGGTACCAGCTGCTGTTGAATTTTCTCATGAAGTACATGCAA 53399

Qy       3909 AACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGT 3968
              |||||  |||||||  ||  |||||||||| ||  | |  |||| || |||| |      |
Db      53400 AACCA-CTTTGAACTTTGGAAGGTACTGGAACCGTCGTGTTTTACTGTCTTGTAAGTGTT 53458

Qy       3969 TAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTA-GAA 4027
              ||   |  |||  |||| || |||||||| ||  || ||| |||||||| |||| |
Db      53459 AAAGAGGCAAAAAGATAAAAACTAACCAACCGTGAGTAGTAGGTTTGGGTCTTTTAGGGC 53518

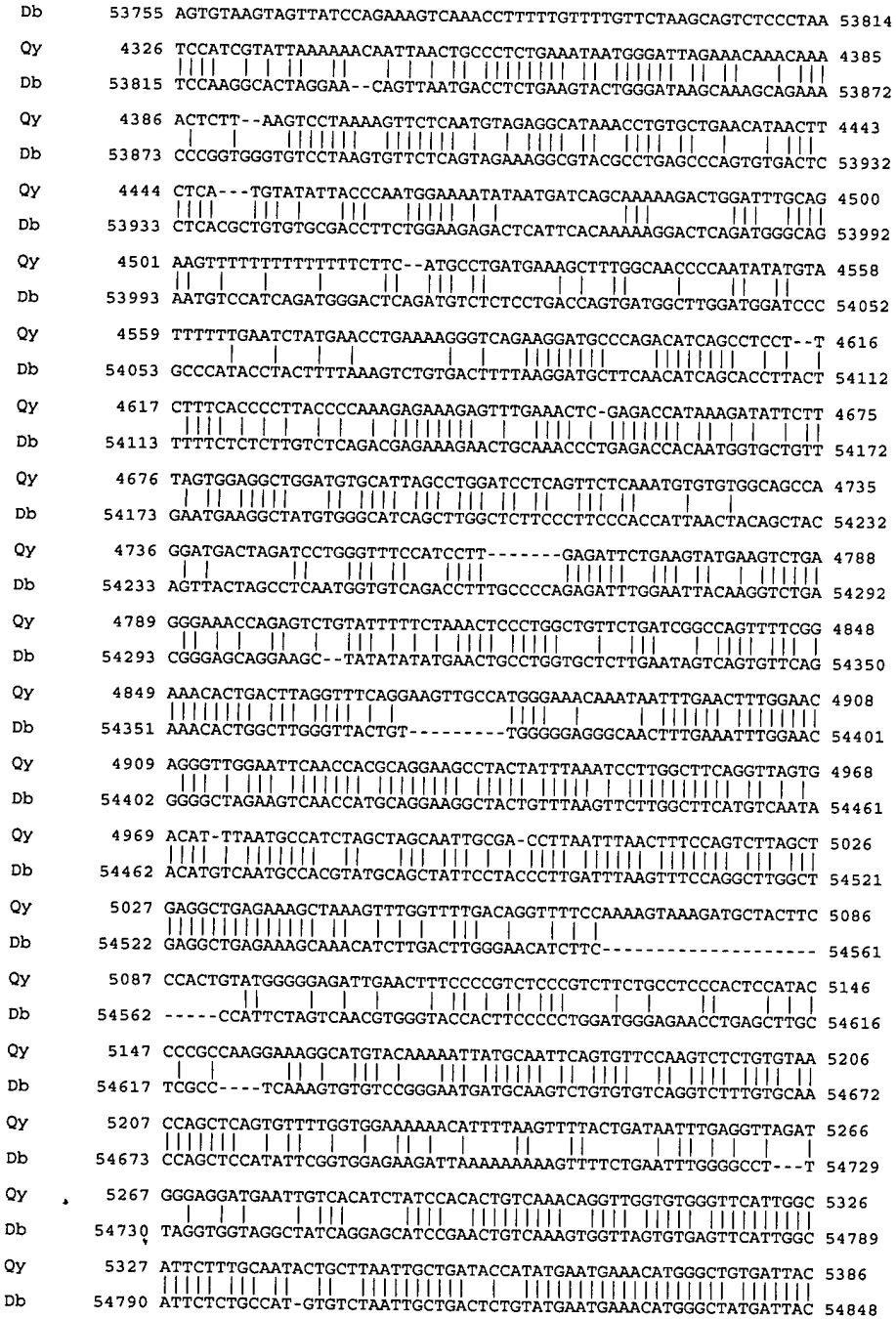
Qy       4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTG-TTATCAGT 4086
              ||  | || || | |  || ||||||||| |  |||||| |||||||||| ||| ||
Db      53519 ACCCAAGAATTCCTCTGTATCTTGTAATCTGTACTTATAACACTACTACTGTTTAACAAG 53578

Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAA-AC 4145
              |||||||||| ||||||   |||||||||||||  | |||||||||||||||| ||| |
Db      53579 AATGCTAAATATGTAAT-CCGTAACATGATTTCTTTACAGAGAAAGCACAATTAAAACAA 53637

Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
              || |||||||||| |||||  |||||| |||||||||||||||||||||| ||||| ||
Db      53638 AACCCTTACTAAGAAGGTGACAAGTTTGGCAGTTTTTGACATTTATATTAAGTAACACGT 53697

Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
              |||||  ||||||||   |||||| |||||  | ||||||  ||||    |   ||||||  ||
Db      53698 TTCTCAATAAAGTA---TAATAGGTTTAGCGGATTAAAGTTAGCAAACACTAGAGAGCAG 53754

Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
              |||  |||||||  |    |       |  ||||    ||| || |  ||  |||| ||
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Db 53755 AGTGTAAGTAGTTATCCAGAAAGTCAAACCTTTTTGTTTTGTTCTAAGCAGTCTCCCTAA 53814
Qy 4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
Db 53815 TCCAAGGCACTAGGAA--CAGTTAATGACCTCTGAAGTACTGGGATAAGCAAAGCAGAAA 53872
Qy 4386 ACTCTT--AAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTT 4443
Db 53873 CCCGGTGGGTGTCCTAAGTGTTCTCAGTAGAAAGGCGTACGCCTGAGCCCAGTGTGACTC 53932
Qy 4444 CTCA---TGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db 53933 CTCACGCTGTGTGCGACCTTCTGGAAGAGACTCATTCACAAAAAGGACTCAGATGGGCAG 53992
Qy 4501 AAGTTTTTTTTTTTTTTCTTC--ATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTA 4558
Db 53993 AATGTCCATCAGATGGGACTCAGATGTCTCTCCTGACCAGTGATGGCTTGGATGGATCCC 54052
Qy 4559 TTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCT--T 4616
Db 54053 GCCCATACCTACTTTTAAAGTCTGTGACTTTTAAGGATGCTTCAACATCAGCACCTTACT 54112
Qy 4617 CTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTC-GAGACCATAAAGATATTCTT 4675
Db 54113 TTTTCTCTCTTGTCTCAGACGAGAAAGAACTGCAAACCCTGAGACCACAATGGTGCTGTT 54172
Qy 4676 TAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCA 4735
Db 54173 GAATGAAGGCTATGTGGGCATCAGCTTGGCTCTTCCCTTCCCACCATTAACTACAGCTAC 54232
Qy 4736 GGATGACTAGATCCTGGGTTTCCATCCTT-------GAGATTCTGAAGTATGAAGTCTGA 4788
Db 54233 AGTTACTAGCCTCAATGGTGTCAGACCTTTGCCCCAGAGATTTGGAATTACAAGGTCTGA 54292
Qy 4789 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 4848
Db 54293 CGGGAGCAGGAAGC--TATATATATGAACTGCCTGGTGCTCTTGAATAGTCAGTGTTCAG 54350
Qy 4849 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 4908
Db 54351 AAACACTGGCTTGGGTTACTGT---------TGGGGGAGGGCAACTTTGAAATTTGGAAC 54401
Qy 4909 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 4968
Db 54402 GGGGCTAGAAGTCAACCATGCAGGAAGGCTACTGTTTAAGTTCTTGGCTTCATGTCAATA 54461
Qy 4969 ACAT-TTAATGCCATCTAGCTAGCAATTGCGA-CCTTAATTTAACTTTCCAGTCTTAGCT 5026
Db 54462 ACATGTCAATGCCACGTATGCAGCTATTCCTACCCTTGATTTAAGTTTCCAGGCTTGGCT 54521
Qy 5027 GAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTC 5086
Db 54522 GAGGCTGAGAAAGCAAACATCTTGACTTGGGAACATCTTC---------- 54561
Qy 5087 CCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATAC 5146
Db 54562 -----CCATTCTAGTCAACGTGGGTACCACTTCCCCCTGGATGGGAGAACCTGAGCTTGC 54616
Qy 5147 CCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAA 5206
Db 54617 TCGCC----TCAAAGTGTGTCCGGGAATGATGCAAGTCTGTGTGTCAGGTCTTTGTGCAA 54672
Qy 5207 CCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGAT 5266
Db 54673 CCAGCTCCATATTCGGTGGAGAAGATTAAAAAAAAAGTTTTCTGAATTTGGGGCCT---T 54729
Qy 5267 GGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGC 5326
Db 54730 TAGGTGGTAGGCTATCAGGAGCATCCGAACTGTCAAAGTGGTTAGTGTGAGTTCATTGGC 54789
Qy 5327 ATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTAC 5386
Db 54790 ATTCTCTGCCAT-GTGTCTAATTGCTGACTCTGTATGAATGAAACATGGGCTATGATTAC 54848
Qy 5387 TGCAATCACTG---TGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAA 5443
Db 54849 TGCAATCACTGTATTGCTTCTAGCAGGTGACGCTTTGGAAGGCACAGAAGCAATAACAAG 54908
Qy 5444 GTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTT 5503
Db 54909 GTACTTGACTACCTACTGGCATAATCTCAATGCAAACCCCAACTTTC--------CCTTT 54960
Qy 5504 TCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATT-AAAAACGAAAACCTGACTAGG 5562
Db 54961 TCACAGTAAGTGTGAAGACTGAGCCAGATTGGCCAATTGAAAAACAAAAACCTGACTAGA 55020
Qy 5563 TTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCAT 5622
Db 55021 GTCTTTCGAGCCAATTAGACTTGAACTACATCCGTCTTTCTAGACTCGTGGCTGGAGCAG 55080
Qy 5623 TCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGAT 5682
Db 55081 TCTGTTTACCACTCA------TTTGCACAGCCTCTGTTTGTTGCTTCTTTTTATTCTGAT 55134
Qy 5683 ATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTT 5742
Db 55135 GTCGCTTTGGGCCTTGCATGACACCATGAAGTTGGATGATACTTCTCAGACCAGCAGTTT 55194
Qy 5743 CCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGT- 5801
Db 55195 CCCATCTTTAGCTGTACCCACCTCTGAGATTCAATGGGAATACGTTCACTTTTGTTTTTT 55254
Qy 5802 ---------- 5801
Db 55255 GAGACAGGGTCTTTCTACGCAGCCCTGGCTGCCCTGGAACTCACTGTGTAAACCAGGCTA 55314
Qy 5802 ---------- 5801
Db 55315 GCCTTGAACTCTCAGAGATCCACTGTCTCTGTACCCCCAGTGCTGGGATTACAGGCATGC 55374
Qy 5802 ----------GTGTTTTCAGCAAATTCCAG 5821
Db 55375 ACCACCACACTCAGCAGGGATACATTTTTATTTTTAAACAGTGTTTTGACTGTATCCTGA 55434
Qy 5822 ATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTAC 5881
Db 55435 TTTGTTTTCTTTCTGGCCTCCTGCAGAGTCCCTGGAAGAAAATTTACCAATCTTTCCTGC 55494
Qy 5882 TTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTT--- 5938
Db 55495 TTTCTATTTTTATGATGACAATCAAAGCTTGCCCGAGGAACACAATTTGTGACTTTTAAA 55554
Qy 5939 TAAACGATTAGTGATGTCCTT---AAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTA 5995
Db 55555 AAAATGATCAATGATGTCCTTAAAAAAATGTGGTCTGCCAACCTGTACAAAATGGTCCTA 55614
Qy 5996 TTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATT 6055
Db 55615 TATTTGTGAAGAGGGACGTAAGATAAAACGATGTTATACATCGATATGTATATATCTGTT 55674
Qy 6056 TCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCG 6115
Db 55675 GCTATGTAGACTTGGAGAATACTGCCAAAATGTGTATGACAAGCTGTATCACTGCCTTTG 55734
Qy 6116 TTTATA-TTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAAT 6174
Db 55735 TTTATATTTTTTTTAACTGTGATATTCCCCACAGGCACGTTAACTGTTGCACTTTTGAAT 55794
Qy 6175 GTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAA 6234
Db 55795 GTCCAAAATTTATATTTTAGAAGTAATAAAGAGAAAAATACTGACATGTTCCCAACATGG 55854
Qy 6235 TGGTGTGGTGAATGTGTGAGAAAAACTAACTTGAT----AGGGTCTACCAATACAAAATG 6290
Db 55855 TGGTGTGGTAAGTGTGTGAGAGCGACTTACTCCATAGGAAGGGTCTTCCAATACAAGATG 55914

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Qy       6291 TATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATAT 6350
              || |  || |||||||||||| |||||||||||||| ||||||||| ||||||||||||
Db      55915 GCTTCCAGATACCCCTGTTCATG-TTTTGTTTTAAAAAGTGTAAATGGAGATCTTTATAT 55973

Qy       6351 TTCAATAAATGATATATAATTTAAAGTTAAA 6381
              |||||||||||||  ||| || ||    | ||
Db      55974 TTCAATAAATGATTTATTATATATGACTTAA 56004
```

RESULT 49
ADZ13912
ID ADZ13912 standard; cDNA; 1047 BP.
XX
AC ADZ13912;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human cancer-associated cDNA #435.
XX
KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
KW cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2005031001-A2.
XX
PD 07-APR-2005.
XX
PF 23-SEP-2004; 2004WO-US031617.
XX
PR 23-SEP-2003; 2003US-00669920.
XX
PA (CHIR) CHIRON CORP.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2005-273395/28.
DR P-PSDB; ADZ13913.
XX
PT Nucleic acid array useful for detecting cancer associated nucleic acid,
PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 1432; 198pp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acids. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated cDNA of the
CC invention.
XX
SQ Sequence 1047 BP; 274 A; 232 C; 271 G; 270 T; 0 U; 0 Other;

Query Match 11.5%; Score 736; DB 14; Length 1047;
Best Local Similarity 98.7%; Pred. No. 1.7e-124;

Matches 764; Conservative 0; Mismatches 5; Indels 5; Gaps 2;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  ||||||||| |||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACAT 772
              |||||||||||||||||||||||||||||||||||||||||||||||||||  || |
Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGGTACTT 1027
```

RESULT 50
ADQ38814
ID ADQ38814 standard; DNA; 1047 BP.
XX
AC ADQ38814;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 477.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004058052-A2.
XX
PD 15-JUL-2004.

XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JJ, Iakoubova O;
XX
DR WPI; 2004-533949/51.
DR P-PSDB; ADQ39642.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 477; 145pp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 1047 BP; 274 A; 231 C; 270 G; 269 T; 0 U; 3 Other;

Query Match 11.5%; Score 734.8; DB 13; Length 1047;
Best Local Similarity 98.3%; Pred. No. 2.8e-124;
Matches 761; Conservative 3; Mismatches 5; Indels 5; Gaps 2;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGRCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACAT 772
              ||||||||||||||||||||||||||||||||:|||||||||||||||||  || |
Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGGTACTT 1027
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Search completed: May 15, 2006, 09:48:47
Job time : 3546 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 08:49:40 ; Search time 15267 Seconds
(without alignments)
19653.210 Million cell updates/sec

Title: US-08-439-095-2
Perfect score: 6413
Sequence: 1 ccattactgttggagctaca.....aaaaaaaaaaaaaaaaaaa 6413

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2615	40.8	3122	10	AY410193	AY410193 Homo sapi
	2	2251	35.1	3122	10	AY410194	AY410194 Pan trogl
	3	2042.6	31.9	3118	10	AY410195	AY410195 Mus muscu
	4	1815.4	28.3	2869	4	AK081664	AK081664 Mus muscu
	5	1804	28.1	2835	4	AK035501	AK035501 Mus muscu
	6	1203.4	18.8	1699	4	BC020405	BC020405 Mus muscu
	7	898.8	14.0	1104	3	BM926494	BM926494 AGENCOURT
	8	799.4	12.5	904	3	BI768268	BI768268 603056437
c	9	796.8	12.4	847	1	AI819719	AI819719 wj11e03.x
	10	788.4	12.3	808	8	CX166250	CX166250 HESC2_38_
	11	772.6	12.0	902	6	CD518236	CD518236 AGENCOURT
	12	751.2	11.7	904	6	CD172287	CD172287 AGENCOURT
	13	744	11.6	746	7	CR736703	CR736703 CR736703
	14	741.2	11.6	765	7	CR791892	CR791892 DKFZp469F
	15	733	11.4	796	1	AU120263	AU120263 AU120263
	16	731	11.4	737	7	CN373040	CN373040 170006004
c	17	729	11.4	742	3	BQ015005	BQ015005 UI-H-ED1-
	18	726.6	11.3	750	1	AL713494	AL713494 DKFZp686B
	19	725.2	11.3	928	6	CA983729	CA983729 AGENCOURT
	20	718	11.2	741	2	BG623357	BG623357 602648396
	21	715	11.1	728	7	CN373044	CN373044 170004239
	22	715	11.1	759	7	CR769595	CR769595 DKFZp469J
	23	714.2	11.1	783	1	AU118489	AU118489 AU118489
c	24	711	11.1	723	5	BQ446932	BQ446932 UI-H-EU1-
c	25	707.8	11.0	711	3	BQ010105	BQ010105 UI-H-ED0-
	26	707.4	11.0	733	7	CN373045	CN373045 170004245
	27	707	11.0	707	6	CB217027	CB217027 NISC_nq11
	28	704.8	11.0	935	5	BU510904	BU510904 AGENCOURT
c	29	702.2	10.9	731	7	CN479805	CN479805 UI-H-EU0-
	30	698.6	10.9	740	8	DR005181	DR005181 TC116256
c	31	696.4	10.9	698	6	CA447048	CA447048 UI-H-ED0-
	32	684	10.7	791	2	BG434752	BG434752 602507957
c	33	681.4	10.6	783	1	AI805230	AI805230 tu44g03.x
c	34	681	10.6	681	2	BG939663	BG939663 cr60b12.x
c	35	679	10.6	698	3	BM972746	BM972746 UI-CF-EC1
	36	666.8	10.4	698	7	CN373046	CN373046 170004180
	37	666.2	10.4	807	7	CO431484	CO431484 UI-M-HX0-
	38	660.2	10.3	677	6	CA392578	CA392578 cs26c11.y
c	39	659.2	10.3	764	1	AI188169	AI188169 qd66c04.x
	40	657.2	10.2	734	7	CO739013	CO739013 SlLE04c22
	41	656.4	10.2	789	7	CK781356	CK781356 UI-M-GV0-
c	42	653.4	10.2	656	3	BQ003864	BQ003864 UI-H-EI1-
c	43	644.6	10.1	699	1	AI857848	AI857848 wl23b06.x
	44	644.2	10.0	931	5	BQ884103	BQ884103 AGENCOURT
c	45	642	10.0	669	1	AI672567	AI672567 wb32g09.x
c	46	641	10.0	730	1	AI422895	AI422895 tf30g02.x
	47	640	10.0	640	7	CN483903	CN483903 hw39g04.y
c	48	632.6	9.9	686	5	BU623579	BU623579 UI-H-FG1-
	49	630.2	9.8	802	5	BQ442880	BQ442880 UI-M-EV0-
	50	627.6	9.8	642	7	CV030074	CV030074 9079 Full
	51	626.4	9.8	795	6	CB522409	CB522409 UI-M-GH0-
	52	625.8	9.8	776	7	CV555649	CV555649 UI-M-HZ0-
	53	624.8	9.7	637	7	CN373041	CN373041 170004243
	54	623.4	9.7	766	6	CB521132	CB521132 UI-M-GH0-
c	55	623.2	9.7	632	1	AI767385	AI767385 wi94g01.x
	56	622.6	9.7	650	5	BX481288	BX481288 DKFZp686G
	57	622.4	9.7	814	6	CB520847	CB520847 UI-M-GH0-
c	58	621.2	9.7	720	1	AI184329	AI184329 qd39e12.x
	59	619.2	9.7	757	6	CF746471	CF746471 UI-M-HE0-
	60	614.8	9.6	743	6	CF744412	CF744412 UI-M-GV0-
	61	611.2	9.5	742	6	CF533631	CF533631 UI-M-GH0-
c	62	610.6	9.5	648	1	AI806205	AI806205 wf26d01.x
	63	608.2	9.5	786	6	CB519658	CB519658 UI-M-GH0-
c	64	606.8	9.5	668	1	AI589118	AI589118 tf81c02.x
	65	604.8	9.4	800	6	CF534720	CF534720 UI-M-GH0-
c	66	603.4	9.4	616	5	BU739951	BU739951 UI-E-EJ0-
c	67	603	9.4	623	3	BQ006823	BQ006823 UI-H-EI1-
c	68	602.6	9.4	645	1	AI654558	AI654558 wb48c07.x
	69	602.6	9.4	772	7	CN535343	CN535343 UI-M-HS0-
	70	602	9.4	654	2	BG616454	BG616454 602614616
	71	600	9.4	600	6	CD677439	CD677439 ho17b01.y
	72	596.8	9.3	787	5	BQ432542	BQ432542 AGENCOURT
	73	596	9.3	781	7	CN525798	CN525798 UI-M-HN0-
c	74	595	9.3	595	1	AW172753	AW172753 xj03a09.x
	75	594.6	9.3	832	8	CX565582	CX565582 UI-M-HA0-
	76	592.8	9.2	596	6	CD671313	CD671313 fg03b01.y
	77	592.6	9.2	615	1	AV653603	AV653603 AV653603
	78	591.2	9.2	798	6	CF746125	CF746125 UI-M-GV0-
c	79	587.6	9.2	676	1	AI360962	AI360962 qy02e06.x
	80	587.4	9.2	615	1	AW605347	AW605347 QV3-DT004
c	81	587.2	9.2	625	1	AI686922	AI686922 tp91c09.x
	82	586.4	9.1	760	6	CF736622	CF736622 UI-M-HD0-
	83	584.8	9.1	601	1	AL036386	AL036386 DKFZp564F
	84	581.4	9.1	583	3	BP270737	BP270737 BP270737
	85	579.8	9.0	592	7	CK823263	CK823263 ij27a12.y
	86	579.2	9.0	720	6	CF731341	CF731341 UI-M-GZ0-
c	87	576.4	9.0	589	1	AV719177	AV719177 AV719177
c	88	575.6	9.0	626	1	AI631199	AI631199 ts93g12.x
	89	574.6	9.0	614	1	AL603591	AL603591 DKFZp686I
	90	573	8.9	582	3	BP348576	BP348576 BP348576
	91	571.4	8.9	582	3	BP339302	BP339302 BP339302
	92	571.4	8.9	584	3	BP204834	BP204834 BP204834
	93	571.4	8.9	836	8	DN125574	DN125574 1139428 M
c	94	569.6	8.9	658	1	AA669381	AA669381 ab90a12.s
	95	569.4	8.9	582	3	BP293414	BP293414 BP293414

	96	568	8.9	583	3	BP288747	BP288747 BP288747
	97	568	8.9	833	7	CN524868	CN524868 UI-M-GH0-
c	98	567.8	8.9	607	1	AI951016	AI951016 wx62c06.x
	99	566.8	8.8	579	3	BM966779	BM966779 ij26d07.y
	100	566.4	8.8	773	7	CK477487	CK477487 AGENCOURT
	101	565.8	8.8	582	3	BP363739	BP363739 BP363739
c	102	563.8	8.8	586	1	AW573235	AW573235 hf34f08.x
	103	563.8	8.8	618	1	AV699068	AV699068 AV699068
	104	560.8	8.7	720	8	DN542929	DN542929 1391721 M
	105	560.6	8.7	593	1	AV697958	AV697958 AV697958
	106	560.6	8.7	756	8	CX758607	CX758607 AGENCOURT
	107	557	8.7	581	3	BP290943	BP290943 BP290943
	108	555.6	8.7	574	3	BP289145	BP289145 BP289145
	109	555.4	8.7	580	3	BP290364	BP290364 BP290364
c	110	554.6	8.6	881	8	DN125930	DN125930 1139812 M
	111	553.6	8.6	716	2	BF529107	BF529107 602042151
c	112	552.2	8.6	579	1	AW182268	AW182268 xj40b03.x
	113	551	8.6	552	3	BM700233	BM700233 UI-E-DW1-
	114	550.4	8.6	564	1	AU280434	AU280434 AU280434
	115	550.2	8.6	557	3	BP344712	BP344712 BP344712
c	116	549.6	8.6	566	5	BU752991	BU752991 UI-1-BB1-
c	117	546.8	8.5	574	1	AA599881	AA599881 ag32e07.s
	118	545.8	8.5	582	3	BP320264	BP320264 BP320264
	119	544.8	8.5	723	2	BG435720	BG435720 602506821
	120	543.8	8.5	578	3	BP220081	BP220081 BP220081
	121	543.4	8.5	660	2	BG927326	BG927326 HNC1-1-B7
	122	543.2	8.5	628	8	DN865723	DN865723 nac17f01.
	123	541.8	8.4	706	6	CF727026	CF727026 UI-M-HB0-
	124	539	8.4	582	3	BP232383	BP232383 BP232383
c	125	538	8.4	539	2	BF196702	BF196702 7m94g04.x
c	126	533	8.3	591	1	AA625689	AA625689 zu86b07.s
c	127	532	8.3	584	1	AU145037	AU145037 AU145037
	128	530.2	8.3	557	3	BP424246	BP424246 BP424246
	129	529.6	8.3	596	1	AV696990	AV696990 AV696990
	130	527.6	8.2	556	3	BP220107	BP220107 BP220107
	131	526.2	8.2	587	3	BP321273	BP321273 BP321273
	132	526.2	8.2	823	2	BG967919	BG967919 602833170
	133	525.4	8.2	647	7	CK393846	CK393846 L0121H06-
c	134	524.8	8.2	786	8	DN643305	DN643305 UMC-bof_0
	135	520.8	8.1	610	1	AV689272	AV689272 AV689272
c	136	519.8	8.1	523	1	AW473224	AW473224 xy13f02.x
	137	518.6	8.1	536	5	BX111508	BX111508 BX111508
	138	518.6	8.1	1390	8	DN692999	DN692999 CGX85-D07
	139	517.2	8.1	766	8	DN535260	DN535260 1371278 M
	140	516.2	8.0	697	6	CF743849	CF743849 UI-M-GI0-
c	141	513.6	8.0	933	5	BX693437	BX693437 BX693437
	142	513.4	8.0	700	7	CV555812	CV555812 UI-M-HZ0-
	143	512.8	8.0	525	3	BM966834	BM966834 ij27a12.y
	144	510.2	8.0	658	7	CN536954	CN536954 UI-M-HS0-
	145	510	8.0	789	6	CF743225	CF743225 UI-M-GV0-
c	146	508.2	7.9	535	3	BM677213	BM677213 UI-E-EO1-
c	147	508.2	7.9	603	1	AA845508	AA845508 ak04c02.s
c	148	508	7.9	533	1	AW887370	AW887370 RC0-OT008
c	149	507.2	7.9	541	1	AI004887	AI004887 ot59d02.s
	150	506	7.9	519	2	BG619837	BG619837 602618012
	151	505.4	7.9	641	8	CX949478	CX949478 UMC-bcl_0
	152	505	7.9	524	3	BM715043	BM715043 UI-E-EJ0-
	153	505	7.9	712	6	CF723563	CF723563 UI-M-GV0-
	154	504.4	7.9	629	7	CN694051	CN694051 E0345C10-
c	155	502.6	7.8	727	7	CO872889	CO872889 BovGen_01
	156	502.6	7.8	788	7	CK781272	CK781272 UI-M-GV0-
	157	501.6	7.8	727	7	CO875768	CO875768 BovGen_04
	158	501.4	7.8	741	6	CF728074	CF728074 UI-M-HB0-
	159	500.8	7.8	581	3	BP215096	BP215096 BP215096
c	160	500.2	7.8	599	1	AA054505	AA054505 zk83b06.s
c	161	499.4	7.8	727	5	BQ782100	BQ782100 UI-R-FF0-
	162	499	7.8	511	6	CB270748	CB270748 1009672 H
c	163	499	7.8	531	1	AA705647	AA705647 zf40c04.s
	164	498.4	7.8	560	3	BP344913	BP344913 BP344913
	165	497	7.7	638	6	CF728798	CF728798 UI-M-HE0-
	166	497	7.7	675	6	CD803107	CD803107 UI-M-GV0-
c	167	497	7.7	724	2	BE630572	BE630572 uu37e04.x
c	168	496.6	7.7	764	7	CN153907	CN153907 941074 MA
c	169	495.2	7.7	878	8	CX389518	CX389518 JGI_XZT37
c	170	494.8	7.7	576	1	AV688375	AV688375 AV688375
	171	494.8	7.7	582	3	BP230744	BP230744 BP230744
	172	493.8	7.7	587	3	BP336054	BP336054 BP336054
	173	493.8	7.7	625	1	AW323855	AW323855 uo77e10.y
	174	493.4	7.7	583	3	BM502402	BM502402 ii33f05.y
	175	493.2	7.7	602	1	AI228644	AI228644 EST225339
	176	493.2	7.7	619	1	AV688357	AV688357 AV688357
c	177	491.4	7.7	603	2	BF470972	BF470972 UI-M-BH3-
	178	490.8	7.7	630	1	AV687046	AV687046 AV687046
	179	490.4	7.6	782	6	CF742988	CF742988 UI-M-HB0-
	180	489.8	7.6	736	7	CK781546	CK781546 UI-M-GV0-
c	181	489.6	7.6	704	8	DN536694	DN536694 1372814 M
	182	489	7.6	494	1	AW021685	AW021685 df26h10.y
c	183	488.4	7.6	490	1	AI952733	AI952733 wq48c08.x
	184	487.8	7.6	513	1	AL710441	AL710441 DKFZp686D
	185	487.4	7.6	707	6	CF734831	CF734831 UI-M-HB0-
	186	485.8	7.6	657	2	BF107419	BF107419 601824037
	187	484.6	7.6	582	3	BP229872	BP229872 BP229872
c	188	482.8	7.5	687	6	CB168250	CB168250 PWQ602701
	189	482.6	7.5	529	1	AA026841	AA026841 zk02f02.r
c	190	482	7.5	482	1	AI192222	AI192222 qc92h06.x
c	191	482	7.5	482	7	CR746416	CR746416 CR746416
	192	481.8	7.5	598	7	CK393917	CK393917 L0123H05-
	193	481.4	7.5	571	7	CN696666	CN696666 E0382H07-
	194	481.2	7.5	1184	6	CD244994	CD244994 AGENCOURT
	195	479.8	7.5	829	8	CX242348	CX242348 NMA05480
	196	479.4	7.5	482	7	CN373043	CN373043 170004240
c	197	478.4	7.5	678	10	AG145715	AG145715 Pan trogl
	198	476.4	7.4	823	8	CX365518	CX365518 JGI_XZT25
c	199	472.6	7.4	520	1	AI056024	AI056024 ow32f09.s
c	200	472.4	7.4	474	1	AI360903	AI360903 qy01f05.x
	201	472.2	7.4	686	7	CR453431	CR453431 CR453431
	202	470.6	7.3	753	7	CN439414	CN439414 BE04019B1
	203	467.6	7.3	722	7	CK031869	CK031869 AGENCOURT
c	204	467.4	7.3	469	2	BE858626	BE858626 7f98e05.x
c	205	467.4	7.3	569	1	AV719090	AV719090 AV719090
	206	466.4	7.3	730	8	CX602494	CX602494 CT02032B2
c	207	465.6	7.3	472	1	AA927919	AA927919 om18f12.s
c	208	465.4	7.3	662	7	CK946234	CK946234 4070764 B
c	209	464.4	7.2	477	1	AA884644	AA884644 am33d09.s
c	210	464	7.2	556	3	BI404804	BI404804 MI-P-H5-a
c	211	463.4	7.2	465	1	AA644680	AA644680 ab87c12.s
	212	462.4	7.2	464	1	AW880717	AW880717 QV0-OT003
	213	462	7.2	463	3	BM721602	BM721602 UI-E-EO1-
c	214	460.8	7.2	464	1	AI335725	AI335725 qt36g06.x
	215	460.6	7.2	547	6	CA895593	CA895593 B0193B06-
	216	460.2	7.2	569	3	BP277058	BP277058 BP277058
c	217	460	7.2	461	1	AI092636	AI092636 qa35d08.x
	218	459.4	7.2	799	8	CX760731	CX760731 AGENCOURT
c	219	459	7.2	630	8	W82312	W82312 me99h11.r1
c	220	458	7.1	516	1	AU146380	AU146380 AU146380
c	221	456.8	7.1	679	8	DN865722	DN865722 nac17f01.
	222	455.2	7.1	548	6	CD552500	CD552500 B0344A02-
	223	453.6	7.1	557	2	BE946229	BE946229 UI-M-BH3-
	224	453	7.1	699	7	CK358956	CK358956 AGENCOURT
c	225	452.8	7.1	542	1	AI921757	AI921757 wo29h01.x
	226	452.6	7.1	560	7	CO431949	CO431949 UI-M-HX0-
	227	452	7.0	476	1	AA043451	AA043451 zk54b09.r
	228	451.2	7.0	923	8	CX950349	CX950349 UMC-bcl_0
	229	449.8	7.0	550	7	CK343841	CK343841 K0800D08-
	230	448.6	7.0	728	7	CK692770	CK692770 ZF101-P00
c	231	448.4	7.0	491	1	AI624526	AI624526 ts17h04.x
	232	448.4	7.0	547	1	AI599570	AI599570 EST251273
c	233	448.2	7.0	613	7	CK343959	CK343959 K0815E03-
	234	448	7.0	740	7	CO892755	CO892755 BovGen_21
	235	447.8	7.0	752	6	CD803651	CD803651 UI-M-GV0-
	236	447.2	7.0	524	7	CN667672	CN667672 A0856H10-
c	237	447	7.0	518	1	AI215060	AI215060 qg52c06.x
	238	446.4	7.0	478	6	CB267839	CB267839 1006745 H
c	239	446.4	7.0	552	1	AI245226	AI245226 qk11f10.x
	240	446.2	7.0	762	8	DN891546	DN891546 nao09d10.
	241	446	7.0	582	3	BP380239	BP380239 BP380239

c 242	445	6.9	445	1	AA969144	AA969144 op50d02.s
243	445	6.9	739	6	CB448178	CB448178 702239 MA
244	443.6	6.9	735	6	CF745466	CF745466 UI-M-GV0-
c 245	442.8	6.9	462	1	AA043452	AA043452 zk54b09.s
246	442.2	6.9	468	1	AL589412	AL589412 DKFZp451O
247	442	6.9	442	8	W70251	W70251 zd49f11.r1
c 248	441.6	6.9	460	1	AI654509	AI654509 wb63d07.x
249	439.4	6.9	537	2	BE103474	BE103474 UI-R-BX0-
c 250	438.4	6.8	657	8	DN541866	DN541866 1390489 M
c 251	438.4	6.8	671	6	CB168247	CB168247 PWQ602701
252	436.6	6.8	640	7	CO894506	CO894506 BovGen_22
253	435.4	6.8	577	7	CN663497	CN663497 A0800G04-
c 254	434.8	6.8	598	7	CK340586	CK340586 C0930G02-
255	434.8	6.8	811	7	CN156021	CN156021 943378 MA
256	432.4	6.7	581	1	AA054366	AA054366 zk83b06.r
257	431.6	6.7	754	2	BF163118	BF163118 601769635
258	429	6.7	693	2	BB865561	BB865561 BB865561
259	428.2	6.7	498	1	AL039890	AL039890 DKFZp434G
c 260	427.4	6.7	597	6	CA774419	CA774419 ik74e03.x
c 261	426.4	6.6	480	1	AA724024	AA724024 ah88e07.s
c 262	424.4	6.6	559	1	AI215058	AI215058 qg52c04.x
263	423.6	6.6	694	8	W78320	W78320 me79f03.r1
264	422.8	6.6	438	5	BX483320	BX483320 DKFZp686N
265	422.8	6.6	506	7	CN693685	CN693685 E0340D01-
266	422.2	6.6	439	5	BX479019	BX479019 DKFZp686I
267	421.8	6.6	645	7	CR551001	CR551001 CR551001
268	421.6	6.6	596	2	BF719290	BF719290 mab38f07.
c 269	420	6.5	420	2	BF477431	BF477431 nac60f12.
270	417.8	6.5	581	7	CN663738	CN663738 A0803H07-
271	417.6	6.5	647	5	BY722174	BY722174 BY722174
272	417	6.5	417	6	CB266178	CB266178 1005083 H
273	415.6	6.5	510	2	BE114274	BE114274 UI-R-BJ1-
274	414.4	6.5	755	8	CV811870	CV811870 AGENCOURT
275	413.6	6.4	509	1	AI137657	AI137657 UI-R-C0-h
276	413.2	6.4	463	8	H02958	H02958 yj46f05.r1
277	412	6.4	758	6	CA371754	CA371754 652337 NC
c 278	411.6	6.4	432	8	H04256	H04256 yj46f05.s1
279	411.4	6.4	581	3	BP291448	BP291448 BP291448
280	411.2	6.4	606	6	CD802671	CD802671 UI-M-GV0-
281	411.2	6.4	885	7	CR849574	CR849574 CR849574
282	410.4	6.4	629	6	CD772183	CD772183 AGENCOURT
283	410.4	6.4	822	2	BF102306	BF102306 601751915
284	409.6	6.4	504	2	BE984896	BE984896 UI-M-CG0p
c 285	408.6	6.4	477	1	AI619541	AI619541 ty49g09.x
c 286	408	6.4	455	1	AI335563	AI335563 qt30f07.x
287	407.8	6.4	885	5	BU107364	BU107364 603111921
c 288	407.2	6.3	608	6	CB427907	CB427907 603517 MA
c 289	407.2	6.3	711	6	CA505634	CA505634 UI-R-FJ0-
290	406	6.3	648	5	BY728496	BY728496 BY728496
291	405	6.3	640	6	CD803536	CD803536 UI-M-GV0-
292	404.6	6.3	423	2	BF929228	BF929228 IL2-NT019
293	404	6.3	474	8	R81879	R81879 yj03a03.r1
c 294	403.6	6.3	522	1	AI040046	AI040046 ox28a06.x
c 295	403.6	6.3	536	1	AI250996	AI250996 qx49f02.x
296	403.6	6.3	727	6	CF728803	CF728803 UI-M-HE0-
297	403.4	6.3	440	8	W56717	W56717 zd14f07.r1
298	403.4	6.3	639	6	CB434442	CB434442 611059 MA
299	400.2	6.2	611	7	CN667545	CN667545 A0855A07-
300	399.8	6.2	626	6	CF744174	CF744174 UI-M-GV0-
c 301	399	6.2	543	6	CA891305	CA891305 B0164H01-
c 302	398.8	6.2	785	7	CK031364	CK031364 AGENCOURT
c 303	398	6.2	422	8	W70252	W70252 zd49f11.s1
304	397.2	6.2	595	3	BM537077	BM537077 ha77h04.g
305	396.8	6.2	468	1	AA041495	AA041495 zf10b06.r
306	396.2	6.2	970	2	BF099663	BF099663 601751691
307	396	6.2	625	6	CD773008	CD773008 AGENCOURT
c 308	395.6	6.2	538	2	BG798108	BG798108 ic09h06.x
309	392.4	6.1	441	3	BM706203	BM706203 UI-E-DW0-
c 310	392.4	6.1	538	2	BE103253	BE103253 UI-R-BX0-
c 311	392.2	6.1	609	1	AW322569	AW322569 uo77e10.x
c 312	392.2	6.1	635	1	AW541540	AW541540 C0146D03-
313	392.2	6.1	770	8	DN441309	DN441309 LIB5338-1
314	391.8	6.1	718	5	BU701262	BU701262 UI-M-EX0-
c 315	391	6.1	629	1	AI232379	AI232379 EST229067
c 316	389.6	6.1	532	2	BE103248	BE103248 UI-R-BX0-
c 317	386.6	6.0	434	1	AA884868	AA884868 am21c01.s
c 318	386.6	6.0	803	7	CK022796	CK022796 AGENCOURT
c 319	386	6.0	626	1	AW320615	AW320615 uo21c04.y
320	384.6	6.0	615	5	BQ396571	BQ396571 NISC_ng21
c 321	383.2	6.0	569	3	BI303917	BI303917 UI-R-DR0-
322	382.2	6.0	649	3	BJ623792	BJ623792 BJ623792
c 323	382	6.0	408	1	AA027043	AA027043 zk02f02.s
324	381.4	5.9	448	8	W00708	W00708 za72h10.r1
c 325	381.4	5.9	470	1	AA888900	AA888900 ak15c03.s
326	381.4	5.9	582	3	BP321319	BP321319 BP321319
c 327	380	5.9	524	3	BI677358	BI677358 ie11g12.x
c 328	379	5.9	515	6	CA889262	CA889262 B0151G10-
329	378	5.9	378	8	F07207	F07207 HSC1YH021 n
c 330	377.4	5.9	515	7	CK340585	CK340585 C0930C03-
c 331	376.4	5.9	514	1	AA964437	AA964437 UI-R-E1-g
332	376	5.9	448	5	BX515644	BX515644 BX515644
333	373.2	5.8	684	1	AI122392	AI122392 uc61e08.r
334	373	5.8	415	1	AW498738	AW498738 EST304239
335	373	5.8	443	1	AA330087	AA330087 EST33768
c 336	372.8	5.8	831	8	DN823208	DN823208 UMC-bof_0
c 337	372.6	5.8	550	3	BM237343	BM237343 K0449E11-
c 338	372.2	5.8	505	6	CA892956	CA892956 B0175G05-
c 339	372	5.8	540	3	BI492624	BI492624 df26h10.w
340	372	5.8	654	3	BJ029667	BJ029667 BJ029667
c 341	371.2	5.8	542	7	CK627326	CK627326 io02c03.y
c 342	370.8	5.8	444	8	W56762	W56762 zd14f07.s1
343	370.4	5.8	556	2	BF180200	BF180200 601808473
344	370.4	5.8	590	8	DN377430	DN377430 LIB38533_
345	369.8	5.8	475	6	CB224855	CB224855 1OM26B03_
346	369.6	5.8	456	2	BE984927	BE984927 UI-M-CG0p
c 347	366.2	5.7	404	1	AI926299	AI926299 wo44c02.x
c 348	365.6	5.7	479	1	AA041261	AA041261 zf10b06.s
c 349	365	5.7	396	2	BF115104	BF115104 hr74d09.x
c 350	365	5.7	502	2	BE118069	BE118069 UI-R-BS1-
351	364.4	5.7	628	7	CN698612	CN698612 E0410C03-
352	363.4	5.7	816	7	CK475525	CK475525 AGENCOURT
353	363.2	5.7	419	8	R52364	R52364 yg75f12.r1
354	363	5.7	582	3	BP377407	BP377407 BP377407
355	362	5.6	404	1	AA055129	AA055129 zf19b03.r
c 356	360.4	5.6	568	6	CA894759	CA894759 B0187F07-
357	360	5.6	1022	2	BF579633	BF579633 602095395
c 358	359.8	5.6	943	5	BU946534	BU946534 703769938
359	358	5.6	359	1	AL044813	AL044813 DKFZp434O
360	357.6	5.6	398	2	BI008373	BI008373 MR4-RT002
c 361	356.2	5.6	500	1	AA851858	AA851858 EST194626
c 362	355.6	5.5	823	6	CF617127	CF617127 AGENCOURT
363	355	5.5	358	8	F07234	F07234 HSC1ZH051 n
c 364	354.6	5.5	613	2	BF147580	BF147580 us39c07.x
c 365	354.4	5.5	487	1	AA925099	AA925099 UI-R-A1-e
366	354.4	5.5	675	7	CK946556	CK946556 4071148 B
367	354	5.5	587	1	AA672117	AA672117 vl11h11.r
c 368	353.8	5.5	692	5	BX676407	BX676407 BX676407
369	353.2	5.5	456	6	CD287960	CD287960 2_F9.abd
370	351.2	5.5	629	3	BJ690723	BJ690723 BJ690723
371	350.6	5.5	527	7	CN666900	CN666900 A0846D11-
c 372	350.4	5.5	368	1	AW293742	AW293742 UI-H-BI2-
373	350.4	5.5	581	3	BP339650	BP339650 BP339650
374	350.4	5.5	717	8	DN863299	DN863299 nac02b12.
375	350	5.5	528	7	CN669951	CN669951 A0886E08-
376	350	5.5	908	6	CA978572	CA978572 AGENCOURT
377	349.6	5.5	439	8	H23349	H23349 ym52h06.r1
378	348	5.4	348	5	BX480820	BX480820 DKFZp686F
c 379	346.2	5.4	426	1	AA147629	AA147629 z152e03.s
380	346.2	5.4	636	7	CO786390	CO786390 BL286A_H1
381	346	5.4	3883	4	AK046795	AK046795 Mus muscu
382	346	5.4	5174	4	BC026713	BC026713 Mus muscu
383	342.8	5.3	681	7	CK981138	CK981138 4113124 B
384	342	5.3	364	2	BE825322	BE825322 PM4-EN000
385	341.6	5.3	476	5	BY003750	BY003750 BY003750
386	341.4	5.3	347	2	BF951540	BF951540 RC6-NN119
387	339.6	5.3	404	2	BE808455	BE808455 213588 MA

388	338.4	5.3	674	7	CN792286 CN792286 4127130 B
389	338	5.3	678	5	BU129216 BU129216 603003665
c 390	337.4	5.3	456	1	AA851857 AA851857 EST194625
391	337.4	5.3	743	7	CK601877 CK601877 AGENCOURT
392	337.2	5.3	406	5	BY268794 BY268794
393	337.2	5.3	474	5	BX669165 BX669165
394	336.4	5.2	777	5	BU232373 BU232373 603407989
c 395	336.2	5.2	494	6	CA884464 CA884464 B0111D08-
396	335.4	5.2	401	6	CA894760 CA894760 B0187F07-
397	335.2	5.2	778	2	BG619305 BG619305 602619435
398	335	5.2	892	2	BF143963 BF143963 601791213
399	335	5.2	3887	4	AK047010 AK047010 Mus muscu
400	334.8	5.2	410	2	BE115015 BE115015 UI-R-BJ1-
401	334.8	5.2	933	5	BU930979 BU930979 AGENCOURT
402	333.8	5.2	409	2	BE114517 BE114517 UI-R-BJ1-
403	332.6	5.2	859	5	BU107213 BU107213 603110006
404	332.4	5.2	406	1	AJ686994 AJ686994
405	332.4	5.2	878	8	DN519732 DN519732 1262404 M
c 406	332	5.2	426	8	H23235 H23235 ym52h06.s1
c 407	331.8	5.2	855	8	DN517024 DN517024 1257528 M
c 408	331	5.2	795	7	CK470972 CK470972 AGENCOURT
c 409	330.6	5.2	791	5	BU480245 BU480245 603846492
c 410	330.4	5.2	357	2	BF876755 BF876755 QV2-ET010
c 411	330.4	5.2	357	2	BF877282 BF877282 QV2-ET010
412	329	5.1	461	2	BE629400 BE629400 uu37e04.y
413	324	5.1	336	1	AA339395 AA339395 EST44473
414	323.4	5.0	437	1	AI002889 AI002889 am95c03.s
415	322.4	5.0	521	3	BI319499 BI319499 ie11g12.y
416	321.8	5.0	869	3	BP142296 BP142296 BP142296
c 417	321.6	5.0	460	3	BM781246 BM781246 MLN1_6_F0
418	319.6	5.0	455	8	H43260 H43260 yp05g08.r1
419	318.6	5.0	737	7	CV116905 CV116905 AGENCOURT
420	318.4	5.0	795	7	CK475330 CK475330 AGENCOURT
421	317.4	4.9	439	7	CK390140 CK390140 K0815E03-
422	317.2	4.9	447	2	BB860546 BB860546 BB860546
c 423	317	4.9	331	1	AA386053 AA386053 EST99846
424	317	4.9	573	3	BJ095894 BJ095894 BJ095894
c 425	316.8	4.9	342	1	AI192411 AI192411 qc98d02.x
426	316.4	4.9	615	6	CA892957 CA892957 B0175G05-
c 427	315.6	4.9	340	8	R52365 R52365 yg75f12.s1
c 428	312.8	4.9	436	1	AI852319 AI852319 UI-M-BH0-
429	312.4	4.9	431	1	AW880224 AW880224 QV0-OT003
430	312.2	4.9	690	2	BB794798 BB794798 BB794798
c 431	311.6	4.9	322	8	T03641 T03641 IB657 Infan
c 432	311	4.8	312	1	AA373369 AA373369 EST85378
433	310.2	4.8	564	6	CB428133 CB428133 603805 MA
434	309.6	4.8	439	6	CB750939 CB750939 AMGNNUC:C
435	308.8	4.8	444	2	BB748814 BB748814 BB748814
c 436	308.4	4.8	415	1	AA074759 AA074759 zm82d04.s
437	308.2	4.8	488	2	BB680883 BB680883 BB680883
438	308	4.8	2960	11	DQ052371 DQ052371 Homo sapi
c 439	307.2	4.8	421	6	CA895755 CA895755 B0194C06-
440	306.4	4.8	357	8	H05849 H05849 yl73c05.r1
c 441	305.8	4.8	388	1	AI928604 AI928604 wp60b11.x
c 442	305.4	4.8	413	3	BI399716 BI399716 MI-P-AY1-
443	305.4	4.8	430	8	R22852 R22852 yg47h07.r1
444	304.4	4.7	352	1	AW945280 AW945280 PM1-EN000
445	304.2	4.7	452	2	BB682534 BB682534 BB682534
c 446	304	4.7	384	1	AI234646 AI234646 EST231208
c 447	303.2	4.7	562	6	CB609284 CB609284 AMGNNUC:U
c 448	303	4.7	423	7	CK344936 CK344936 L0012A03-
c 449	302.8	4.7	603	2	BG065542 BG065542 H3032D03-
c 450	302.8	4.7	746	1	AW537708 AW537708 G0120F08-
c 451	302	4.7	573	3	BM502125 BM502125 ii33f05.x
452	301.4	4.7	332	8	H87699 H87699 yw15h01.r1
c 453	301.4	4.7	471	1	AI454175 AI454175 UI-R-A0-a
c 454	301	4.7	379	8	H90646 H90646 yw29c07.s1
455	300.8	4.7	3647	4	BC036028 BC036028 Homo sapi
456	300.6	4.7	385	2	BE757548 BE757548 212014 MA
c 457	299.4	4.7	345	1	AV686006 AV686006 AV686006
c 458	299.2	4.7	416	2	BE104824 BE104824 UI-R-BX0-
c 459	297.8	4.6	775	8	CV981683 CV981683 UMC-bmix_
460	297.4	4.6	583	7	CN692119 CN692119 E0318F03-
461	297.2	4.6	645	8	CV783910 CV783910 UI-M-HY0p
462	295.8	4.6	779	6	CA511669 CA511669 UI-R-FJ0-
463	295.6	4.6	412	6	CB801421 CB801421 AMGNNUC:N
464	294.6	4.6	465	6	CA895756 CA895756 B0194C06-
c 465	294.4	4.6	312	1	AI358839 AI358839 qy18f06.x
466	294.2	4.6	850	7	CO400347 CO400347 AGENCOURT
c 467	294	4.6	649	5	BX669660 BX669660 BX669660
c 468	293.8	4.6	325	2	BF507965 BF507965 UI-H-BI4-
c 469	293	4.6	486	8	H05743 H05743 yl73c05.s1
470	292.8	4.6	550	2	BG620314 BG620314 602618614
471	292.4	4.6	733	6	CA367245 CA367245 643019 NC
472	291.4	4.5	651	6	CA334084 CA334084 NISC_1s05
473	289.4	4.5	343	8	H91571 H91571 yw29c07.r1
474	288.6	4.5	636	7	CN697605 CN697605 E0396G03-
475	288.4	4.5	303	1	AA370894 AA370894 EST82607
476	288.2	4.5	318	1	AA373565 AA373565 EST85622
477	287.8	4.5	575	6	CA889263 CA889263 B0151G10-
478	287.4	4.5	526	1	AJ681805 AJ681805 AJ681805
479	283.2	4.4	857	6	CF616434 CF616434 AGENCOURT
480	283	4.4	428	2	BE576046 BE576046 dc32g07.y
481	282.8	4.4	375	2	BE654995 BE654995 UI-M-BH0-
c 482	282.6	4.4	383	2	BE116462 BE116462 UI-R-BS1-
483	282.4	4.4	951	5	BQ934272 BQ934272 AGENCOURT
484	282.2	4.4	842	7	CO419508 CO419508 GGEZHC101
485	282	4.4	348	1	AV725098 AV725098 AV725098
486	282	4.4	483	2	BF556140 BF556140 UI-R-A1-e
487	282	4.4	629	9	CE017391 CE017391 tigr-gss-
c 488	281.6	4.4	401	1	AI849619 AI849619 UI-M-AH1-
489	281.4	4.4	467	5	BY003749 BY003749 BY003749
c 490	281.4	4.4	725	8	DN640961 DN640961 UMC-bend_
491	280.8	4.4	373	1	AA457678 AA457678 aa92h01.s
c 492	280.8	4.4	392	1	AA899414 AA899414 UI-R-E0-c
493	280.4	4.4	3616	4	AK080326 AK080326 Mus muscu
494	279.8	4.4	703	6	CD615160 CD615160 56083323J
c 495	279.8	4.4	725	8	DN640706 DN640706 UMC-bend_
496	278.8	4.3	464	6	CA884465 CA884465 B0111D08-
497	278.8	4.3	3312	4	AK004947 AK004947 Mus muscu
498	278.8	4.3	3687	4	AK079247 AK079247 Mus muscu
499	278.8	4.3	3822	4	BC050024 BC050024 Mus muscu
c 500	277.6	4.3	408	2	BF720868 BF720868 mab38f07.

ALIGNMENTS

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RESULT 1
AY410193
LOCUS       AY410193               3122 bp    DNA     linear   GSS 16-DEC-2003
DEFINITION  Homo sapiens PDGFRA gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY410193
VERSION     AY410193.1  GI:39766161
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3122)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3122)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
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  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
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Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
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Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
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RESULT 2
AY410194

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DEFINITION  Pan troglodytes PDGFRA gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY410194
VERSION     AY410194.1  GI:39766162
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 3122)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3122)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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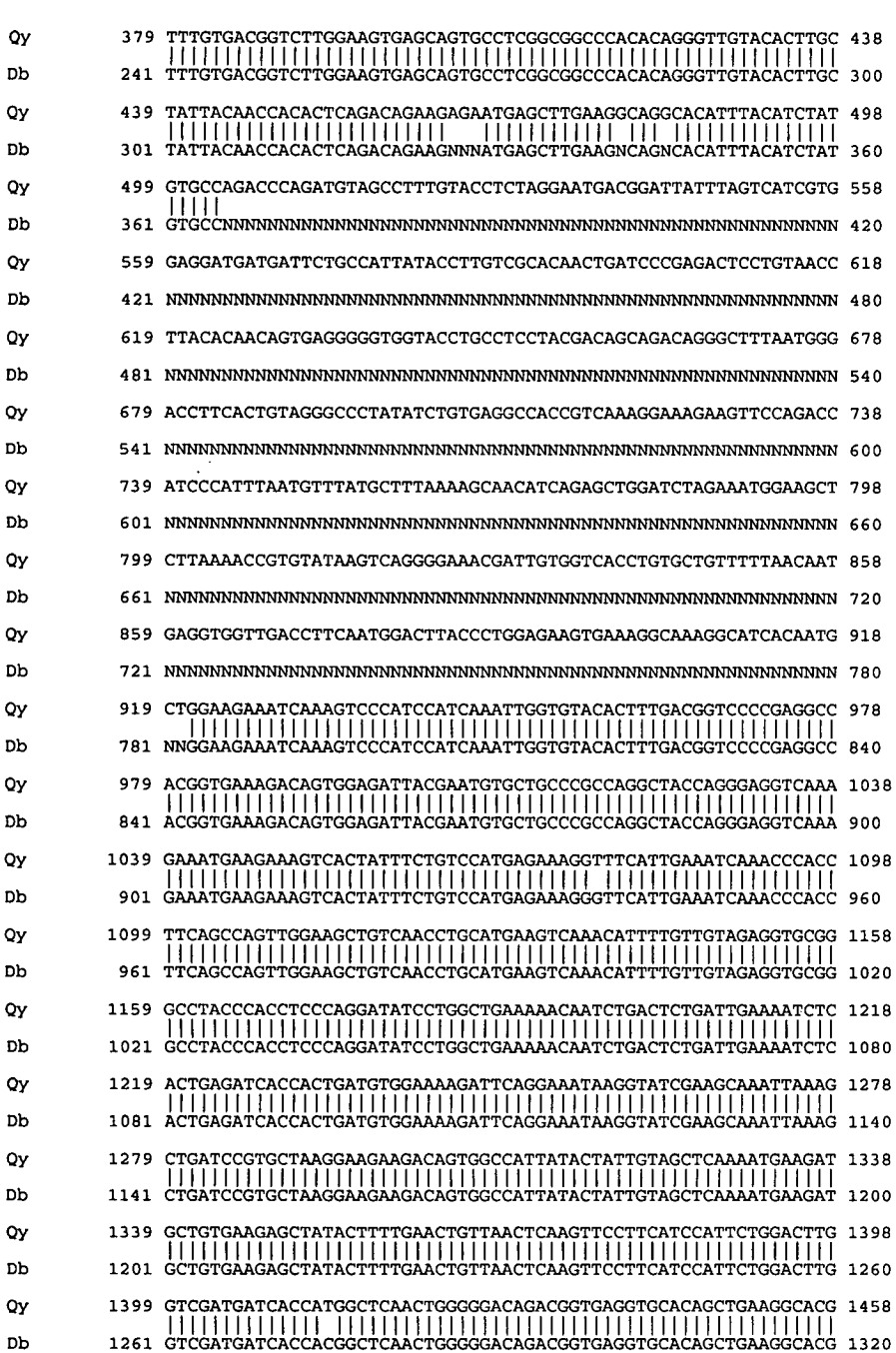
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Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
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Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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DEFINITION  Mus musculus PDGFRA gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY410195
VERSION     AY410195.1  GI:39766163
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3118)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 3118)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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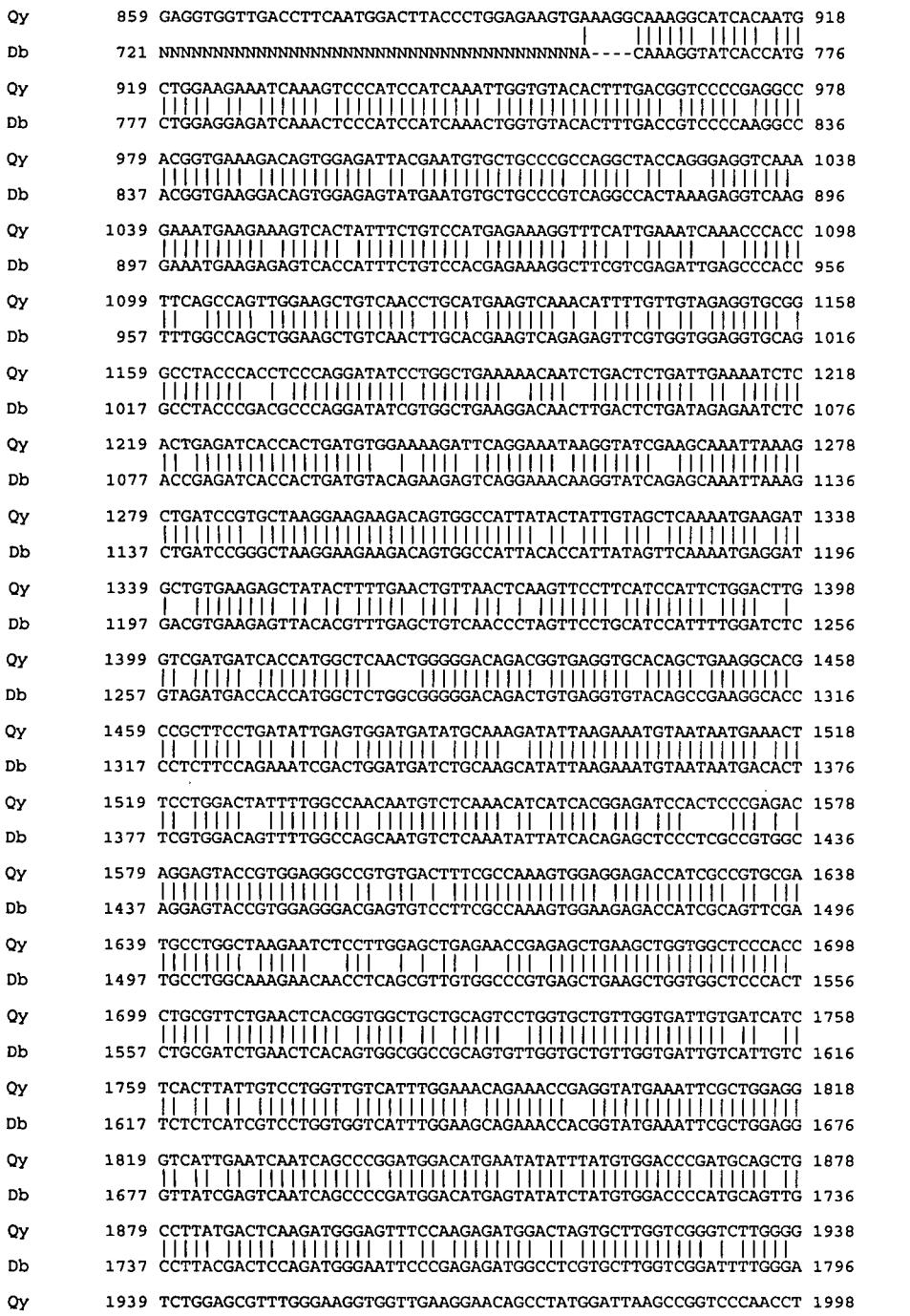
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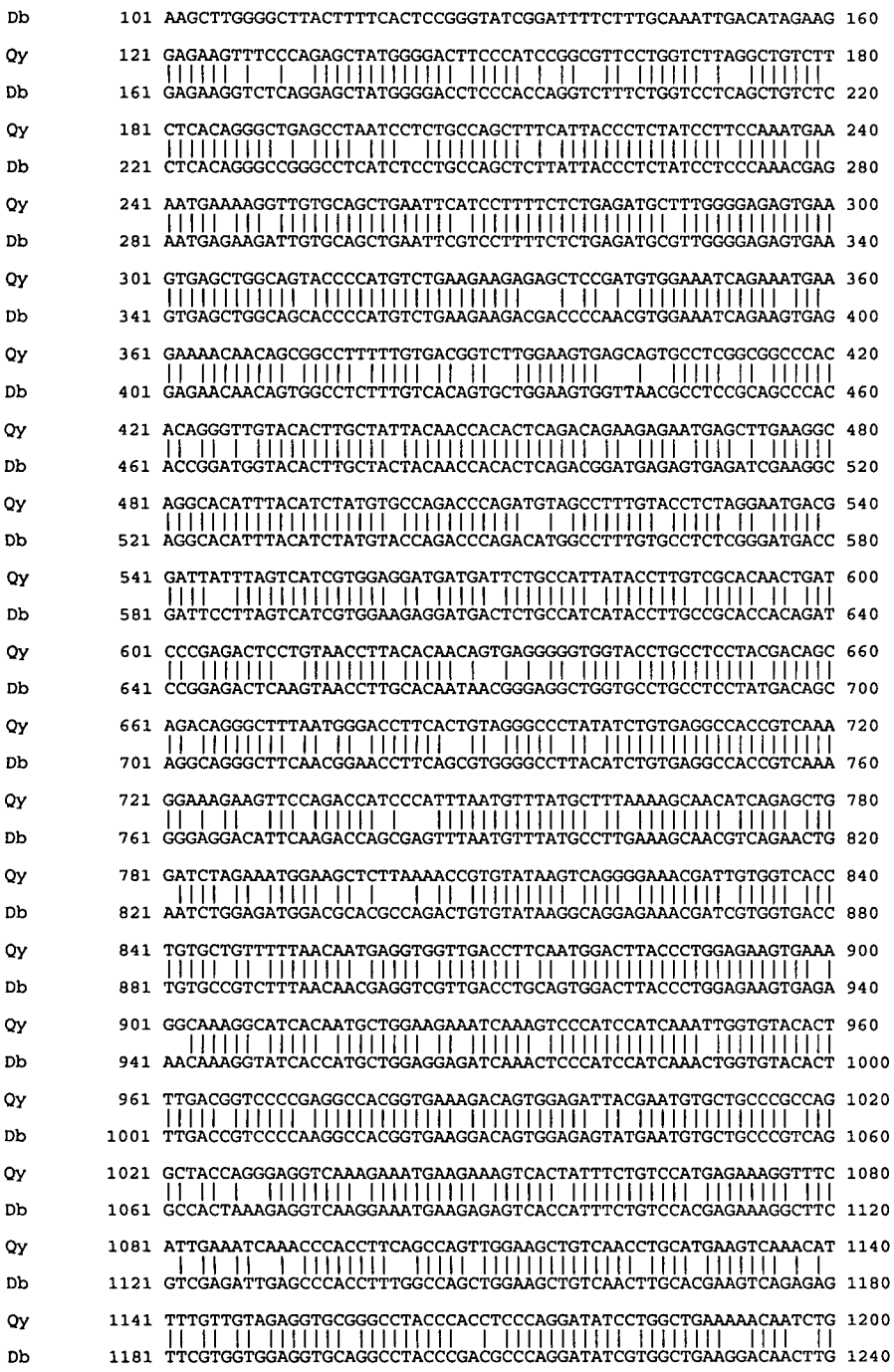
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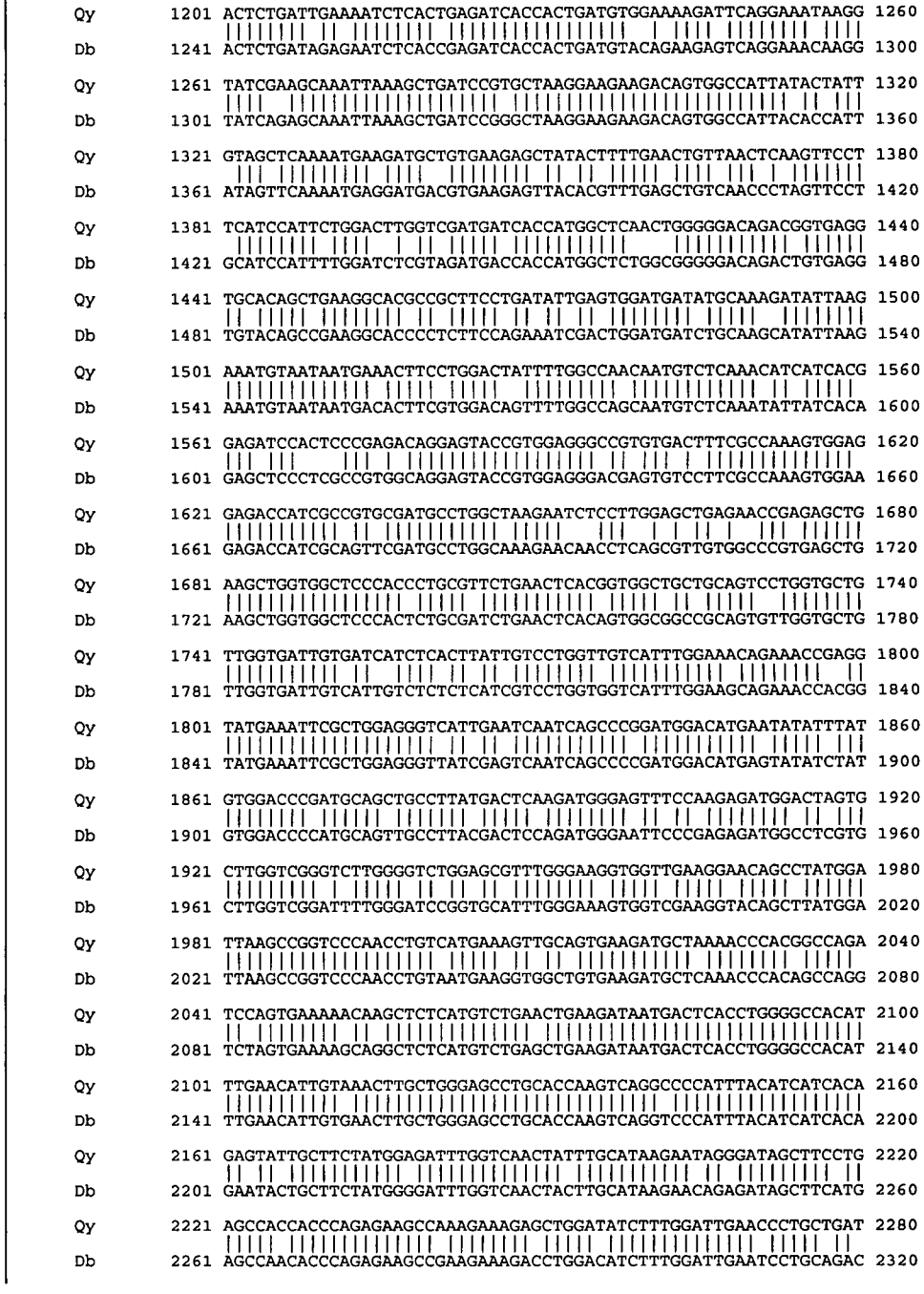
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ACCESSION AK081664
VERSION AK081664.1 GI:26349286
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2869)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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KHIKKCNNDTSWTVLASNVSNIITELPRRGRSTVEGRVSFAKVEETIAVRCLAKNNLS
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AVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTKSGPIYIITEYCFYGDL
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polyA_site 2869
/note="putative"
ORIGIN

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Best Local Similarity 83.9%; Pred. No. 0;
Matches 2064; Conservative 0; Mismatches 396; Indels 1; Gaps 1;

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Db         42 CCATTACTGTTGGAGCTTGAGGGAGAGAAACAAACGGAGGA-GCTGCGGGGAAGGACTGG 100

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Qy       2461 G 2461
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RESULT 5
AK035501

LOCUS	AK035501 2835 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530057A20 product:platelet derived growth factor receptor, alpha polypeptide, full insert sequence.
ACCESSION	AK035501
VERSION	AK035501.1 GI:26084653
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2835)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES	Location/Qualifiers
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ORIGIN

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Best Local Similarity 83.9%; Pred. No. 0;
Matches 2063; Conservative 0; Mismatches 395; Indels 2; Gaps 2;

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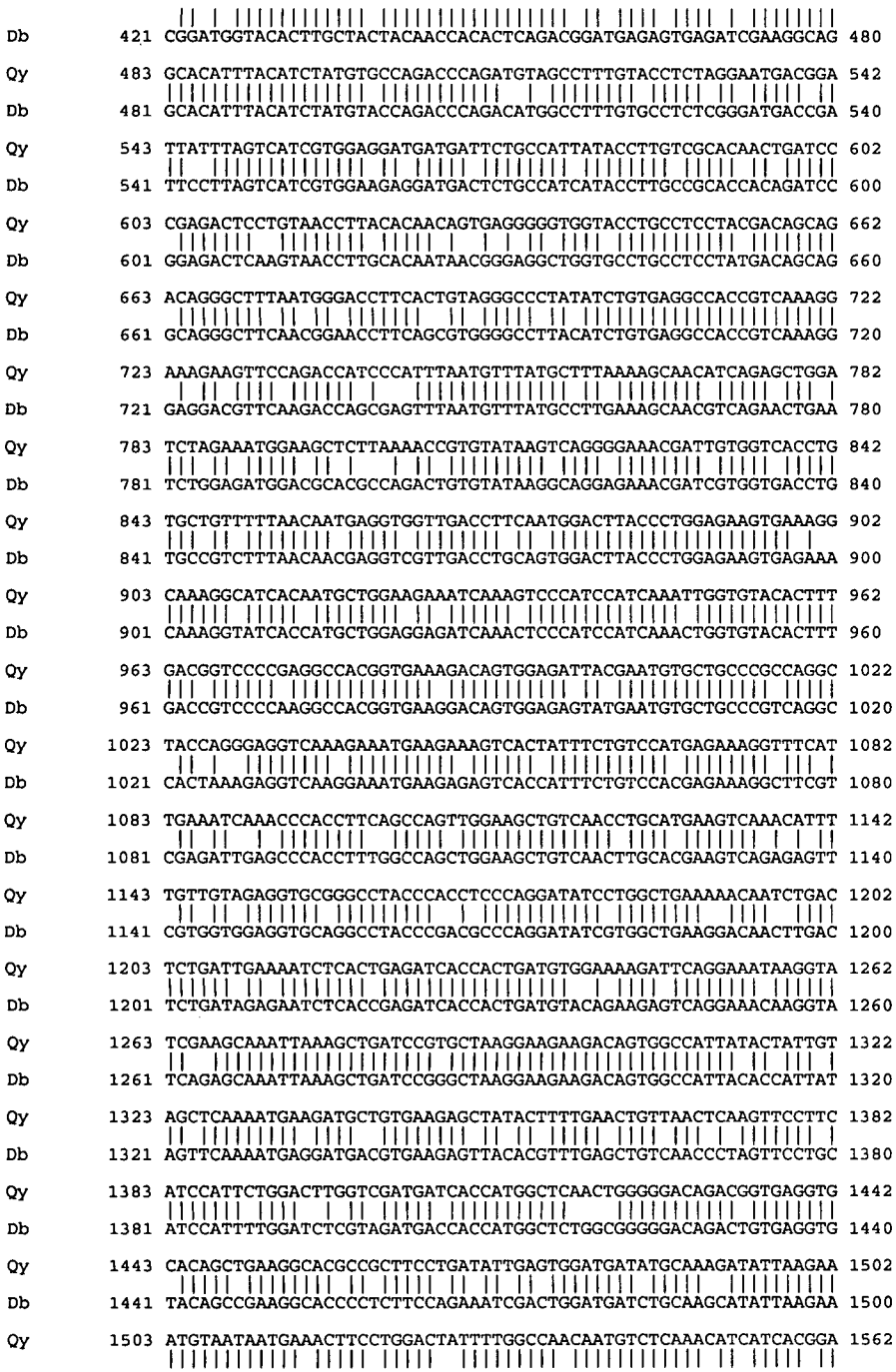
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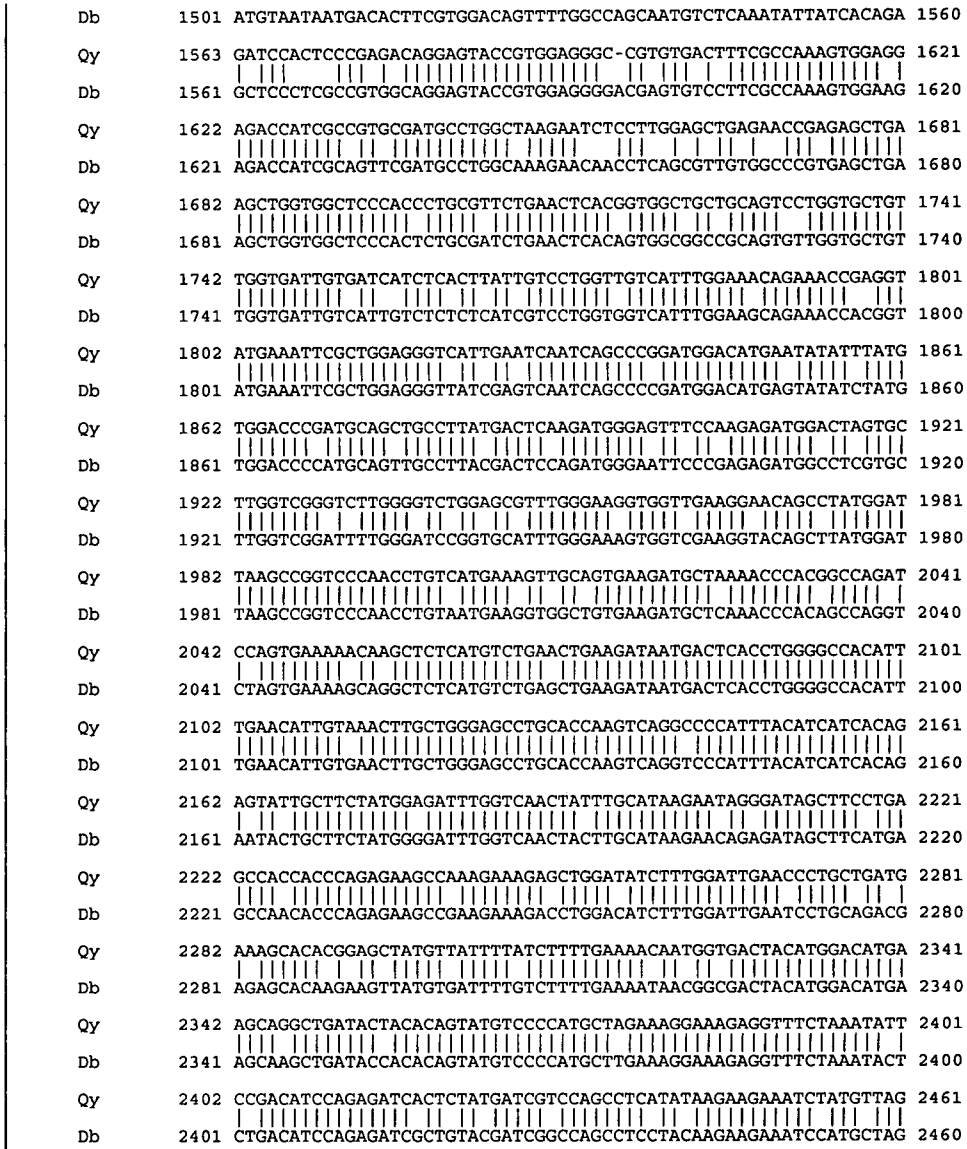
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RESULT 6
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LOCUS BC020405 1699 bp mRNA linear HTC 01-JUN-2005
DEFINITION Mus musculus platelet derived growth factor receptor, alpha polypeptide, mRNA (cDNA clone IMAGE:3979390).
ACCESSION BC020405
VERSION BC020405.1 GI:18043003
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1699)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
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            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1699)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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            This clone was selected for full length sequencing because it
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Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
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Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
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Qy        899 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 958
              |  |||||| ||||| |||||||| || |||||| |||||||||||||| |||||||||
Db        871 GAAACAAAGGTATCACCATGCTGGAGGAGATCAAACTCCCATCCATCAAACTGGTGTACA 930

Qy        959 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1018
              ||||||| |||||| |||||||||||| |||||||||| || ||||||||||||||| |
Db        931 CTTTGACCGTCCCCAAGGCCACGGTGAAGGACAGTGGAGAGTATGAATGTGCTGCCCGTC 990

Qy       1019 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTT 1078
              |||| || |  |||||||| |||||||||| |||||| |||||||||||||| ||||||||
Db        991 AGGCCACTAAAGAGGTCAAGGAAATGAAGAGAGTCACCATTTCTGTCCACGAGAAAGGCT 1050

Qy       1079 TCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAAC 1138
              || | || ||  | |||||||  ||||| |||||||||||||| |||| ||||||| |
Db       1051 TCGTCGAGATTGAGCCCACCTTTGGCCAGCTGGAAGCTGTCAACTTGCACGAAGTCAGAG 1110

Qy       1139 ATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATC 1198
              | || || || ||||||| |||||||||  | |||||||||| ||||||||  ||||
```

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Db       1111 AGTTCGTGGTGGAGGTGCAGGCCTACCCGACGCCCAGGATATCGTGGCTGAAGGACAACT 1170

Qy       1199 TGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAA 1258
              |||||||||| || |||||||| |||||||||||||||||  | |||| |||||||| ||
Db       1171 TGACTCTGATAGAGAATCTCACCGAGATCACCACTGATGTACAGAAGAGTCAGGAAACAA 1230

Qy       1259 GGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTA 1318
              ||||||  |||||||||||||||||||| |||||||||||||||||||||||||||| || |
Db       1231 GGTATCAGAGCAAATTAAAGCTGATCCGGGCTAAGGAAGAAGACAGTGGCCATTACACCA 1290

Qy       1319 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1378
              || ||| ||||||||| |||| |||||||| || || ||||| |||| ||| | |||||
Db       1291 TTATAGTTCAAAATGAGGATGACGTGAAGAGTTACACGTTTGAGCTGTCAACCCTAGTTC 1350

Qy       1379 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1438
              || |||||||| |||| | || ||||| ||||||||||    |||||||||| ||||
Db       1351 CTGCATCCATTTTGGATCTCGTAGATGACCACCATGGCTCTGGCGGGGGACAGACTGTGA 1410

Qy       1439 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1498
              |||| ||||| |||||||| || ||||| || || || |||||||| ||||| ||||||
Db       1411 GGTGTACAGCCGAAGGCACCCCTCTTCCAGAAATCGACTGGATGATCTGCAAGCATATTA 1470

Qy       1499 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1558
              |||||||||||||||| ||||| ||||| ||||||||| |||||||||||| || ||||
Db       1471 AGAAATGTAATAATGACACTTCGTGGACAGTTTTGGCCAGCAATGTCTCAAATATTATCA 1530

Qy       1559 CGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1618
              | ||| |||    ||| | |||||||||||||||||| || ||| | ||||||||||||
Db       1531 CAGAGCTCCCTCGCCGTGGCAGGAGTACCGTGGAGGGACGAGTGTCCTTCGCCAAAGTGG 1590

Qy       1619 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1678
              | |||||||||| || |||||||||| |||||   |||  | | || |   ||| ||||
Db       1591 AAGAGACCATCGCAGTTCGATGCCTGGCAAAGAACAACCTCAGCGTTGTGGCCCGTGAGC 1650

Qy       1679 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGC 1727
              |||||||||||||||||| ||||| |||||||||| ||||| || ||
Db       1651 TGAAGCTGGTGGCTCCCACTCTGCGATCTGAACTCACAGTGGCGGCCGC 1699


RESULT 7
BM926494
LOCUS       BM926494               1104 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6644826 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5766882
            5', mRNA sequence.
ACCESSION   BM926494
VERSION     BM926494.1  GI:19376873
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12824  row: d  column: 19
            High quality sequence stop: 688.
FEATURES             Location/Qualifiers
     source          1. .1104
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5766882"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_122"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             14.0%;  Score 898.8;  DB 3;  Length 1104;
  Best Local Similarity   93.2%;  Pred. No. 1.8e-195;
  Matches  982;  Conservative    0;  Mismatches   66;  Indels    6;  Gaps    4;

Qy       4639 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 4698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 70

Qy       4699 GCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCC 4758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCC 130

Qy       4759 ATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACT 4818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 ATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACT 190

Qy       4819 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 4878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 250

Qy       4879 ATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCT 4938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCT 310

Qy       4939 ACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCG 4998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCG 370

Qy       4999 ACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACA 5058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 ACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACA 430

Qy       5059 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 5118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 490

Qy       5119 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 5178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 550

Qy       5179 CAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTT 5238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 CAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTT 610

Qy       5239 AAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTG 5298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 AAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTG 670

Qy       5299 TCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACC 5358
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Db        671 TCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACC 730

Qy       5359 ATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTT 5418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 ATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTT 790

Qy       5419 TGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAA 5478
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        791 TGGAAGATGCAGAAGCCATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAA 850
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Qy       5479 GCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAG-CCAGATTGGCC 5537
             |||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||
Db        851 GCCCCAACTTTCTTATCCNACTTTTTCATAGTAAGTGCGAAGACTGAGCCCAGATTGGCC 910

Qy       5538 AATTAAAAAC--GAAAACCTGACTAG--GTTCTGTAG-AGCCAATTAGACTTGAAATACG 5592
             ||||||||||   ||| |||||||||  |||||||||| |||||||||||||||| ||
Db        911 AATTAAAAACCGAAAACCCTGACTAGNNGTTCTGTAGAAGCCAATTAGACTTGGAAATAC 970

Qy       5593 TTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAG 5652
              || |||    |   | |      | |||      |    ||       | ||   |  ||
Db        971 GTTTTGTGNTTTCTAGGAATCACCCAGCTCAAGGCAATTCTGGTTTTATCGGCTCCACTC 1030

Qy       5653 CCTTATTTTGTTGGTGCTTTGCATTTTGATATTG 5686
              |      || ||    || ||  | |||    |||
Db       1031 CTCCCCTTGGTACAGGCCTTTTAATTTTGNNTTG 1064
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RESULT 8
BI768268
LOCUS BI768268 904 bp mRNA linear EST 25-SEP-2001
DEFINITION 603056437F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205969 5', mRNA sequence.
ACCESSION BI768268
VERSION BI768268.1 GI:15759846
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11516 row: i column: 10
High quality sequence stop: 775.

FEATURES Location/Qualifiers
source 1. .904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5205969"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.5%; Score 799.4; DB 3; Length 904;
Best Local Similarity 96.4%; Pred. No. 1.4e-172;
Matches 861; Conservative 0; Mismatches 26; Indels 6; Gaps 4;

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Qy         21 GGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGTGGGCACGCTCTTT 80
              |||||||||||||||||| |||||||||||||| |   |||||||||||||||||||
Db          1 GGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGTGGGCACGCTCTTT 57

Qy         81 ACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTAT 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 ACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTAT 117

Qy        141 GGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTAAT 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 GGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTAAT 177

Qy        201 CCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAGCT 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 CCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAGCT 237

Qy        261 GAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCAT 320
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        238 GAATTCATCCTTTTCTCTGAGATGC-TTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCAT 296

Qy        321 GTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTTTT 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTTTT 356

Qy        381 TGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGCTA 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGCTA 416

Qy        441 TTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 TTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 476

Qy        501 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 536

Qy        561 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 596

Qy        621 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 680
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Db        597 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 656

Qy        681 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACCAT 740
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Db        657 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGACAGAAGTTCCAGA-CAT 715

Qy        741 CCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCTCT 800
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Qy        801 TAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAATG- 859
              ||| ||||||||| ||||||||||||||||||||||||||||||||| ||||| |||||
Db        776 TAACACCGTGTATCAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGCTTTTACCAATGA 835

Qy        860 AGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATC 912
              |||||||||||||||  |||  |  ||  | ||  |  | |  |||||| |
Db        836 AGGTGGTTGACCTTCATAGGAACTTACCCTGGGAGAAGTGAAGGCAAGGCACC 888
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RESULT 9
AI819719/c
LOCUS AI819719 847 bp mRNA linear EST 21-DEC-1999
DEFINITION wj11e03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402524 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI819719
VERSION AI819719.1 GI:5438798
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 847)

```
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1047   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 468.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2402524"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid12"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1323912-1325831, 1471368-1472903 and
                     1492104-1493255). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             12.4%;  Score 796.8;  DB 1;  Length 847;
  Best Local Similarity   97.6%;  Pred. No. 5.3e-172;
  Matches  829;  Conservative    0;  Mismatches   18;  Indels    2;  Gaps    2;

Qy       5136 CCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAG 5195
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Db        847 CCACTCCATACCCGGCCAAAGAAAGGCATGAAC-AAAATTAAGCAATTCAGTGTTCCAAG 789

Qy       5196 TCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATT 5255
             |||| |||||||||||   |||| ||||||| |||||||||| |||||||||||||| ||
Db        788 TCTCGGTGTAACCAGTCAAGTG-TTTGGTGAAAAAAACATTTAAAGTTTTACTGATATTT 730

Qy       5256 TGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTG 5315
             |||||||||||||||| |||||||||||||||||||||||||  |||||||| ||||||
Db        729 TGAGGTTAGATGGGAGAATGAATTGTCACATCTATCCACACTGCAAAACAGGTGGGTGTG 670

Qy       5316 GGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGG 5375
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGTTCATGGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGG 610

Qy       5376 GCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCA 5435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCA 550

Qy       5436 ATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATC 5495
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 ATAATANAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATC 490

Qy       5496 CAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCT 5555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCT 430

Qy       5556 GACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCT 5615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCT 370

Qy       5616 CAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCA 5675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCA 310

Qy       5676 TTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCA 5735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCA 250

Qy       5736 GCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGT 5795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGT 190

Qy       5796 GTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCA 5855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCA 130

Qy       5856 GAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCT 5915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCT 70

Qy       5916 GAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCA 5975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCA 10

Qy       5976 ATCTGTACA 5984
             | |||||||
Db          9 ACCTGTACA 1


RESULT 10
CX166250
LOCUS       CX166250                808 bp    mRNA    linear   EST 23-DEC-2004
DEFINITION  HESC2_38_B05.g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
            IMAGE:7469892 5', mRNA sequence.
ACCESSION   CX166250
VERSION     CX166250.1  GI:56796330
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 808)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
             cDNA Library Preparation: Express Genomics, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15771  row: c  column: 10
            Seq primer: JENREV (CAGGAAACAGCTATGACC)
            High quality sequence stop: 808.
FEATURES             Location/Qualifiers
     source          1. .808
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7469892"
                     /sex="male"
                     /tissue_type="human embryonic stem cells differentiated to
                     an early endodermal cell type"
                     /cell_type="human embryonic stem cells"
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/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_258"
/note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early endodermal cell type. Cell line id and NIH Registry designation is BG01. Positive for GATA4, MixL1, Msx1, HNF4alpha expression; negative for AFP expression. Passage number 40. cDNA primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH_MGC_259). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 12.3%; Score 788.4; DB 8; Length 808;
Best Local Similarity 99.4%; Pred. No. 4.5e-170;
Matches 803; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

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Qy       3927 AAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAA 3986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAA 60

Qy       3987 TAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCA 4046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCA 120

Qy       4047 TATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAAT 4106
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAAT 180

Qy       4107 GTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAGTAGGTGAT 4166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAGTAGGTGAT 240

Qy       4167 GAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGTATGGTAAT 4226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGTATGGTAAT 300

Qy       4227 AGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCAG 4286
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCAG 360

Qy       4287 GAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAAAAAACAAT 4346
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAAAAAACAAT 420

Qy       4347 TAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCTAAAAGTTC 4406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCTAAAAGTTC 480

Qy       4407 TCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGAA 4466
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGAA 540

Qy       4467 AATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG----TTTTTTTTTTTTTTCTTCA 4522
             ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db        541 AATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTTTTCTTCA 600

Qy       4523 TGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAA 4582
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAA 660

Qy       4583 AGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAA 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAA 720

Qy       4643 GAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCT 4702
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCT 780

Qy       4703 GGATCCTCAGTTCTCAAATGTGTGTGGC 4730
             |||||||||||||||||||||||||||||
Db        781 GGATCCTCAGTTCTCAAATGTGTGTGGC 808
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RESULT 11
CD518236
LOCUS CD518236 902 bp mRNA linear EST 06-JUN-2003
DEFINITION AGENCOURT_14375939 NIH_MGC_181 Homo sapiens cDNA clone IMAGE:30407320 5', mRNA sequence.
ACCESSION CD518236
VERSION CD518236.1 GI:31449954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 902)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM488 row: h column: 17
High quality sequence stop: 645.
FEATURES Location/Qualifiers
source 1. .902
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30407320"
/tissue_type="White Matter"
/dev_stage="Unknown"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 12.0%; Score 772.6; DB 6; Length 902;
Best Local Similarity 93.4%; Pred. No. 2e-166;
Matches 827; Conservative 0; Mismatches 56; Indels 2; Gaps 2;

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Qy       5079 GCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCA 5138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCA 60

Qy       5139 CTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCT 5198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCT 120

Qy       5199 CTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGA 5258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGA 180
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Qy       5259 GGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGT 5318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGT 240

Qy       5319 TCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCT 5378
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Db         241 TCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCT 300

Qy       5379 GTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATA 5438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATA 360

Qy       5439 ATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAA 5498
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Db         361 ATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAA 420

Qy       5499 CTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGAC 5558
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Db         421 CTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGAC 480

Qy       5559 TAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAA 5618
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Db         481 TAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAA 540

Qy       5619 GCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTT 5678
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Db         541 GCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTT 600

Qy       5679 TGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCA 5738
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCA 660

Qy       5739 GTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTG 5798
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Db         661 GTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTG 720

Qy       5799 TGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTT-GGCCTCCTGCAAAGTCTCCAG- 5856
             |||||||||||     |||| |||| |||||||||||| ||||||||||||||||||||| 
Db         721 TGTGTGTTTTTCAGCAATTTCAGAATTGTTTCCTTTTGGGCCTCCTGCAAAGTCTCCAGA 780

Qy       5857 AAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTG 5916
             |||||||||||  ||||||||    || | |  || | ||||    |||     ||| | 
Db         781 AAGAAAATTTGCANATCTTTCCNTACTTTTCTAATTTTTATGAATGACAATCAAAGCCCG 840

Qy       5917 AGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAA 5961
                |  |       | ||| | |||  ||  | |     ||||
Db         841 GCCCTGAGAAAACACTATTTTGTGAACTTTTTTTAAACGAATTAA 885
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RESULT 12
CD172287
LOCUS       CD172287                904 bp    mRNA    linear   EST 19-MAY-2003
DEFINITION  AGENCOURT_14063908 NIH_MGC_181 Homo sapiens cDNA clone
            IMAGE:30377372 5', mRNA sequence.
ACCESSION   CD172287
VERSION     CD172287.1  GI:30853685
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: NDAM441  row: h  column: 21
             High quality sequence start: 23
             High quality sequence stop: 672.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:30377372"
                     /tissue_type="White Matter"
                     /dev_stage="Unknown"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_181"
                     /note="Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV
                     (destroyed); Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.42 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN
```

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  Query Match             11.7%;  Score 751.2;  DB 6;  Length 904;
  Best Local Similarity   96.4%;  Pred. No. 1.7e-161;
  Matches  811;  Conservative    0;  Mismatches   24;  Indels    6;  Gaps    4;

Qy       4403 GTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAAT 4462
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 GATCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAAT 91

Qy       4463 GGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTCTTCA 4522
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         92 GGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTTCTTCA 150

Qy       4523 TGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAA 4582
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        151 TGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAA 210

Qy       4583 AGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAA 4642
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAA 270

Qy       4643 GAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCT 4702
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Db        271 GAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCT 330

Qy       4703 GGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCC 4762
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 GGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCC 390

Qy       4763 TTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCT 4822
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Db        391 TTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCT 450

Qy       4823 GGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGG 4882
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Db        451 GGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGG 510

Qy       4883 GAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTA 4942
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTA 570

Qy       4943 TTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCT 5002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCT 630

Qy       5003 TAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTT 5062
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Db        631 TAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTT 690

Qy       5063 TTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCC 5122
             ||||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        691 TTCCANAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTTCCCGTCTCC 750
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Qy       5123 CGTCTTCTGCCTCCCACTCCATACCCC-GCCAAGGAAAGGCATGTACAAAAA-TTATGCA 5180
             ||||||||||||||||||||||||||| |||| | ||||||||||||||||| |||||||
Db        751 CGTCTTCTGCCTCCCACTCCATACCCCGGCCAGGAAAAGGCATGTACAAAAATTTATGCA 810

Qy       5181 ATTCAGTGTTCCAA---GTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237
             |||||||| | |||    ||| |||  | |     |||||||||||  | ||||| | |
Db        811 ATTCAGTGGTTCAAAGTCTCTGTGTAAACCAGCTCCAGTGTTTTGGGTGGAAAAAAACAT 870

Qy       5238 T 5238
             |
Db        871 T 871


RESULT 13
CR736703
LOCUS       CR736703                746 bp    mRNA    linear   EST 10-DEC-2004
DEFINITION  CR736703 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998A121830
            ; IMAGE:744851 5', mRNA sequence.
ACCESSION   CR736703
VERSION     CR736703.1  GI:51586445
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
            Peters,M., Radelof,U. and Schneider,D.
  TITLE     I.M.A.G.E. cDNA Clone Collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; IMAGp998A121830.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES              Location/Qualifiers
     source           1. .746
                      /organism="Homo sapiens"
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                      /db_xref="taxon:9606"
                      /clone="IMAGp998A121830 ; IMAGE:744851"
                      /sex="male"
                      /lab_host="DH10B"
                      /clone_lib="Soares_testis_NHT"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was prepared from mRNA obtained from Clontech
                      Laboratories, Inc., and primed with  a Not I - oligo(dT)
                      primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                      Double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Not I and cloned into the Not I
                      and Eco RI sites of the modified pT7T3 vector. Library
                      went through one round of normalization to Cot5, and was
                      constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match           11.6%;  Score 744;  DB 7;  Length 746;
  Best Local Similarity  99.7%;  Pred. No. 7.5e-160;
  Matches  744;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5648 TACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATC 5707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATC 60

Qy       5708 ATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCT 5767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCT 120

Qy       5768 GAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGT 5827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGT 180

Qy       5828 TTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTA 5887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTA 240

Qy       5888 TTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATT 5947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATT 300

Qy       5948 AGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGA 6007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGA 360

Qy       6008 GGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACT 6067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACT 420

Qy       6068 TGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTT 6127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTT 480

Qy       6128 TAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTAT 6187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTAT 540

Qy       6188 ATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAAT 6247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAAT 600

Qy       6248 GTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTG 6307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTG 660

Qy       6308 TTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATAT 6367
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCATGTTTTTGNTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATAT 720

Qy       6368 AATTTAAAGTTAAAAAAAAAAAAAAA 6393
             ||||||||| ||||||||||||||||
Db        721 AATTTAAAGNTAAAAAAAAAAAAAA 746


RESULT 14
CR791892
LOCUS       CR791892                765 bp    mRNA    linear   EST 01-OCT-2004
DEFINITION  DKFZp469F1764_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
            DKFZp469F1764 5', mRNA sequence.
ACCESSION   CR791892
VERSION     CR791892.1  GI:53710732
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
```

```
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
            ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F1764
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES              Location/Qualifiers
     source           1. .765
                      /organism="Pongo pygmaeus"
                      /mol_type="mRNA"
                      /db_xref="taxon:9600"
                      /clone="DKFZp469F1764"
                      /tissue_type="kidney"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="469 (synonym: pkid1)"
                      /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
ORIGIN

  Query Match             11.6%;  Score 741.2;  DB 7;  Length 765;
  Best Local Similarity   97.9%;  Pred. No. 3.3e-159;
  Matches  749;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       3497 GGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTA 3556
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db          1 GGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCAGGGAGCCTTCTA 60

Qy       3557 AATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCT 3616
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||
Db         61 AATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAGTGCCT 120

Qy       3617 CAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCA 3676
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCA 180

Qy       3677 CAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATAC 3736
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 CAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAGCAGACACAATTTATAC 240

Qy       3737 TGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGAT 3796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGAT 300

Qy       3797 TGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCC 3856
             |||||||||| |||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 TGTATTAACTGTCTTCTTTGGACTTCTGAAGAGACCACTCCATCCATCCATGTACTTCCT 360

Qy       3857 TCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTT 3916
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        361 TCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCACTT 420

Qy       3917 TTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGA 3976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGA 480

Qy       3977 TAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAA 4036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAA 540

Qy       4037 CTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAAT 4096
             |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        541 CTCATTTTCATATTGTAATCTACATTTATAATACTACTACTGTTATCAGTAATGCTAAAT 600

Qy       4097 GTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTA 4156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTA 660

Qy       4157 AGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAA 4216
             |||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||
Db        661 AGTAGGTGATGAGTTTGACAGTTTTTGACATTTACATTAAATAACATGTTTTTCTATAAA 720

Qy       4217 GTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGA 4261
             |||||||||||||||||||||||||||||||| |||||||||||| | |
Db        721 GTATGGTAATAGCTTTAGTGAATTAAATTNAGTTGAGCATANANA 765


RESULT 15
AU120263
LOCUS       AU120263                 796 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU120263 HEMBB1 Homo sapiens cDNA clone HEMBB1000313 5', mRNA
            sequence.
ACCESSION   AU120263
VERSION     AU120263.1  GI:10935498
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES              Location/Qualifiers
     source           1. .796
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="HEMBB1000313"
                      /tissue_type="whole embryo, mainly body"
                      /dev_stage="embryo, 10 weeks"
                      /clone_lib="HEMBB1"
                      /note="Vector: pME18SFL3"
ORIGIN

  Query Match             11.4%;  Score 733;  DB 1;  Length 796;
  Best Local Similarity   97.9%;  Pred. No. 2.6e-157;
  Matches  774;  Conservative    0;  Mismatches   12;  Indels    5;  Gaps    3;

Qy       3851 CTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAA 60

Qy       3911 CCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTA 3970
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTA 120

Qy       3971 AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCC 4030
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTCAGAAGCC 180

Qy       4031 TGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATG 4090
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATG 240

Qy       4091 CTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCC 4150
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCC 300

Qy       4151 TTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTC 4210
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                    ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        301 TTACTAAGTAGGTGATGAGTTTGACAGTTTTTGGCATTTATATTAAATAACATGTTTCTC 360

Qy       4211 TATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAA 4270
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAA 420

Qy       4271 AAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCAT 4330
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCAT 480

Qy       4331 CGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCT 4390
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCT 540

Qy       4391 TAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGT 4450
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Db        541 TAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGT 600

Qy       4451 ATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTT 4509
                ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        601 ATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTT 660

Qy       4510 TTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATC 4569
                ||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||
Db        661 TTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGNATTTTTTGAATC 720

Qy       4570 TATGAACCTGAAAAGGGTCA--GAAGGATGCCCAGACATCA--GCCTCCTTCTTTCACCC 4625
                ||||||||||||||||||    | ||||||||||||| |   ||||||||||||||||
Db        721 TATGAACCTGAAAAGGGTCAANAANGGATGCCCAGACATTAAGCCCTCCTTCTTTCACCC 780

Qy       4626 CTTACCCCAAA 4636
                | |  ||| ||
Db        781 CCTTACCCCAA 791
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RESULT 16
CN373040
LOCUS CN373040 737 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600430637 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN373040
VERSION CN373040.1 GI:47372974
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 737)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 737 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .737
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
ORIGIN

Query Match 11.4%; Score 731; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 7.4e-157;
Matches 731; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5275 GAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTG 5334
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Db          7 GAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTG 66

Qy       5335 CAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCA 5394
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Db         67 CAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCA 126

Qy       5395 CTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTA 5454
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Db        127 CTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTA 186

Qy       5455 CCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGT 5514
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGT 246

Qy       5515 GCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCC 5574
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCC 306

Qy       5575 AATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGC 5634
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 AATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGC 366

Qy       5635 TCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGC 5694
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Db        367 TCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGC 426

Qy       5695 CTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACA 5754
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACA 486

Qy       5755 AATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAA 5814
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Db        487 AATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAA 546

Qy       5815 ATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCT 5874
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Db        547 ATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCT 606

Qy       5875 TTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC 5934
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Db        607 TTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC 666

Qy       5935 TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCT 5994
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Db        667 TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCT 726

Qy       5995 ATTTTTGTGAA 6005
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Db        727 ATTTTTGTGAA 737
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RESULT 17
BQ015005/c
LOCUS BQ015005 742 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-ED1-ayc-m-16-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone IMAGE:5836983 3', mRNA sequence.
ACCESSION BQ015005
VERSION BQ015005.1 GI:19739906
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
            191-218, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5836983"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED1"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
                     containing the following tissue(s): Chondrosarcoma cell
                     line CS5. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED1
                     TAG_SEQ=CGTCAAGGCT"
ORIGIN

  Query Match            11.4%;  Score 729;  DB 3;  Length 742;
  Best Local Similarity  99.6%;  Pred. No. 2.1e-156;
  Matches  740;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       5654 CTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGG 5713
             |||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||
Db        742 CTTATTTTGTTGGTGCTNTGCATTTTGATANTGCTGTGAGCCTTGCATGACATCATGAGG 683

Qy       5714 CCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTT 5773
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTT 623

Qy       5774 GTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTT 5833
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        622 GTATATGACTGCATTTGTGGGTGTGTGTGT-TTTTCAGCAAATTCCAGATTTGTTTCCTT 564

Qy       5834 TTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTA 5893
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTA 504

Qy       5894 TGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGAT 5953
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 TGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGAT 444

Qy       5954 GTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACA 6013
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACA 384

Qy       6014 TAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGA 6073
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGA 324

Qy       6074 ATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTG 6133
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTG 264

Qy       6134 TGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTA 6193
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 TGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTA 204

Qy       6194 GAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGA 6253
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGA 144

Qy       6254 GAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATG 6313
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATG 84

Qy       6314 TTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTA 6373
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 TTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTA 24

Qy       6374 AAGTTAAAAAAAAAAAAAAAAAA 6396
             |||||||||||||||||||||||
Db         23 AAGTTAAAAAAAAAAAAAAAAAA 1


RESULT 18
AL713494
LOCUS       AL713494                750 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686B119_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686B119 5', mRNA sequence.
ACCESSION   AL713494
VERSION     AL713494.1  GI:19696850
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686B119) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686B119"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
```

cDNA-collection"
ORIGIN

Query Match 11.3%; Score 726.6; DB 1; Length 750;
Best Local Similarity 99.2%; Pred. No. 7.6e-156;
Matches 740; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```
Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GGAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 64

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 124

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 184

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 244

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 304

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 364

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 424

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 484

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        485 CGGATTATTTAGTCATCGTGGAGGATGATGGTTCTGCCATTATACCTTGTCGCACAACTG 544

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 604

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        605 GCAGACAGGGCTTTAATGGGACCTTCACTGTANGGCCCTATATCTGTGAGGCCACCGTCA 664

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTT-ATGCTTTAAAAGCAACATCAGAG 777
              |||||||||||||||||||||||||||||| |||| |||||| ||||||||||||||||
Db        665 AAGGAAAGAAGTTCCAGACCATCCCATTTAACGTTTNATGCTTAAAAAGCAACATCAGAG 724

Qy        778 CTGGATCTAGAAATGGAAGCTCTTAA 803
              |||||||||||||||||||||||||
Db        725 CTGGATCTAGAAATGGAAGCTCTTAA 750
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RESULT 19
CA983729
LOCUS CA983729 928 bp mRNA linear EST 06-JAN-2003
DEFINITION AGENCOURT_11293166 NIH_MGC_164 Mus musculus cDNA clone IMAGE:30144193 5', mRNA sequence.
ACCESSION CA983729
VERSION CA983729.1 GI:27516383
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0056 row: e column: 02
High quality sequence stop: 685.
FEATURES Location/Qualifiers
source 1. .928
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30144193"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_164"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI; Non-normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 10.5 and 11.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.8k bp. Priming sequence: 5'GACTAGTTCTAGATCGCGAGCGGCCGCCC(T) 3'. Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
ORIGIN

Query Match 11.3%; Score 725.2; DB 6; Length 928;
Best Local Similarity 87.1%; Pred. No. 1.7e-155;
Matches 807; Conservative 0; Mismatches 119; Indels 1; Gaps 1;

```
Qy       2543 TTGCCCGAGGAATGGAGTTTT-TGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCT 2601
              |||| |||||||||| |||| ||||||| |||||||||||||||||| || ||||||||
Db          1 TTGCTCGAGGAATGGAATTTTNTGGCTTCGAAAAATTGTGTCCACCGGGACCTGGCTGCC 60

Qy       2602 CGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGA 2661
              |||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||
Db         61 CGCAACGTCCTCCTGGCGCAAGGAAAAATTGTGAAGATCTGTGATTTTGGCCTGGCCAGA 120

Qy       2662 GACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGG 2721
              |||||||||| ||||| ||||| ||||| |||||||||| || ||||| |||||||||
Db        121 GACATCATGCACGATTCCAACTACGTGTCAAAAGGCAGTACTTTCCTGCCTGTGAAGTGG 180

Qy       2722 ATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTAT 2781
              ||||| || |||||||||| |||||||||||||||||| |||||||| |||||||| |||
Db        181 ATGGCACCCGAGAGCATCTTCGACAACCTCTACACCACGCTGAGTGACGTCTGGTCCTAT 240

Qy       2782 GGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTG 2841
              |||||||||||||||| |||||||||||||||||||| || || || ||||||||||||
Db        241 GGCATTCTGCTCTGGGAAATCTTTTCCCTTGGTGGCACACCCTATCCTGGCATGATGGTC 300

Qy       2842 GATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCT 2901
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||| ||
Db        301 GATTCTACTTTCTACAATAAGATCAAGAGTGGATACCGGATGGCCAAACCTGACCATGCC 360

Qy       2902 ACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCC 2961
              |||||||||||||| |||||||||| | |||||||||||||||| ||||||||||||
Db        361 ACCAGTGAAGTCTATGAGATCATGGTGCAGTGCTGGAACAGTGAGCCCGAGAAGAGACCC 420

Qy       2962 TCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGT 3021
              ||||| |||||||| || ||||| |||||||| ||| |||| |||||||| || |||||||
Db        421 TCCTTCTACCACCTCAGCGAGATAGTGGAGAACCTGTTGCCGGGACAATACAAGAAGAGT 480

Qy       3022 TATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGT 3081
              |||||||| |||||||||||||||| |||||||||||||| || ||||||||||||||||
Db        481 TATGAAAAGATTCACCTGGACTTCCTAAAGAGTGACCATCCGGCCGTGGCACGCATGCGG 540
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Qy       3082 GTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAG 3141
             ||||||||  ||  |||||  |||||  ||||||||  ||||||||  ||  ||  ||  |||||||||
Db        541 GTGGACTCTGATAATGCGTACATCGGTGTCACTTACAAAAATGAAGAGGATAAGCTGAAG 600

Qy       3142 GACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCT 3201
             ||||||||  |||||  |||||  ||  ||||||||||||||||||||||||||||||||  ||
Db        601 GACTGGGAAGGTGGCCTGGACGAACAGAGACTGAGCGCTGACAGTGGCTACATCATCCCC 660

Qy       3202 CTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGC 3261
             |||||  ||||||||||||||  ||  ||||||||  ||||||||||||||||||||||||
Db        661 CTGCCAGACATTGACCCTGTTCCAGAGGAGGAAGACCTGGGCAAGAGGAACAGACACAGC 720

Qy       3262 TCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAG 3321
             ||  |||||  ||  ||||||||||||||  |||||  ||||||||  ||||||||||||  |||||
Db        721 TCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCNTCAAG 780

Qy       3322 AGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCA 3381
             ||||||||||||||||  ||  ||||||||||||||||  |||||  ||  |||||  ||  ||
Db        781 AGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATTCCTCG 840

Qy       3382 GACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGG 3441
             ||  ||||||||||  |||||  |     |    |   |    ||||   |  ||   ||  |  ||
Db        841 GAACTGGTGGAAGAAAGCTTTCCTGTAACTGACCACGCTCCGGGTATCATCTTCTCCGGG 900

Qy       3442 GGCCACCTCTGGATCCCGTTCAGAAAA 3468
               |||  ||||  ||||     |  |  |||
Db        901 AGCCTCCTCGGGATAAACCTTAAGAAA 927


RESULT 20
BG623357
LOCUS       BG623357                741 bp    mRNA    linear   EST 18-APR-2001
DEFINITION  602648396F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4769926 5',
            mRNA sequence.
ACCESSION   BG623357
VERSION     BG623357.1  GI:13674728
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1635  row: p  column: 23
            High quality sequence stop: 723.
FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4769926"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_79"
                     /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.3
                     kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             11.2%;  Score 718;  DB 2;  Length 741;
  Best Local Similarity   98.9%;  Pred. No. 7.3e-154;
  Matches  732;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy       5310 GGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAA 5369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAA 60

Qy       5370 ACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCA 5429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCA 120

Qy       5430 GAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTT 5489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTT 180

Qy       5490 CTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGA 5549
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 CTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGANTGGCCAATTAAAAACGA 240

Qy       5550 AAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATC 5609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATC 300

Qy       5610 ACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGC 5669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGC 360

Qy       5670 TTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTC 5729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTC 420

Qy       5730 AGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTT 5789
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        421 AGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTCGTATATGACTGCATTT 480

Qy       5790 GTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAG 5849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAG 540

Qy       5850 TCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGC 5909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGC 600

Qy       5910 CGGCCTGAGAAACACTA-TTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGG 5968
             ||  |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGNGCTGAGAAACACTATTTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGG 660

Qy       5969 TCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATG 6028
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||  |||||||  |||||
Db        661 TCTGGCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATTAGATAAACTGATG 720

Qy       6029 TTATACATCAATATGTATAT 6048
             ||||||||||||||||||||
Db        721 TTATACATCAATATGTATAT 740


RESULT 21
CN373044
LOCUS       CN373044                728 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000423958053 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN373044
VERSION     CN373044.1  GI:47372978
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 728   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from embryoid body outgrowths derived from hES cell lines
                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

  Query Match           11.1%;  Score 715;  DB 7;  Length 728;
  Best Local Similarity   99.9%;  Pred. No. 3.6e-153;
  Matches  726;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       2168 GCTTCTATGGAGA-TTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 2226
             ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db             2 GCTTCTATGGAGAGTTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 61

Qy       2227 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 2286
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            62 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 121

Qy       2287 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 2346
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           122 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 181

Qy       2347 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 2406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           182 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 241

Qy       2407 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 2466
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           242 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 301

Qy       2467 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 2526
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           302 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 361

Qy       2527 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 2586
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           362 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 421

Qy       2587 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 2646
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           422 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 481

Qy       2647 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 2706
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           482 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 541

Qy       2707 CTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGT 2766
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           542 CTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGT 601

Qy       2767 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           602 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 661

Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           662 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 721

Qy       2887 AAGCCTG 2893
             |||||||
Db           722 AAGCCTG 728


RESULT 22
CR769595
LOCUS       CR769595                759 bp    mRNA    linear   EST 23-SEP-2004
DEFINITION  DKFZp469J1429_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
            DKFZp469J1429 5', mRNA sequence.
ACCESSION   CR769595
VERSION     CR769595.1  GI:52613623
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
            Deutschenbaur,S., et al.)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert. Clone from S. Wiemann,
            Molecular Genome Analysis, German Cancer Research Center (DKFZ);
            Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
            (Martinsried/Germany) within the cDNA sequencing consortium of the
            German Genome Project. This clone (DKFZp469J1429) is available at
            the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
            Berlin, Germany. Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469J1429
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Pongo pygmaeus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9600"
                     /clone="DKFZp469J1429"
                     /tissue_type="kidney"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="469 (synonym: pkid1)"
                     /note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
ORIGIN

  Query Match           11.1%;  Score 715;  DB 7;  Length 759;
  Best Local Similarity   98.2%;  Pred. No. 3.6e-153;
  Matches  743;  Conservative    0;  Mismatches   12;  Indels    2;  Gaps    2;

Qy       3608 GCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAAT 3667
             ||| |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db             1 GCAGTGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGNGATAGATGGATAAGGGAAT 60

Qy       3668 AATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACAC 3727
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db            61 AATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAGCAGACAC 120
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Qy       3728 AATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTG 3787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTG 180

Qy       3788 TGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATT 3847
             |||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||
Db        181 TGTTTAGATTGTATTAACTGTCTTCTTTGGACTTCTGAAGAGACCACTCCATCCATCCATT 240

Qy       3848 GTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAA 3907
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTACTTCCTTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAA 300

Qy       3908 AAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTG 3967
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACCACTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTG 360

Qy       3968 TTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAA 4027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAA 420

Qy       4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTA 4087
             ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        421 GCCTGACAACTCATTTTCATATTGTAATCTACATTTATAATACTACTACTGTTATCAGTA 480

Qy       4088 ATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAA 4147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAA 540

Qy       4148 TCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTT 4207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTT 600

Qy       4208 CTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAG 4267
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        601 TTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGNTGAGCATAGAGAACAAAG 660

Qy       4268 T-AAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAAT 4326
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAAT 720

Qy       4327 CCATCGTATTAAAAAAC-AATTAACTGCCCTCTGAAA 4362
             |||||||||||||||| |||||||||||||||| ||
Db        721 CCATCGTATTAAAAAACAAATTAACTGCCCTCTGGAA 757


RESULT 23
AU118489
LOCUS       AU118489                783 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU118489 HEMBA1 Homo sapiens cDNA clone HEMBA1003698 5', mRNA
            sequence.
ACCESSION   AU118489
VERSION     AU118489.1  GI:10933545
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HEMBA1003698"
                     /tissue_type="whole embryo, mainly head"
                     /dev_stage="embryo, 10 weeks"
                     /clone_lib="HEMBA1"
                     /note="Vector: pME18SFL3"
ORIGIN

  Query Match           11.1%;  Score 714.2;  DB 1;  Length 783;
  Best Local Similarity   98.0%;  Pred. No. 5.5e-153;
  Matches  753;  Conservative    0;  Mismatches   11;  Indels    4;  Gaps    3;

Qy       4873 GTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGG 4932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGG 60

Qy       4933 AAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCA 4992
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCA 120

Qy       4993 ATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTT 5052
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTT 180

Qy       5053 TTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTT 5112
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTT 240

Qy       5113 CCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAA 5172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAA 300

Qy       5173 ATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAA 5232
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        301 ATTATGCAATTCAGTGTTCCAAGTCTCTGTG--ACCAGCTCAGTGTTTTGGTGGAAAAAA 358

Qy       5233 CATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCC 5292
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 CATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCC 418

Qy       5293 ACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCT 5352
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 ACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCT 478

Qy       5353 GATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATG 5412
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 GATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATG 538

Qy       5413 ATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCA 5472
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 ATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCA 598

Qy       5473 ATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGAT 5532
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGAT 658

Qy       5533 TGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACG 5592
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        659 TGGCCAATTAAAAACGAAAACCTGACTAGGNTCTGTAGAGCCAATTAGACTTGAAATACG 718

Qy       5593 TTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             |||| | |||||||||| ||||| |||||||||| |      | | |||
Db        719 TTTG-GGTTCTAGAATC-CAGCTNAAGCATTCTGNTATCGTCACTCTC 764


RESULT 24
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BQ446932/c
LOCUS       BQ446932                723 bp    mRNA    linear   EST 29-MAY-2002
DEFINITION  UI-H-EU1-bac-i-01-0-UI.s1 NCI_CGAP_Ct1 Homo sapiens cDNA clone
            UI-H-EU1-bac-i-01-0-UI 3', mRNA sequence.
ACCESSION   BQ446932
VERSION     BQ446932.1  GI:21250044
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
            191-218, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .723
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EU1-bac-i-01-0-UI"
                     /tissue_type="Osteoarthritic Cartilage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ct1"
                     /note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ct1 is a normalized cDNA library containing the
                     following tissue(s): Osteoarthritic Cartilage The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=osteoarthritic cartilage
                     TAG_LIB=UI-H-EU1
                     TAG_SEQ=TGATCACGCT"
ORIGIN
```

Query Match 11.1%; Score 711; DB 5; Length 723;
Best Local Similarity 99.7%; Pred. No. 3e-152;
Matches 722; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy       5673 GCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGT 5732
             |||||||||||  |||||||||||||||||||||||||||||||||||| ||||||||
Db        723 GCATTTTGATANTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAA-TTCTCAGT 665

Qy       5733 CCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTG 5792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTG 605

Qy       5793 GGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCT 5852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        604 GGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCT 545

Qy       5853 CCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGG 5912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGG 485

Qy       5913 CCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTG 5972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTG 425

Qy       5973 CCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTAT 6032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTAT 365

Qy       6033 ACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTAT 6092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 ACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTAT 305

Qy       6093 GACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCAC 6152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCAC 245

Qy       6153 ATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGA 6212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGA 185

Qy       6213 TACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGG 6272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 TACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGG 125

Qy       6273 GTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGT 6332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGT 65

Qy       6333 AAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAA 6392
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          64 AAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAA 5

Qy       6393 AAAA 6396
              ||||
Db           4 AAAA 1
```

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RESULT 25
BQ010105/c
LOCUS       BQ010105                711 bp    mRNA    linear   EST 26-MAR-2002
DEFINITION  UI-H-ED0-axz-k-23-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
            IMAGE:5835790 3', mRNA sequence.
ACCESSION   BQ010105
VERSION     BQ010105.1  GI:19735006
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
            191-218, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
```

```
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .711
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5835790"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED0"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
                     the following tissue(s): Chondrosarcoma cell line CS5. The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED0
                     TAG_SEQ=CGTCAAGGCT"
ORIGIN

  Query Match             11.0%;  Score 707.8;  DB 3;  Length 711;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-151;
  Matches  709;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5686 GCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCA 5745
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        711 GCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTATCAGTCCAGCAGTTTCCA 652

Qy       5746 GTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGT 5805
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGT 592

Qy       5806 TTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATT 5865
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 TTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATT 532

Qy       5866 TGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACT 5925
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 TGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACT 472

Qy       5926 ATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAA 5985
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 ATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAA 412

Qy       5986 AATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTA 6045
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 AATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTA 352

Qy       6046 TATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATC 6105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATC 292

Qy       6106 ACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCA 6165
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        291 ACTGCCTTCGTTTATATTTCTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCA 232

Qy       6166 CTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTC 6225
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 CTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTC 172

Qy       6226 CCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACA 6285
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACA 112

Qy       6286 AAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTT 6345
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 AAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTT 52

Qy       6346 TATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 6396
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          51 TATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 1


RESULT 26
CN373045
LOCUS       CN373045                733 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000424507422 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN373045
VERSION     CN373045.1  GI:47372979
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 733   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, embryoid bodies
                     derived from H1, H7 and H9 cells"
                     /clone_lib="GRN_EB"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from embryoid body outgrowths derived from hES cell lines
                     H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                     conditions."
ORIGIN

  Query Match             11.0%;  Score 707.4;  DB 7;  Length 733;
  Best Local Similarity   99.9%;  Pred. No. 2e-151;
  Matches  708;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2457 GTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATT 2516
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 GGTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATT 84

Qy       2517 GGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAA 2576
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAA 144

Qy       2577 TTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAA 2636
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 TTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAA 204

Qy       2637 GATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGG 2696
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGG 264

Qy       2697 CAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACAC 2756
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REFERENCE   1  (bases 1 to 935)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. David Rowe
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14066  row: n  column: 02
            High quality sequence stop: 610.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6505633"
                     /tissue_type="undifferentiated limb"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_134"
                     /note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
                     Cloned unidirectionally. Primer: Oligo dT. Average insert
                     size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match            11.0%;  Score 704.8;  DB 5;  Length 935;
  Best Local Similarity  87.8%;  Pred. No. 8.4e-151;
  Matches  815;  Conservative    0;  Mismatches  107;  Indels    6;  Gaps    4;

Qy       2053 CAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTA 2112
              || ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CAGGCTCTCATGTCTGAGCTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTG 60

Qy       2113 AACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTC 2172
              |||||||||||||||||||||||||||| ||||||||||||||||||| || ||||||
Db         61 AACTTGCTGGGAGCCTGCACCAAGTCAGGTCCCATTTACATCATCACAGAATACTGCTTC 120

Qy       2173 TATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCA 2232
              ||||| |||||||||||||| |||||||||| || ||||||||| ||||||| ||||||
Db        121 TATGGGGATTTGGTCAACTACTTGCATAAGAACAGAGATAGCTTCATGAGCCAACACCCA 180

Qy       2233 GAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGG 2292
              |||||||| |||||||| ||||| |||||||||||||| ||||| || || |||||| |
Db        181 GAGAAGCCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGCAGACGAGAGCACAAGA 240

Qy       2293 AGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGAT 2352
              || ||||| ||||| |||||||||| || || |||||||||||||||||||| ||||||
Db        241 AGTTATGTGATTTTGTCTTTTGAAAATAACGGCGACTACATGGACATGAAGCAAGCTGAT 300

Qy       2353 ACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAG 2412
              || |||||||||||||||||| |||||||||||||||||||||| || |||||||||
Db        301 ACCACACAGTATGTCCCCATGCTTGAAAGGAAAGAGGTTTCTAAATACTCTGACATCCAG 360

Qy       2413 AGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTC 2472
              ||||| || || ||||| |||||||| || |||||||||| ||| ||||||||||||||
Db        361 AGATCGCTGTACGATCGGCCAGCCTCCTACAAGAAGAAATCCATGCTAGACTCAGAAGTC 420

Qy       2473 AAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTC 2532
              |||||||||||||| || ||| |||| || || || |||||  ||||| | |||||||||
Db        421 AAAAACCTCCTTTCGGACGATGACTCCGAGGGTCTGACTTTGCTGGATCTATTGAGCTTC 480

Qy       2533 ACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGAT 2592
              |||||||||||||| |||||||||| |||||||||| |||||||||||||||||| ||
Db        481 ACCTATCAAGTTGCTCGAGGAATGGAATTTTTGGCTTCGAAAAATTGTGTCCACCGGGAC 540

Qy       2593 CTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGC 2652
              |||||||| |||||||||||||||| |||||||||||||||||||||||||| ||||||
Db        541 CTGGCTGCCCGCAACGTCCTCCTGGCGCAAGGAAAAATTGTGAAGATCTGTGATTTTGGC 600

Qy       2653 CTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCC 2712
              |||||||||||||||||||| ||||| ||||| ||||| |||||||||| || |||||
Db         601 CTGGCCAGAGACATCATGCACGATTCCAACTACGTGTCAAAAGGCAGTACTTTCCTGCCT 660

Qy       2713 GTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTC 2772
              |||||||||||||| || |||||||||| |||||||||||||||| |||||||| |||
Db         661 GTGAAGTGGATGGCACCCGAGAGCATCTTCGACAACCTCTACACCACGCTGAGTGACGTC 720

Qy       2773 TGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGC 2832
              ||||| |||||||||||||||||||| |||||||||||||||||||| || || || |||
Db         721 TGGTCCTATGGCATTCTGCTCTGGGAAATCTTTTCCCTTGGTGGCACACCCTATCCTGGC 780

Qy       2833 ATGAT-GGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACC-GGATGGCCAAGC 2890
              ||||| ||| |||||||||||||| ||| |||| ||||||| |||| |||||||||| |
Db         781 ATGATGGGTCGATTCTACTTTCTACCATAGGATCCAGAGTGGATACCGGGATGGCCAAAC 840

Qy       2891 CTGACCACGCTACCAGTGAAGTCTACG-AGATCATGGTGAAATGCTGGAACAGTGAG--- 2946
              ||||||  || ||  | |||| ||| | | |||||| ||  ||||| ||| |  | |
Db         841 CTGACCTGGCCACAGGGGAAGCCTATGAAAATCATGCTGCCATGCTTGAAAACGGGGAGC 900

Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACC 2974
              ||  |||||||||||  ||||   ||||
Db         901 CCCCAGAAGAGACCCCTCTTTCTACACC 928


RESULT 29
CN479805/c
LOCUS       CN479805                731 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-EU0-azk-d-15-0-UI.s1 NCI_CGAP_Car1 Homo sapiens cDNA clone
            UI-H-EU0-azk-d-15-0-UI 3', mRNA sequence.
ACCESSION   CN479805
VERSION     CN479805.1  GI:46548659
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 620-727, >MER5B#DNA/MER1_type
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EU0-azk-d-15-0-UI"
                     /tissue_type="Osteoarthritic Cartilage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Car1"
                     /note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Car1 is a cDNA library containing the following
                     tissue(s): Osteoarthritic Cartilage The library was
```

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCACGCT.
TAG_TISSUE=osteoarthritic cartilage
TAG_LIB=UI-H-EU0
TAG_SEQ=TGATCACGCT"

ORIGIN

Query Match 10.9%; Score 702.2; DB 7; Length 731;
Best Local Similarity 99.6%; Pred. No. 3.2e-150;
Matches 704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       4752 GGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTT 4811
             || |||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        724 GGGTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGAGAAACCAGAGTCTGTATTTTT 665

Qy       4812 CTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGA 4871
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        664 CTAAACTCCCTGGCTGTTCTGATCGCCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGA 605

Qy       4872 AGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAG 4931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAG 545

Qy       4932 GAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGC 4991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGC 485

Qy       4992 AATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGT 5051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 AATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGT 425

Qy       5052 TTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTT 5111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTT 365

Qy       5112 TCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAA 5171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAA 305

Qy       5172 AATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAA 5231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAA 245

Qy       5232 ACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATC 5291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATC 185

Qy       5292 CACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGC 5351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGC 125

Qy       5352 TGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGAT 5411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGAT 65

Qy       5412 GATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 5458
             ||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 18
```

RESULT 30
DR005181
LOCUS DR005181 740 bp mRNA linear EST 17-MAY-2005
DEFINITION TC116256 Human prostate, large insert, pCMV expression library Homo sapiens cDNA clone TC116256 5' similar to Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA sequence.
ACCESSION DR005181
VERSION DR005181.1 GI:66265054
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
TITLE High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
JOURNAL Unpublished (2005)
COMMENT Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 5prime forward vector primer, OriGene Technologies Inc.

FEATURES Location/Qualifiers
source 1. .740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC116256"
/tissue_type="Prostate"
/clone_lib="Human prostate, large insert, pCMV expression library"
/note="Organ: Prostate; Vector: pCMV6-XL4; Site_1: EcoR1; Site_2: XhoI/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Query Match 10.9%; Score 698.6; DB 8; Length 740;
Best Local Similarity 99.1%; Pred. No. 2.1e-149;
Matches 734; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

```
Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGC-GGAATAACATCG-G 118
              |||||||||||||||||||||||| |||||||||||||||||| |||||||||||| |
Db          1 AGGCCGTGGGCACGCTCTTTACTCC-TGTGTGGGACATTCATTGCTGGAATAACATCGNG 59

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 119

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TTCTCACATTTTTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 179

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 239

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 299

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 359

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 419

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 479

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 539

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 599

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 659

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 778
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 719

Qy        779 TGGATCTAGAAATGGAAGCTC 799
                |||||||||||||||||||||
Db        720 TGGATCTAGAAATGGAAGCTC 740


RESULT 31
CA447048/c
LOCUS       CA447048                698 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-ED0-aya-m-14-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
            UI-H-ED0-aya-m-14-0-UI 3', mRNA sequence.
ACCESSION   CA447048
VERSION     CA447048.1  GI:24811461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
            191-218, >AT_rich#Low_complexity (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-ED0-aya-m-14-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED0"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
                     the following tissue(s): Chondrosarcoma cell line CS5. The
                     library was constructed according to Bonaldo, Lennon and
                     Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site. Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED0
                     TAG_SEQ=CGTCAAGGCT"
ORIGIN

  Query Match             10.9%;  Score 696.4;  DB 6;  Length 698;
  Best Local Similarity   99.9%;  Pred. No. 6.8e-149;
  Matches  697;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5699 CATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATG 5758
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATG 639

Qy       5759 CTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTC 5818
                ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 CTCCCACTTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTC 579

Qy       5819 CAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAAATTTGCCAATCTTTCC 5878
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAAATTTGCCAATCTTTCC 519

Qy       5879 TACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTT 5938
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 TACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTT 459

Qy       5939 TAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTT 5998
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 TAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTT 399

Qy       5999 TTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCT 6058
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 TTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCT 339

Qy       6059 ATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTT 6118
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTT 279

Qy       6119 ATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCC 6178
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCC 219

Qy       6179 AAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGT 6238
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGT 159

Qy       6239 GTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGA 6298
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGA 99

Qy       6299 ATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAA 6358
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          98 ATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAA 39

Qy       6359 ATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 6396
                |||||||||||||||||||||||||||||||||||||
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Db         38 ATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 1


RESULT 32
BG434752
LOCUS       BG434752                791 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602507957F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4604846 5',
            mRNA sequence.
ACCESSION   BG434752
VERSION     BG434752.1  GI:13341258
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 791)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1341  row: b  column: 15
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
     source          1. .791
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4604846"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_79"
                     /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.3
                     kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            10.7%;  Score 684;  DB 2;  Length 791;
  Best Local Similarity  95.5%;  Pred. No. 5e-146;
  Matches  747;  Conservative    0;  Mismatches   30;  Indels    5;  Gaps    4;

Qy       5219 TTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAAT 5278
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 TTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAAT 69

Qy       5279 TGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAAT 5338
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAAT 129

Qy       5339 ACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGT 5398
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGT 189

Qy       5399 GCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 5458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 249

Qy       5459 CTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGA 5518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGA 309

Qy       5519 AGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATT 5578
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        310 AGACTGAGCCAGATTGGCCAATTAAAAGCGAAAACCTGACTAGGTTCTGTAGAGCCAATT 369

Qy       5579 AGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCAC 5638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCAC 429

Qy       5639 TCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTG 5698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 TCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTG 489

Qy       5699 CATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATG 5758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 CATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATG 549

Qy       5759 CTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTC 5818
             |||||||||||||      ||||||||||||||||||||||||||||| ||||||||||||
Db        550 CTCCCACCTGAATTGTATATTGACTGCATTTGTGGGTGTGTGTGTGTCTTCAGCAAATTC 609

Qy       5819 CAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCC 5878
             |||| |||||||||||||||||||||||||||||||||||||||||||| |    ||||
Db        610 CAGA-TTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCAATCTTTTC- 667

Qy       5879 TACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACT-ATTTGTGACTTT 5937
                 |||||||||||||||||||||||||||| ||||      || |||| ||||||||||||
Db        668 -TACTTCTATTTTTATGATGACAATCAAAGGCGGCTGAGAAACCACTAATTTGTGACTTT 726

Qy       5938 TTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATT 5997
                | || |||||||||||||| |||||||||||||  | |||||||| ||| ||||||| |
Db        727 TAAACCGATTAGTGATGTCTTTAAAATGTGGTCTTGC-ATCTGTACCAAAGGGTCCTAAT 785

Qy       5998 TT 5999
                ||
Db        786 TT 787


RESULT 33
AI805230/c
LOCUS       AI805230                783 bp    mRNA    linear   EST 07-MAR-2000
DEFINITION  tu44g03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253940 3'
            similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI805230
VERSION     AI805230.1  GI:5391723
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1053   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
```

```
     source          1. .783
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2253940"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             10.6%;  Score 681.4;  DB 1;  Length 783;
  Best Local Similarity   93.5%;  Pred. No. 2e-145;
  Matches  733;  Conservative    0;  Mismatches   47;  Indels    4;  Gaps    2;

Qy       5597 TGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTT 5656
             |||   || |    |   ||||||  |||  ||||||||||||||| | || ||||||
Db        782 TGTGGTTATAGATCCCAGTCAAGCCATCTTGTTATCGCTCACTCTCCATGGTCCAGCCTA 723

Qy       5657 ATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCG 5716
               ||| |||| |||||||||||||| |||| ||||||||||||||||||||||||||||||
Db        722 TTTTGGTTGATGCTTTGCATTTTAATATGGCTGTGAGCCTTGCATGACATCATGAGGCCG 663

Qy       5717 GATGAAACTTCTCAGTCC--AGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTG 5774
               |||||  | ||  |||||       || |||||||||  |||||||||||| | | ||||
Db        662 AATGAANCCTCCAAGTCCCAGCAGTTTCCCAGTCCTACAAAATGCTCCCACTTAATTTTG 603

Qy       5775 TATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTT 5834
             |||||||||||||||||||||||||||||||||       || | ||||||||||||||||
Db        602 TATATGACTGCATTTGTGGGTGTGTGTGTGTTT--CAGCAAATTCAGATTTGTTTCCTTT 545

Qy       5835 TGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTAT 5894
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 TGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTAT 485

Qy       5895 GATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATG 5954
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATG 425

Qy       5955 TCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACAT 6014
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 TCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACAT 365

Qy       6015 AAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAA 6074
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 AAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAA 305

Qy       6075 TACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGT 6134
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGT 245

Qy       6135 GATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAG 6194
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAG 185

Qy       6195 AAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAG 6254
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 AAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAG 125

Qy       6255 AAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGT 6314
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGT 65

Qy       6315 TTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAA 6374
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 TTTTTTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAA 5

Qy       6375 AGTT 6378
             ||||
Db          4 AGTT 1


RESULT 34
BG939663/c
LOCUS       BG939663                681 bp    mRNA    linear   EST 20-JUN-2002
DEFINITION  cr60b12.x1 Human bone marrow stromal cells Homo sapiens cDNA clone
            HBMSC_cr60b12 3', mRNA sequence.
ACCESSION   BG939663
VERSION     BG939663.1  GI:14339035
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 681)
  AUTHORS   Jia,L., Young,M.F., Powell,J., Yang,L., Ho,N.C., Hotchkiss,R.,
            Robey,P.G. and Francomano,C.A.
  TITLE     Gene expression profile of human bone marrow stromal cells:
            high-throughput expressed sequence tag sequencing analysis
  JOURNAL   Genomics 79 (1), 7-17 (2002)
   PUBMED   11827452
COMMENT     Contact: Libin Jia
            Medical Genetics Branch
            National Human Genome Research Institute
            10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
            Tel: 301-402-4877
            Fax: 301-496-7157
            Email: libin@helix.nih.gov
            DNA Sequencing and analyses by National Institutes of Health
            Intramural Sequencing Center (NISC).
            Plate: 60  row: b  column: 12
            Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .681
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="HBMSC_cr60b12"
                     /sex="mixed"
                     /tissue_type="bone marrow stroma"
                     /dev_stage="mixed"
                     /lab_host="XL1-Blue MRF'/SOLR"
                     /clone_lib="Human bone marrow stromal cells"
                     /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
                     mRNA made from human bone marrow stroma, cDNA made by
                     oligo-dT priming. Directionally cloned. Size-selected for
                     average insert size >0.5 kb. Library constructed by Dr.
                     Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library
                     supplied by Dr. Libin Jia (NHGRI)"
ORIGIN

  Query Match             10.6%;  Score 681;  DB 2;  Length 681;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-145;
  Matches  681;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5731 GTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTG 5790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTG 622

Qy       5791 TGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGT 5850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGT 562

Qy       5851 CTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCC 5910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 CTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCC 502
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Qy       5911 GGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTC 5970
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTC 442

Qy       5971 TGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTT 6030
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTT 382

Qy       6031 ATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTT 6090
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTT 322

Qy       6091 ATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGC 6150
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 ATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGC 262

Qy       6151 ACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAA 6210
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAA 202

Qy       6211 GATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATA 6270
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATA 142

Qy       6271 GGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGT 6330
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGT 82

Qy       6331 GTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAA 6390
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 GTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAA 22

Qy       6391 AAAAAAAAAAAAAAAAAAAA 6411
             ||||||||||||||||||||
Db          21 AAAAAAAAAAAAAAAAAAAA 1
```

RESULT 35
BM972746/c
LOCUS BM972746 698 bp mRNA linear EST 20-FEB-2003
DEFINITION UI-CF-EC1-abr-e-02-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-abr-e-02-0-UI 3', mRNA sequence.
ACCESSION BM972746
VERSION BM972746.1 GI:19590337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 1-53, >AT_rich#Low_complexity (matched compliment)
191-218, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .698
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-abr-e-02-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.
TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

ORIGIN

Query Match 10.6%; Score 679; DB 3; Length 698;
Best Local Similarity 99.1%; Pred. No. 6.9e-145;
Matches 693; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy       5698 GCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAAT 5757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 GCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAAT 639

Qy       5758 GCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATT 5817
             |||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        638 GCTCCCACTTGAATTTGTATATGACTGCATTTGTGGGTGTGTGT-TGTTTTCAGCAAATT 580

Qy       5818 CCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTC 5877
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CCAGATTTATTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTC 520

Qy       5878 CTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTT 5937
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 TTACTTTCTATTTGTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTT 460

Qy       5938 TTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATT 5997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 TTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATT 400

Qy       5998 TTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTC 6057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 TTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTC 340

Qy       6058 TATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTT 6117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        339 TATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCGTCGTT 280

Qy       6118 TATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTC 6177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 TATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTC 220

Qy       6178 CAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGG 6237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 CAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGG 160
```

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Qy       6238 TGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACG 6297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACG 100

Qy       6298 AATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATA 6357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 AATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATA 40

Qy       6358 AATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 6396
             ||||||||||||||||||||||||||||||||||||||||
Db          39 AATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAA 1


RESULT 36
CN373046
LOCUS       CN373046                698 bp    mRNA    linear   EST 16-MAY-2004
DEFINITION  17000418008530 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CN373046
VERSION     CN373046.1  GI:47372980
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Lebkowski,J and Stanton,L.W.
  TITLE     Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
  JOURNAL   Nat. Biotechnol. 22 (6), 707-716 (2004)
   PUBMED   15146197
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 698   Std Error: 0.00.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cells, cell lines H1, H7, and
                     H9"
                     /clone_lib="GRN_ES"
                     /note="oligo dT primed, full-length enriched cDNA library
                     from undifferentiated hES cell lines H1 (p32), H7 (p29),
                     and H9 (p26) maintained in feeder-free conditions"
ORIGIN

  Query Match             10.4%;  Score 666.8;  DB 7;  Length 698;
  Best Local Similarity   98.6%;  Pred. No. 4.5e-142;
  Matches  684;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    1;

Qy         21 GGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGTGGGCACGCTCTTT 80
              | |||| | | ||||||||| ||||||||||||||    | ||||||||||||||||||||
Db          3 GAGAGAAACAGAGGAGGAGACTGCAAGAGATCATT---GGAGGCCGTGGGCACGCTCTTT 59

Qy         81 ACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTAT 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 ACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTAT 119

Qy        141 GGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTAAT 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTAAT 179

Qy        201 CCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAGCT 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAGCT 239

Qy        261 GAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCAT 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCAT 299

Qy        321 GTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTTTT 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTTTT 359

Qy        381 TGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGCTA 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGCTA 419

Qy        441 TTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 500
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        420 TTACAACCACACTCAGACAGAAGATAATGAGCTTGAAGGCAGGCACATTTACATCTATGT 479

Qy        501 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTGGA 539

Qy        561 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTT 599

Qy        621 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 ACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGGAC 659

Qy        681 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACC 714
              |||||||||||||||||||||||||||||||||
Db        660 CTTCACTGTAGGGCCCTATATCTGTGAGGCCACC 693


RESULT 37
CO431484
LOCUS       CO431484                807 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  UI-M-HX0-csd-n-08-0-UI.r1 NIH_BMAP_HX0 Mus musculus cDNA clone
            IMAGE:30685663 5', mRNA sequence.
ACCESSION   CO431484
VERSION     CO431484.1  GI:49677778
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 807)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .807
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30685663"
                     /tissue_type="whole eye"
                     /dev_stage="newborn (1, 5, 15 days) and embryonic (15, 16,
                     17, 18 dpc)"
```

/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HX0"
/note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site .Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AATAATTACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match 10.4%; Score 666.2; DB 7; Length 807;
Best Local Similarity 89.8%; Pred. No. 6.3e-142;
Matches 724; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

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Qy       2560 TTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCA 2619
             |||||||||||| |||||||||||||||||| || |||||||| ||||||||||||||||||
Db             2 TTTTTGGCTTCGAAAAATTGTGTCCACCGGGACCTGGCTGCCCGCAACGTCCTCCTGGCG 61

Qy       2620 CAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCG 2679
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||| |||||
Db            62 CAAGGAAAAATTGTGAAGATCTGTGATTTTGGCCTGGCCAGAGACATCATGCACGATTCC 121

Qy       2680 AACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATC 2739
             ||||| ||||| |||||||||||| || ||||| |||||||||||||| || |||||||||
Db           122 AACTACGTGTCAAAAGGCAGTACTTTCCTGCCTGTGAAGTGGATGGCACCCGAGAGCATC 181

Qy       2740 TTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAG 2799
             || |||||||||||||||| |||||||| |||||||| ||||||||||||||||||||||
Db           182 TTCGACAACCTCTACACCACGCTGAGTGACGTCTGGTCCTATGGCATTCTGCTCTGGGAA 241

Qy       2800 ATCTTTTCCCTT-GGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAA 2858
             |||||||||||| |||||||| || || || |||||||||||| ||||||||||||||||||
Db           242 ATCTTTTCCCTTGGGTGGCACACCCTATCCTGGCATGATGGTCGATTCTACTTTCTACAA 301

Qy       2859 TAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGA 2918
             |||||||||||||||| |||||||||||||| |||||||| || |||||||||||||| ||
Db           302 TAAGATCAAGAGTGGATACCGGATGGCCAAACCTGACCATGCCACCAGTGAAGTCTATGA 361

Qy       2919 GATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAG 2978
             ||||||||| | |||||||||||||||| |||||||||||||||| |||||||| ||
Db           362 GATCATGGTGCAGTGCTGGAACAGTGAGCCCGAGAAGAGACCCTCCTTCTACCACCTCAG 421

Qy       2979 TGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCT 3038
             |||||  |||||||| ||| |||| |||||||| || ||||||||||||| |||||||||
Db           422 CGAGATAGTGGAGAACCTGTTGCCGGGACAATACAAGAAGAGTTATGAAAAGATTCACCT 481

Qy       3039 GGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGC 3098
             ||||||||| |||||||||||||| || |||||||||||||| |||||||| || |||||
Db           482 GGACTTCCTAAAGAGTGACCATCCGGCCGTGGCACGCATGCGGGTGGACTCTGATAATGC 541

Qy       3099 ATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCT 3158
             |||||  |||||||| |||||||| || || || |||||||||||||||| |||||  ||
Db           542 GTACATCGGTGTCACTTACAAAAATGAAGAGGATAAGCTGAAGGACTGGGAAGGTGGCCT 601

Qy       3159 GGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCC 3218
             |||  || |||||||||||||||||||||||||||||||| || |||||  ||||||||||
Db           602 GGACGAACAGAGACTGAGCGCTGACAGTGGCTACATCATCCCCCTGCCAGACATTGACCC 661

Qy       3219 TGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGA 3278
             |||  || |||||||| ||||||    |||||||||||||||||||| ||||| || |||||
Db           662 TGTTCCAGAGGAGGAAGACCTGNNGCAGAGGAACAGACACAGCTCACAGACTTCGGAAGA 721

Qy       3279 GAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCAT 3338
             |||||||||  ||||| |||||||| ||||||||||||  ||||||||||||||||||||
Db           722 GAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCATNCAGAGAGAGGACGAGACCAT 781

Qy       3339 TGAAGACATCGACATGATGGACGACA 3364
                  || |||||||||||||||||| ||||
Db            782 CGAGGACATCGACATGATGGATGACA 807
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RESULT 38
CA392578
LOCUS CA392578 677 bp mRNA linear EST 06-NOV-2002
DEFINITION cs26c11.y1 Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs26c11 5', mRNA sequence.
ACCESSION CA392578
VERSION CA392578.1 GI:24725431
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 677)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants
JOURNAL Mol. Vis. 8 (4), 205-220 (2002)
PUBMED 12107410
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 26 row: c column: 11
Seq primer: M13RP1 reverse primer (ABI).
FEATURES Location/Qualifiers
source 1. .677
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs26c11"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp. <http://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 10.3%; Score 660.2; DB 6; Length 677;
Best Local Similarity 99.4%; Pred. No. 1.5e-140;
Matches 673; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy       5539 ATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTG 5598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db              1 ATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTG 60

Qy       5599 TTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTAT 5658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        61 TTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTAT 120

Qy      5659 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 5718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 180

Qy      5719 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 5778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 240

Qy      5779 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 5838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 300

Qy      5839 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 360

Qy      5899 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC-TTTTTAAACGATTAGTGATGTCC 5957
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       361 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTTAAACGATTAGTGATGTCC 420

Qy      5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 480

Qy      6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 540

Qy      6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 600

Qy      6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 660

Qy      6198 TAATAAAAAGAAAGATA 6214
             ||||||||| ||| | |
Db       661 TAATAAAAAAAAAAAAA 677


RESULT 39
AI188169/c
LOCUS       AI188169                764 bp    mRNA    linear   EST 28-OCT-1998
DEFINITION  qd66c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734438
            3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR
            RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI188169
VERSION     AI188169.1  GI:3739378
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 764)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1078   Std Error: 0.00
            Seq primer: -40UP from Gibco

            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
     source          1. .764
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1734438"
                     /sex="male"
                     /lab_host="DH10B"
                     /clone_lib="Soares_testis_NHT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match             10.3%;  Score 659.2;  DB 1;  Length 764;
  Best Local Similarity   96.8%;  Pred. No. 2.6e-140;
  Matches  736;  Conservative    0;  Mismatches   18;  Indels    6;  Gaps    6;

Qy      5623 TCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGAT 5682
             ||||||||||||||| |  |||||||||||| |||||||||| |||||||| |||||||||
Db       754 TCTGTTTATCGCTCATTTCCCCTTGTACAGCTTTATTTTGTGGGTGCTTT-CATTTTGAT 696

Qy      5683 ATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTT 5742
             |||||||||||||||||||| |||||||||||  ||| ||||||||||||||||||||||
Db       695 ATTGCTGTGAGCCTTGCATGAC-TCATGAGGCCGAATG-AACTTCTCAGTCCAGCAGTTC 638

Qy      5743 CCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTG 5802
             | ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       637 CAAGTCCTAACAATTGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTG 578

Qy      5803 TGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAA 5862
             || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       577 TG-TTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTG-AAAGTCTCCAGAAGAAG 520

Qy      5863 ATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAAC 5922
             |||||  |||||||||| ||||||||||||||||||||||||||  ||||||  |||| |
Db       519 ATTTG-CAATCTTTCCAACTTTCTATTTTTATGATGACAATCAAAAGCGGCCTTAGAACC 461

Qy      5923 ACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTA 5982
               | |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       460 CCCATTTGTGACTTTTAAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTA 401

Qy      5983 CAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATAT 6042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       400 CAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATAT 341

Qy      6043 GTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGT 6102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       340 GTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGT 281

Qy      6103 ATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTT 6162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       280 ATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTT 221

Qy      6163 GCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATG 6222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       220 GCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATG 161

Qy      6223 TTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAAT 6282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       160 TTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAAT 101

Qy      6283 ACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGAT 6342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        100 ACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGAT 41

Qy       6343 CTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAA 6382
              |||||||||||||||||||||||||||||||||||||||||
Db         40 CTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAA 1


RESULT 40
CO739013
LOCUS       CO739013                734 bp    mRNA    linear   EST 29-JUL-2004
DEFINITION  S1LE04c22c05f1 squirrel embryo library 1 Spermophilus lateralis
            cDNA clone 22c05 5', mRNA sequence.
ACCESSION   CO739013
VERSION     CO739013.1  GI:50826283
KEYWORDS    EST.
SOURCE      Spermophilus lateralis (golden-mantled ground squirrel)
  ORGANISM  Spermophilus lateralis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
REFERENCE   1  (bases 1 to 734)
  AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
            Rogers,J. and Cossins,A.R.
  TITLE     Microarray analysis of transcriptional changes during hibernation
            in the golden mantled ground squirrel, Spermophilus lateralis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 22  row: c  column: 05
            Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
            High quality sequence stop: 734.
FEATURES             Location/Qualifiers
     source          1. .734
                     /organism="Spermophilus lateralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:76772"
                     /clone="22c05"
                     /sex="male and female"
                     /tissue_type="embryo"
                     /dev_stage="embryonic"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel embryo library 1"
                     /note="Vector: pFLC; Site_1: SalI GTCGAG; Site_2: BamHI
                     GGATCC; Normalized and subtracted cDNA library prepared
                     from embryos"
ORIGIN

  Query Match             10.2%;  Score 657.2;  DB 7;  Length 734;
  Best Local Similarity   93.5%;  Pred. No. 7.3e-140;
  Matches  686;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy       2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
              |||||||||||||||| || ||||| || ||||| |||||||||||||||||||||||||
Db          1 GGCATCCAGAGATCACTGTACGATCGCCCGGCCTCGTATAAGAAGAAATCTATGTTAGAC 60

Qy       2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
              ||||||||||||||||||||||||||| |||||||||||||||||| |||||||||
Db         61 TCAGAAGTCAAAAACCTCCTTTCAGATGACAACTCAGAAGGCCTTACTTTGTTGGATTTG 120

Qy       2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        121 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCCAAAAATTGTGTC 180

Qy       2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
              ||||| || |||||||||||||| |||||||| |||||||| || ||||||||||||||||
Db        181 CACCGGGACCTGGCTGCTCGCAATGTCCTCCTAGCACAAGGGAAGATTGTGAAGATCTGT 240

Qy       2644 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2703
              |||||||||||||||| |||||||||| |||||||||| |||||||| ||||| |||
Db        241 GACTTTGGCCTGGCCAGGGACATCATGCACGATTCGAACTACGTGTCGAAGGGCAGCACC 300

Qy       2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
              || || || |||||||||||||| || ||||||||||||||||||||||||||||| |||
Db        301 TTCCTTCCTGTGAAGTGGATGGCCCCGGAGAGCATCTTTGACAACCTCTACACCACGCTG 360

Qy       2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
              || |||||||||||||||| |||||||||||||||||||| |||||||||| ||
Db        361 AGCGATGTCTGGTCTTATGGGATTCTGCTCTGGGAGATCTTTTCTCTTGGTGGCACACCC 420

Qy       2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
              ||||| |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        421 TACCCTGGCATGATGGTGGATTCTACTTTCTACAACAAGATCAAGAGTGGGTACCGGATG 480

Qy       2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
              |||||||||||||| || |||||||||||||| |||||||||| | ||||||||||
Db        481 GCCAAGCCTGACCATGCCACCAGTGAAGTCTATGAGATCATGGTGCAGTGCTGGAACAGT 540

Qy       2944 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3003
              ||||| |||||||||||||||| |||||||||| ||||| |||||||||| ||||||
Db        541 GAGCCAGAGAAGAGACCCTCCTTCTACCACCTGAGCGAGATAGTGGAGAATCTTCTGCCT 600

Qy       3004 GGACAATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGACAGTATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCC 660

Qy       3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        661 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGCGTCACCTACAAAAAT 720

Qy       3124 GAGGAAGACAAGCT 3137
              || ||||||||||||
Db        721 GAAGAAGACAAGCT 734


RESULT 41
CK781356
LOCUS       CK781356                789 bp    mRNA    linear   EST 23-FEB-2004
DEFINITION  UI-M-GV0-clr-c-14-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
            IMAGE:30621661 5', mRNA sequence.
ACCESSION   CK781356
VERSION     CK781356.1  GI:42747034
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .789
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30621661"
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/tissue_type="whole brain"
/dev_stage="1,5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GV0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction,ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 10.2%; Score 656.4; DB 7; Length 789;
Best Local Similarity 89.4%; Pred. No. 1.1e-139;
Matches 705; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Qy       1986 CCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAG 2045
             |||||||||||||||| ||||| || || |||||||||| |||||||| ||||| || ||
Db          1 CCGGTCCCAACCTGTAATGAAGGTGGCTGTGAAGATGCTCAAACCCACAGCCAGGTCTAG 60

Qy       2046 TGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAA 2105
             |||||| || |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 TGAAAAGCAGGCTCTCATGTCTGAGCTGAAGATAATGACTCACCTGGGGCCACATTTGAA 120

Qy       2106 CATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTA 2165
             |||||| |||||||||||||||||||||||||||| |||||||||||||||||| ||
Db        121 CATTGTGAACTTGCTGGGAGCCTGCACCAAGTCAGGTCCCATTTACATCATCACAGAATA 180

Qy       2166 TTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCA 2225
             |||||||||| |||||||||||||| |||||||||| || ||||||||| |||||||
Db        181 CTGCTTCTATGGGGATTTGGTCAACTACTTGCATAAGAACAGAGATAGCTTCATGAGCCA 240

Qy       2226 CCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAG 2285
             |||||||||||||| |||||||| ||||| |||||||||||||| ||||| || || ||
Db        241 ACACCCAGAGAAGCCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGCAGACGAGAG 300

Qy       2286 CACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCA 2345
             |||| | || ||||| ||||| |||||||||||| || || ||||||||||||||||||||
Db        301 CACAAGAAGTTATGTGATTTTGTCTTTTGAAAATAACGGCGACTACATGGACATGAAGCA 360

Qy       2346 GGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGA 2405
             |||||||| |||||||||||||||||||| ||||||||||||||||||||||| || ||
Db        361 AGCTGATACCACACAGTATGTCCCCATGCTTGAAAGGAAAGAGGTTTCTAAATACTCTGA 420

Qy       2406 CATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTC 2465
             |||||||||||| || || ||||| |||||||| || |||||||||| ||| |||||||
Db        421 CATCCAGAGATCGCTGTACGATCGGCCAGCCTCCTACAAGAAGAAATCCATGCTAGACTC 480

Qy       2466 AGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTT 2525
             |||||||||||||||||||| || ||| |||| || || || |||||  ||||| | ||
Db        481 AGAAGTCAAAAACCTCCTTTCGGACGATGACTCCGAGGGTCTGACTTTGCTGGATCTATT 540

Qy       2526 GAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCA 2585
             |||||||||||||||||||| |||||||||| |||||||||| ||||||||||||||||
Db        541 GAGCTTCACCTATCAAGTTGCTCGAGGAATGGAATTTTTGGCTTCGAAAAATTGTGTCCA 600

Qy       2586 CCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGA 2645
             ||| || |||||||| |||||||||||||||||| || ||||||||||||||||||||||
Db        601 CCGGGACCTGGCTGCCCGCAACGTCCTCCTGGCGCANGGAAAAATTGTGAAGATCTGTGA 660

Qy       2646 CTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTT 2705
             |||||||||| |||||||||||||||| ||||| ||||| |||||  |||||||||| ||
Db        661 TTTTGGCCTGGGCAGAGACATCATGCACGATTCCAACTACGTGTCANAAGGCAGTACTTT 720
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Qy       2706 TCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAG 2765
             ||||| |||||||||||||| || |||||||||| ||| |||||||||||| |||||
Db        721 CCTGCCTGTGAAGTGGATGGCACCCGAGAGCATCTTCGACNACCTCTACACCACGCTGAG 780

Qy       2766 TGATGTCTG 2774
             ||| |||||
Db        781 TGACGTCTG 789
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RESULT 42
BQ003864/c
LOCUS BQ003864 656 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-EI1-azf-j-21-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone IMAGE:5848052 3', mRNA sequence.
ACCESSION BQ003864
VERSION BQ003864.1 GI:19728764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 656)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 1-54, >AT_rich#Low_complexity (matched compliment) 192-219, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .656
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5848052"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EI1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EI1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGCAC.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-EI1
TAG_SEQ=ACACTTGCAC"

ORIGIN

Query Match 10.2%; Score 653.4; DB 3; Length 656;
Best Local Similarity 99.7%; Pred. No. 5.4e-139;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       5742 TCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGT 5801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 TCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGT 597

Qy       5802 GTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAA 5861
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        596 GTGTTTTCAGCAAATTCCAGATTTGTTTCCTTNTGGCCTCCTGCAAAGTCTCCAGAAGAA 537

Qy       5862 AATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAA 5921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 AATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAA 477

Qy       5922 CACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGT 5981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 CACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGT 417

Qy       5982 ACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATA 6041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATA 357

Qy       6042 TGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTG 6101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTG 297

Qy       6102 TATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGT 6161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGT 237

Qy       6162 TGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACAT 6221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 TGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACAT 177

Qy       6222 GTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAA 6281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 GTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAA 117

Qy       6282 TACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGA 6341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 TACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGA 57

Qy       6342 TCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAA 6397
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         56 TCTTTATATTTCAATAAATGATATATAATTTAAAGTTTAAAAAAAAAAAAAAAAAA 1
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RESULT 43
AI857848/c
LOCUS AI857848 699 bp mRNA linear EST 07-MAR-2000
DEFINITION wl23b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425715 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI857848
VERSION AI857848.1 GI:5511464
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 699)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2085 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
FEATURES Location/Qualifiers
source 1. .699
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2425715"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
ORIGIN

Query Match 10.1%; Score 644.6; DB 1; Length 699;
Best Local Similarity 96.7%; Pred. No. 5.8e-137;
Matches 678; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy       5692 AGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTA 5751
             |||| ||||||||| |||||| |||||||||||||     |||   |||||||  ||||||
Db        699 AGCCCTGCATGACA-CATGAGCCCGGATGAAACTTTCAGGTCAGCCAGTTTCAGGTCCTA 641

Qy       5752 ACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAG 5811
             |||||||||||||||||| |||||||||||||||||||||||||||| | ||||
Db        640 ACAAATGCTCCCACCTGATTTTGTATATGACTGCATTTGTGNGTGTGTGTGTG-TNTCAG 582

Qy       5812 CAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAAATTTGCCAA 5871
             |||||||    ||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        581 CAAATTCAGATTTGTTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAAATTTGCCAA 522

Qy       5872 TCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGT 5931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 TCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGT 462

Qy       5932 GACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGT 5991
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGT 402

Qy       5992 CCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATG 6051
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 CCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATG 342

Qy       6052 TATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCC 6111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 TATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCC 282

Qy       6112 TTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTG 6171
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 TTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTG 222

Qy       6172 AATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAA 6231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 AATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAC 162

Qy       6232 CAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGT 6291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 CAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGT 102

Qy       6292 ATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATT 6351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATT 42

Qy       6352 TCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAA 6392
             ||||||||||||||||||||||||||||||||||||||||||
Db         41 TCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAA 1
```

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RESULT 44
BQ884103
LOCUS       BQ884103                 931 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8681893 Lupski_sciatic_nerve Homo sapiens cDNA clone
            IMAGE:6197264 5', mRNA sequence.
ACCESSION   BQ884103
VERSION     BQ884103.1  GI:22276111
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 931)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13607  row: a  column: 09
            High quality sequence stop: 511.
FEATURES             Location/Qualifiers
     source          1. .931
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6197264"
                     /sex="male"
                     /tissue_type="sciatic nerve"
                     /dev_stage="adult, 70 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_sciatic_nerve"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.87 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated  by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match           10.0%;  Score 644.2;  DB 5;  Length 931;
  Best Local Similarity   95.1%;  Pred. No. 7.7e-137;
  Matches  697;  Conservative    0;  Mismatches   33;  Indels    3;  Gaps    3;

Qy       5545 AACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTA 5604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 AACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTA 71

Qy       5605 GAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTT 5664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 GAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTT 131

Qy       5665 GGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAAC 5724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAAC 191

Qy       5725 TTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTG 5784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 TTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTG 251

Qy       5785 CATTTGTGGGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTG 5844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 CATTTGTGGGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTG 311

Qy       5845 CAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATC 5904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 CAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATC 371

Qy       5905 AAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAAT 5964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAAT 431

Qy       5965 GTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAAT 6024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAAT 491

Qy       6025 GATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAA 6084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        492 GATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCCAA 551

Qy       6085 ACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCC 6144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 ACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCC 611

Qy       6145 ACA-GGCACATTAACTGTTGCACTTTTGAAT-GTCCAAAATTTATATTTTAGAAATAATA 6202
             ||| ||||| ||||||| ||  ||||||||| |||||||||||||||||||||||| ||
Db        612 ACAGGGCACCTTAACTGGTGGCCTTTTGAATGGTCCAAAATTTATATTTTAGAAATATTA 671

Qy       6203 AAAA-GAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACT 6261
             |||| ||||||| ||| |||| |||| |||  | ||   || |    || | | |  |
Db        672 AAAAGGAAAGATCCTTCCATGGTCCCCAAAACAAGGGTGGGGGGGAATGGGTGGAGCAAA 731

Qy       6262 AACTTGATAGGGT 6274
             ||||   | || |
Db        732 AACTAACTTGGAT 744


RESULT 45
AI672567/c
LOCUS       AI672567                 669 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wb32g09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307424 3'
            similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI672567
VERSION     AI672567.1  GI:4852298
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1364   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="IMAGE:2307424"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 10.0%; Score 642; DB 1; Length 669;
Best Local Similarity 99.3%; Pred. No. 2.3e-136;
Matches 664; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Qy       5714 CCGGATGAAACTTCTCAGT-CCAGCAGTTT-CCAGTCCTAACAAATGCTCCCACCTGAAT 5771
             |||||||||||||||||||| |||||||||| |||||||||||||||||||||||||| |||||
Db        669 CCGGATGAAACTTCTCAGTNCCAGCAGTTTCCCAGTCCTAACAAATGCTCCCACNTGAAT 610

Qy       5772 TTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCC 5831
             ||||||||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db        609 TTGTATATGACTGCATTTGTGNGTGTGTGTGTNTTCAGCAAATTCCAGATTTGTTTCC 550

Qy       5832 TTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTT 5891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 TTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTT 490

Qy       5892 TATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTG 5951
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTG 430

Qy       5952 ATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGA 6011
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 ATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGA 370

Qy       6012 CATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGA 6071
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGA 310

Qy       6072 GAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAAC 6131
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Db        309 GAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAAC 250

Qy       6132 TGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTT 6191
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 TGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTT 190

Qy       6192 TAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGT 6251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGT 130

Qy       6252 GAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCA 6311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCA 70

Qy       6312 TGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATT 6371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 TGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATT 10

Qy       6372 TAAAGTTAA 6380
             |||||||||
Db          9 TAAAGTTAA 1
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RESULT 46
AI422895/c
LOCUS AI422895 730 bp mRNA linear EST 30-MAR-1999
DEFINITION tf30g02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2097746 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI422895
VERSION AI422895.1 GI:4268826
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1552 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 364.
FEATURES Location/Qualifiers
source 1. .730
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2097746"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 10.0%; Score 641; DB 1; Length 730;
Best Local Similarity 95.7%; Pred. No. 4e-136;
Matches 689; Conservative 0; Mismatches 28; Indels 3; Gaps 3;

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Qy       5659 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 5718
             ||  |||||| |       ||     |||||||||||| |||||| ||||||||| | |||
Db        717 TTATTTGGTGGTGCTTGCATTTGATATGCTGTGAGCCNTGCATG-CATCATGAGCCNGGA 659

Qy       5719 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 5778
             || |||||||  ||||||||||||||||||||| |||||||||||||||| ||||||||
Db        658 TG-AACTTCTAGGTCCAGCAGTTTCCAGTCCTAAC-AATGCTCCCACCTGATTTTGTATA 601

Qy       5779 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 5838
             |||||||||||||||||||||||||||||      ||||||  ||||||||||||||||||
Db        600 TGACTGCATTTGTGGGTGTGTGTGTGTTTCAGCAAAATTCANGATTTGTTTCCTTTTGGC 541

Qy       5839 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 481

Qy       5899 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 5958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 421
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Qy       5959 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 6018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 361

Qy       6019 TAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACT 6078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         360 TAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACT 301

Qy       6079 GCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATA 6138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         300 GCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATA 241

Qy       6139 ATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAAT 6198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         240 ATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAAT 181

Qy       6199 AATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAA 6258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         180 AATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAA 121

Qy       6259 ACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTT 6318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         120 ACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTT 61

Qy       6319 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 6378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          60 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 1
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RESULT 47
CN483903

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LOCUS       CN483903                640 bp    mRNA    linear   EST 26-APR-2004
DEFINITION  hw39g04.y2 Human primary human ocular pericytes. Unamplified (hw)
            Homo sapiens cDNA clone hw39g04 5', mRNA sequence.
ACCESSION   CN483903
VERSION     CN483903.1  GI:46565407
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Tsai,J.Y. and Wistow,G.
  TITLE     Expressed sequence tag analysis of cultured primary human ocular
            pericytes
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 39  row: g  column: 04
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="hw39g04"
                     /cell_type="pericytes"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Human primary human ocular pericytes.
                     Unamplified (hw)"
                     /note="Organ: Eye; Vector: pSport1; RNA was extracted from
                     primary human pericytes in culture. A directionally cloned
                     cDNA library in the pSPORT1 vector (Invitrogen) was
                     constructed at Bioserve Biotechnology (Laurel MD)
                     essentially following the protocols of the SuperScript
                     Plasmid System full details of which are contained in the
                     manufacturer's Instruction manual
                     (http://www.lifetech.com/). First strand synthesis was
                     carried out using a Not I primer-adapter
                     [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. cDNA was
                     cloned in Not I/Sal I sites. EST analysis was performed at
                     the NIH Intramural Sequencing Center (NISC)."
ORIGIN
```

```
  Query Match             10.0%;  Score 640;  DB 7;  Length 640;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-136;
  Matches  640;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5169 AAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAA 5228
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Db          1 AAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAA 60

Qy       5229 AAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCT 5288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCT 120

Qy       5289 ATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAAT 5348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAAT 180

Qy       5349 TGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCA 5408
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCA 240

Qy       5409 GATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAAT 5468
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Db        241 GATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAAT 300

Qy       5469 CTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCC 5528
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCC 360

Qy       5529 AGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAA 5588
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAA 420

Qy       5589 TACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGT 5648
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Db        421 TACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGT 480

Qy       5649 ACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCA 5708
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCA 540

Qy       5709 TGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTG 5768
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTG 600

Qy       5769 AATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 5808
             |||||||||||||||||||||||||||||||||||||||||
Db        601 AATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 640
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RESULT 48
BU623579/c

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LOCUS       BU623579                686 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FG1-bgg-j-03-0-UI.s1 NCI_CGAP_FG1 Homo sapiens cDNA clone
            UI-H-FG1-bgg-j-03-0-UI 3', mRNA sequence.
ACCESSION   BU623579
VERSION     BU623579.1  GI:23289794
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 686)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
```

```
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .686
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FG1-bgg-j-03-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FG1"
                     /note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FG1 is a normalized cDNA library obtained from a
                     pool of mRNA from 2 cell lines from Enchondroma tissues.
                     The library was constructed according to Bonaldo, Lennon
                     and Soares, Genome Research, 6:791-806, 1996. First strand
                     cDNA synthesis was primed with an oligo-dT primer
                     containing a Not I site.  Double stranded cDNA was ligated
                     to an EcoR I adaptor, digested with Not I, and cloned
                     directionally into pT7T3-Pac vector. The oligonucleotide
                     used to prime the synthesis of first-strand cDNA contains
                     a library tag sequence that is located between the Not I
                     site and the (dT)18 tail. The sequence tag for this
                     library is CGGTCACTC. The cell lines were provided by Dr.
                     James Martin from the University of Iowa.
                     TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
                     TAG_LIB=UI-H-FG1
                     TAG_SEQ=CGGTCACTC"
ORIGIN

  Query Match             9.9%;  Score 632.6;  DB 5;  Length 686;
  Best Local Similarity   98.6%;  Pred. No. 3.4e-134;
  Matches  638;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        895 GTGAAAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTG 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 GTGAAAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTG 627

Qy        955 TACACTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCC 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 TACACTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCC 567

Qy       1015 CGCCAGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAA 1074
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CGCCAGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAA 507

Qy       1075 GGTTTCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTC 1134
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GGGTTCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTC 447

Qy       1135 AAACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAAC 1194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 AAACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAAC 387

Qy       1195 AATCTGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAA 1254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AATCTGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAA 327

Qy       1255 ATAAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTAT 1314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 ATAAGGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTAT 267
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Qy       1315 ACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAA 1374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 ACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAA 207

Qy       1375 GTTCCTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACG 1434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTTCCTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACG 147

Qy       1435 GTGAGGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGAT 1494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GTGAGGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGAT 87

Qy       1495 ATTAAGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAA 1541
              ||||||||||||||||||||||||||||||| |   ||  | || ||
Db          86 ATTAAGAAATGTAATAATGAAACTTCCTGGAATCCATTTTCTAAAAA 40
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RESULT 49
BQ442880
LOCUS       BQ442880                 802 bp    mRNA    linear   EST 29-MAY-2002
DEFINITION  UI-M-EV0-bxf-c-18-0-UI.r1 NIH_BMAP_EV0 Mus musculus cDNA clone
            IMAGE:5707337 5', mRNA sequence.
ACCESSION   BQ442880
VERSION     BQ442880.1  GI:21245992
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 802)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, Univeristy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
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                     Site_2: Not I; The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured mRNa was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was size selected according to mRNA size fraction,
                     ligated with EcoR I adaptor, digested with Not I, and then
                     cloned directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA
                     tail, is GTGCGTGGAA. This library was created for the
                     University of Iowa Mouse Brain Molecular Anatomy Project
                     (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                     System', supported by National Instututes of Mental Health
                     (NIMH), Hemin Chin, Ph.D., program coordinator."
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ORIGIN

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RESULT 50
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DEFINITION  9079 Full Length cDNA from the Mammalian Gene Collection Homo
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ACCESSION   CV030074
VERSION     CV030074.1  GI:51488295
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
            Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
            Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
            Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
            Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
  TITLE     Human ORFeome Version 1.1: a Platform for Reverse Proteomics
  JOURNAL   Genome Res. (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
            results from a PCR reaction using an MGC full-length cDNA as
            template DNA and ORF specific primers
            PCR PRimers
            FORWARD: ATGGGGACTTCCCATCCG
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                      Donor vector. Reference : MGC (Mammalian Gene Collection)
                      Program Team, Generation and Initial Analysis of more than
                      15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
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ORIGIN

  Query Match             9.8%;  Score 627.6;  DB 7;  Length 642;
  Best Local Similarity   99.4%;  Pred. No. 4.7e-133;
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Job time : 15308 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:39:07 ; Search time 722 Seconds
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6399.4	99.8	6412	3	US-09-769-987-1	Sequence 1, Appli
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3	6364.4	99.2	6378	3	US-09-919-497-40	Sequence 40, Appl
4	6364.4	99.2	6378	3	US-09-949-016-832	Sequence 832, App
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6	4777	74.5	6373	3	US-08-461-917-1	Sequence 1, Appli
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10	4765.6	74.3	6375	2	US-08-460-510-5	Sequence 5, Appli
11	4765.6	74.3	6375	2	US-08-460-490-5	Sequence 5, Appli
12	4765.6	74.3	6375	6	PCT-US92-00730-5	Sequence 5, Appli
13	4765.6	74.3	6375	6	PCT-US92-00862-5	Sequence 5, Appli
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15	4037.2	63.0	4100	2	US-08-460-510-3	Sequence 3, Appli
16	4037.2	63.0	4100	2	US-08-460-490-3	Sequence 3, Appli
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19	3838.8	59.9	4054	2	US-08-180-195-35	Sequence 35, Appl
20	3838.8	59.9	4054	2	US-08-477-329-35	Sequence 35, Appl
21	3838.8	59.9	4054	2	US-08-475-458-35	Sequence 35, Appl
22	3838.8	59.9	4054	3	US-08-980-400-35	Sequence 35, Appl
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108	220	3.4	4111	3	US-09-375-248-1	Sequence 1, Appli
109	220	3.4	4195	2	US-08-340-011-1	Sequence 1, Appli
110	220	3.4	4195	3	US-08-901-710-1	Sequence 1, Appli
111	220	3.4	4195	3	US-09-169-079-1	Sequence 1, Appli
112	220	3.4	4416	3	US-08-795-430-1	Sequence 1, Appli
113	220	3.4	4416	3	US-09-355-700-1	Sequence 1, Appli
114	220	3.4	4416	3	US-08-601-132-36	Sequence 36, Appl
115	220	3.4	4416	3	US-08-671-573B-36	Sequence 36, Appl
116	220	3.4	4416	3	US-09-631-092B-36	Sequence 36, Appl
117	220	3.4	4416	3	US-09-534-376A-1	Sequence 1, Appli
118	220	3.4	4425	2	US-08-222-616-31	Sequence 31, Appl
119	220	3.4	4425	3	US-08-446-648-31	Sequence 31, Appl
120	220	3.4	4425	3	US-09-023-655-889	Sequence 889, App
121	220	3.4	4425	3	US-09-982-610-31	Sequence 31, Appl
122	220	3.4	4425	6	PCT-US95-04228-31	Sequence 31, Appl
123	220	3.4	4795	2	US-08-340-011-3	Sequence 3, Appli
124	220	3.4	4795	3	US-08-901-710-3	Sequence 3, Appli
125	220	3.4	4795	3	US-09-169-079-3	Sequence 3, Appli
126	220	3.4	5406	2	US-07-813-593-3	Sequence 3, Appli
127	220	3.4	5406	2	US-07-977-451-5	Sequence 5, Appli
128	220	3.4	5406	2	US-07-946-507-3	Sequence 3, Appli
129	220	3.4	5406	2	US-08-252-517-5	Sequence 5, Appli
130	220	3.4	5406	2	US-07-906-397A-5	Sequence 5, Appli
131	220	3.4	5406	2	US-08-601-891-5	Sequence 5, Appli
132	220	3.4	5406	2	US-09-021-324-5	Sequence 5, Appli
133	220	3.4	5406	3	US-09-872-136B-5	Sequence 5, Appli
134	220	3.4	5406	3	US-09-919-408A-5	Sequence 5, Appli
135	220	3.4	5406	6	PCT-US92-02750-7	Sequence 7, Appli
136	220	3.4	5406	6	PCT-US92-05401-5	Sequence 5, Appli
137	220	3.4	5406	6	PCT-US92-09893-5	Sequence 5, Appli
138	220	3.4	5470	2	US-08-443-861-1	Sequence 1, Appli
139	220	3.4	5470	3	US-08-193-829B-1	Sequence 1, Appli
140	220	3.4	5470	3	US-09-967-655-10	Sequence 10, Appl
141	220	3.4	5470	3	US-09-766-678-1	Sequence 1, Appli
c 142	220	3.4	6827	2	US-08-222-616-17	Sequence 17, Appl
c 143	220	3.4	6827	3	US-08-446-648-17	Sequence 17, Appl
c 144	220	3.4	6827	3	US-09-982-610-17	Sequence 17, Appl
c 145	220	3.4	6827	6	PCT-US95-04228-17	Sequence 17, Appl
146	220	3.4	9108	3	US-08-446-648-45	Sequence 45, Appl
147	220	3.4	9108	3	US-09-982-610-45	Sequence 45, Appl
148	220	3.4	9108	6	PCT-US95-04228-45	Sequence 45, Appl
149	213.4	3.3	4014	3	US-09-119-014D-5	Sequence 5, Appli
150	213.4	3.3	7680	3	US-09-953-318-3	Sequence 3, Appli
151	213.4	3.3	7718	3	US-09-976-594-244	Sequence 244, App
152	211.4	3.3	1894	3	US-07-912-122-3	Sequence 3, Appli
153	211.4	3.3	1894	6	PCT-US93-06404-3	Sequence 3, Appli
154	204.2	3.2	6055	3	US-09-953-318-10	Sequence 10, Appl
155	199.4	3.1	4071	3	US-09-098-707A-1	Sequence 1, Appli
156	199.4	3.1	4071	3	US-09-483-539-1	Sequence 1, Appli
157	199.4	3.1	4071	3	US-10-100-405A-1	Sequence 1, Appli
158	199.4	3.1	4071	3	US-10-022-939-1	Sequence 1, Appli
159	199.4	3.1	5830	3	US-09-967-655-3	Sequence 3, Appli
160	199.4	3.1	5830	3	US-09-949-016-327	Sequence 327, App
161	199.4	3.1	5831	3	US-09-949-016-3982	Sequence 3982, Ap
162	198	3.1	4236	2	US-08-810-116-7	Sequence 7, Appli
163	198	3.1	4236	2	US-07-930-548A-7	Sequence 7, Appli
164	196.8	3.1	601	3	US-09-949-016-34259	Sequence 34259, A
165	196.8	3.1	601	3	US-09-949-016-58538	Sequence 58538, A
166	193.4	3.0	2449	3	US-09-949-016-1248	Sequence 1248, Ap
167	193.4	3.0	5993	3	US-09-383-630-1	Sequence 1, Appli
168	193.4	3.0	5993	3	US-09-383-630-2	Sequence 2, Appli
169	185	2.9	2049	3	US-09-099-749-10	Sequence 10, Appl
170	184.4	2.9	933	2	US-08-701-191A-4	Sequence 4, Appli
171	184.4	2.9	933	3	US-09-664-526-4	Sequence 4, Appli
172	184.4	2.9	1056	2	US-08-701-191A-5	Sequence 5, Appli
173	184.4	2.9	1056	3	US-09-664-526-5	Sequence 5, Appli
174	184.4	2.9	2360	3	US-09-023-655-1288	Sequence 1288, Ap
175	184.4	2.9	2469	2	US-07-997-133-2	Sequence 2, Appli
176	184.4	2.9	2469	6	US-07-997-133-2	Sequence 2, Appli
177	184.4	2.9	2662	2	US-08-451-822A-14	Sequence 14, Appl
178	184.4	2.9	2662	3	US-08-323-430-14	Sequence 14, Appl
179	184.4	2.9	2733	2	US-08-371-001-14	Sequence 14, Appl
180	184.4	2.9	2733	6	PCT-US96-00331-14	Sequence 14, Appl
181	182.8	2.9	2469	2	US-08-459-296-1	Sequence 1, Appli
182	180.4	2.8	1875	2	US-08-070-165F-3	Sequence 3, Appli
183	180.4	2.8	1875	2	US-08-885-418-3	Sequence 3, Appli
184	178.6	2.8	3306	3	US-09-954-556-10	Sequence 10, Appl
185	177.4	2.8	3503	2	US-07-631-717A-1	Sequence 1, Appli
186	177.4	2.8	3503	2	US-08-166-717D-1	Sequence 1, Appli
187	176	2.7	2903	3	US-09-949-016-5033	Sequence 5033, Ap
188	173.6	2.7	2675	2	US-08-070-165F-5	Sequence 5, Appli
189	173.6	2.7	2675	2	US-08-885-418-5	Sequence 5, Appli
190	173.6	2.7	2681	2	US-08-070-165F-9	Sequence 9, Appli
191	173.6	2.7	2681	2	US-08-885-418-9	Sequence 9, Appli
192	167.4	2.6	8083	3	US-09-383-630-4	Sequence 4, Appli
193	167.4	2.6	8083	3	US-09-383-630-5	Sequence 5, Appli
194	164.8	2.6	4890	3	US-09-677-046A-3	Sequence 3, Appli
195	162.6	2.5	2387	3	US-09-949-016-2268	Sequence 2268, Ap
196	162.4	2.5	1839	2	US-08-070-165F-7	Sequence 7, Appli
197	162.4	2.5	1839	2	US-08-885-418-7	Sequence 7, Appli
198	159.4	2.5	2310	2	US-08-471-570-9	Sequence 9, Appli
199	159.4	2.5	2650	3	US-09-954-556-28	Sequence 28, Appl
200	159.4	2.5	2676	2	US-08-471-570-7	Sequence 7, Appli
201	159.4	2.5	3080	3	US-09-954-556-25	Sequence 25, Appl
202	159.4	2.5	3244	3	US-09-954-556-24	Sequence 24, Appl
203	159.4	2.5	3416	2	US-08-451-822A-15	Sequence 15, Appl
204	159.4	2.5	3416	3	US-08-323-430-15	Sequence 15, Appl
205	159.4	2.5	4268	3	US-09-954-556-3	Sequence 3, Appli
206	159.2	2.5	3025	3	US-09-954-556-23	Sequence 23, Appl
207	158.8	2.5	2923	3	US-09-954-556-20	Sequence 20, Appl
208	157.8	2.5	2826	3	US-09-954-556-21	Sequence 21, Appl
209	157.8	2.5	2868	3	US-09-954-556-19	Sequence 19, Appl
210	157.8	2.5	2941	3	US-09-954-556-18	Sequence 18, Appl
211	157.2	2.5	601	3	US-09-949-016-34267	Sequence 34267, A
212	157.2	2.5	601	3	US-09-949-016-58546	Sequence 58546, A
213	155.4	2.4	4943	3	US-09-677-046A-7	Sequence 7, Appli
214	155.4	2.4	5170	3	US-09-677-046A-5	Sequence 5, Appli
215	155.4	2.4	5220	3	US-09-677-046A-1	Sequence 1, Appli
216	155.2	2.4	3944	3	US-09-949-016-1876	Sequence 1876, Ap
217	155.2	2.4	3944	3	US-09-949-016-1877	Sequence 1877, Ap
218	155.2	2.4	3944	3	US-09-949-016-1878	Sequence 1878, Ap
219	155.2	2.4	3944	3	US-09-949-016-1879	Sequence 1879, Ap
220	155.2	2.4	3944	3	US-09-949-016-1880	Sequence 1880, Ap
221	155.2	2.4	3944	3	US-09-949-016-1881	Sequence 1881, Ap
222	155.2	2.4	3944	3	US-09-949-016-1882	Sequence 1882, Ap
223	155.2	2.4	3944	3	US-09-949-016-1883	Sequence 1883, Ap
224	146	2.3	4209	3	US-09-949-016-1101	Sequence 1101, Ap
225	146	2.3	4383	3	US-09-949-016-54	Sequence 54, Appl
226	146	2.3	4384	3	US-09-949-016-1800	Sequence 1800, Ap
227	146	2.3	4384	3	US-09-949-016-1801	Sequence 1801, Ap
228	146	2.3	4384	3	US-09-949-016-1802	Sequence 1802, Ap
229	146	2.3	4384	3	US-09-949-016-1803	Sequence 1803, Ap
230	146	2.3	4508	6	PCT-US93-06251-34	Sequence 34, Appl
231	146	2.3	5615	3	US-09-949-016-1104	Sequence 1104, Ap
232	146	2.3	5616	3	US-09-949-016-2895	Sequence 2895, Ap
233	146	2.3	5616	3	US-09-949-016-2896	Sequence 2896, Ap
234	146	2.3	5616	3	US-09-949-016-2897	Sequence 2897, Ap
235	146	2.3	5616	3	US-09-949-016-2898	Sequence 2898, Ap
236	146	2.3	7003	3	US-09-949-016-1102	Sequence 1102, Ap
237	146	2.3	7005	3	US-09-949-016-2891	Sequence 2891, Ap
238	146	2.3	7005	3	US-09-949-016-2892	Sequence 2892, Ap
239	146	2.3	7005	3	US-09-949-016-2893	Sequence 2893, Ap
240	146	2.3	7005	3	US-09-949-016-2894	Sequence 2894, Ap
241	133.2	2.1	1683	3	US-09-866-510-23	Sequence 23, Appl
242	125.6	2.0	601	3	US-09-949-016-34276	Sequence 34276, A
243	125.6	2.0	601	3	US-09-949-016-58555	Sequence 58555, A

244	124.8	1.9	873	3	US-09-949-016-5347	Sequence 5347, Ap
245	121.2	1.9	2742	2	US-08-286-305A-2	Sequence 2, Appli
246	121.2	1.9	2742	2	US-08-441-104A-2	Sequence 2, Appli
247	121.2	1.9	2742	2	US-08-440-816A-2	Sequence 2, Appli
248	121.2	1.9	2742	3	US-09-417-381A-2	Sequence 2, Appli
249	121.2	1.9	3611	2	US-08-445-640-1	Sequence 1, Appli
250	121.2	1.9	3611	3	US-08-170-558-1	Sequence 1, Appli
251	121.2	1.9	3611	3	US-08-447-314-1	Sequence 1, Appli
252	121.2	1.9	3611	3	US-08-445-461-1	Sequence 1, Appli
253	121.2	1.9	3611	3	US-09-223-490-1	Sequence 1, Appli
254	118.8	1.9	2674	3	US-09-817-180-1	Sequence 1, Appli
255	118.8	1.9	2674	3	US-10-003-295-1	Sequence 1, Appli
256	116.4	1.8	3785	2	US-08-445-640-9	Sequence 9, Appli
257	116.4	1.8	3785	3	US-08-170-558-9	Sequence 9, Appli
258	116.4	1.8	3785	3	US-08-447-314-9	Sequence 9, Appli
259	116.4	1.8	3785	3	US-08-445-461-9	Sequence 9, Appli
260	116.4	1.8	3785	3	US-09-223-490-9	Sequence 9, Appli
261	116	1.8	4541	3	US-09-949-002-58	Sequence 58, Appl
262	112.6	1.8	2869	2	US-08-374-834-2	Sequence 2, Appli
263	112.6	1.8	2869	2	US-08-644-271-2	Sequence 2, Appli
264	112.6	1.8	2869	3	US-09-077-955-2	Sequence 2, Appli
265	112.6	1.8	2869	3	US-10-016-283-2	Sequence 2, Appli
266	111.8	1.7	2440	2	US-08-160-861-2	Sequence 2, Appli
267	111.8	1.7	2442	2	US-08-542-363-3	Sequence 3, Appli
268	111.8	1.7	2442	3	US-09-100-089-3	Sequence 3, Appli
269	111.8	1.7	2442	3	US-09-670-827-3	Sequence 3, Appli
270	111.8	1.7	2442	3	US-09-827-949-3	Sequence 3, Appli
271	111.8	1.7	2608	2	US-08-160-861-1	Sequence 1, Appli
272	111.8	1.7	6226	2	US-08-542-363-1	Sequence 1, Appli
273	111.8	1.7	6226	3	US-09-100-089-1	Sequence 1, Appli
274	111.8	1.7	6226	3	US-09-670-827-1	Sequence 1, Appli
275	111.8	1.7	6226	3	US-09-827-949-1	Sequence 1, Appli
276	111.6	1.7	3307	2	US-08-456-647B-5	Sequence 5, Appli
277	111.6	1.7	3307	2	US-08-237-401A-5	Sequence 5, Appli
278	110.4	1.7	3845	2	US-08-220-240A-4	Sequence 4, Appli
279	108.8	1.7	3845	3	US-09-949-016-1898	Sequence 1898, Ap
280	106.8	1.7	1891	3	US-09-949-016-1947	Sequence 1947, Ap
281	106	1.7	2208	6	PCT-US95-08493-1	Sequence 1, Appli
282	106	1.7	2580	6	PCT-US95-08493-18	Sequence 18, Appl
283	106	1.7	2604	6	PCT-US95-08493-20	Sequence 20, Appl
284	104.6	1.6	2015	3	US-09-023-655-1105	Sequence 1105, Ap
285	104.6	1.6	2015	3	US-10-007-010-3	Sequence 3, Appli
286	104.6	1.6	2056	3	US-09-949-016-4544	Sequence 4544, Ap
287	103.6	1.6	2607	3	US-09-715-249-7	Sequence 7, Appli
288	103.6	1.6	2610	2	US-08-374-834-17	Sequence 17, Appl
289	103.6	1.6	2610	2	US-08-644-271-28	Sequence 28, Appl
290	103.6	1.6	2610	3	US-09-077-955-32	Sequence 32, Appl
291	103.6	1.6	2610	3	US-10-016-283-32	Sequence 32, Appl
292	102.8	1.6	1548	3	US-09-099-053-1	Sequence 1, Appli
293	101.2	1.6	1467	3	US-09-579-182-2	Sequence 2, Appli
294	101.2	1.6	1590	2	US-08-278-089A-3	Sequence 3, Appli
295	101.2	1.6	1601	2	US-07-934-393B-3	Sequence 3, Appli
296	101.2	1.6	1601	2	US-08-838-957A-3	Sequence 3, Appli
297	101.2	1.6	4175	2	US-07-934-393B-1	Sequence 1, Appli
298	101.2	1.6	4175	2	US-08-278-089A-1	Sequence 1, Appli
299	101.2	1.6	4175	2	US-08-838-957A-1	Sequence 1, Appli
300	101.2	1.6	4176	2	US-08-278-089A-5	Sequence 5, Appli
301	101.2	1.6	4176	2	US-08-838-957A-5	Sequence 5, Appli
302	100.4	1.6	2301	2	US-08-306-691B-23	Sequence 23, Appl
303	100.4	1.6	2301	3	US-09-167-206-3	Sequence 3, Appli
304	100.4	1.6	2301	6	PCT-US93-06251-78	Sequence 78, Appl
305	100.4	1.6	2820	2	US-08-286-305A-4	Sequence 4, Appli
306	100.4	1.6	2820	2	US-08-441-104A-4	Sequence 4, Appli
307	100.4	1.6	2820	2	US-08-440-816A-4	Sequence 4, Appli
308	100.4	1.6	2820	3	US-09-417-381A-4	Sequence 4, Appli
309	100	1.6	2437	2	US-08-456-647B-3	Sequence 3, Appli
310	100	1.6	2437	2	US-08-237-401A-3	Sequence 3, Appli
311	99.8	1.6	1574	3	US-09-173-581-12	Sequence 12, Appl
312	99.8	1.6	1574	3	US-09-420-915-12	Sequence 12, Appl
313	99.8	1.6	4125	3	US-09-949-016-3697	Sequence 3697, Ap
314	99.2	1.5	2463	2	US-08-339-578-1	Sequence 1, Appli
315	98.4	1.5	4041	3	US-09-569-611C-1	Sequence 1, Appli
316	98.4	1.5	4866	3	US-09-949-016-4526	Sequence 4526, Ap
317	98.2	1.5	2129	3	US-09-016-434-1452	Sequence 1452, Ap
318	98.2	1.5	4138	2	US-08-323-474-1	Sequence 1, Appli
319	98.2	1.5	4138	3	US-09-949-016-75	Sequence 75, Appl
320	98.2	1.5	4138	6	PCT-US93-06093-1	Sequence 1, Appli
321	98	1.5	3321	2	US-08-484-438-5	Sequence 5, Appli
322	98	1.5	5484	3	US-09-632-580A-3	Sequence 3, Appli
323	98	1.5	5501	2	US-08-484-438-1	Sequence 1, Appli
324	98	1.5	5555	2	US-08-484-438-3	Sequence 3, Appli
325	96.8	1.5	2770	3	US-08-426-509A-5	Sequence 5, Appli
326	96.8	1.5	2770	3	US-08-232-545-5	Sequence 5, Appli
327	96.8	1.5	2770	3	US-09-977-261-5	Sequence 5, Appli
328	96.8	1.5	2770	6	PCT-US95-05008-5	Sequence 5, Appli
329	96.8	1.5	2863	3	US-09-023-655-1389	Sequence 1389, Ap
330	96.8	1.5	3227	2	US-08-372-892-3	Sequence 3, Appli
331	96.8	1.5	3227	3	US-09-919-497-2	Sequence 2, Appli
332	96.8	1.5	3254	2	US-08-372-892-1	Sequence 1, Appli
333	96.8	1.5	4987	3	US-09-949-016-1724	Sequence 1724, Ap
c 334	96.8	1.5	7607	2	US-08-222-616-19	Sequence 19, Appl
c 335	96.8	1.5	7607	3	US-08-446-648-19	Sequence 19, Appl
c 336	96.8	1.5	7607	3	US-09-982-610-19	Sequence 19, Appl
c 337	96.8	1.5	7607	6	PCT-US95-04228-19	Sequence 19, Appl
338	96	1.5	1212	3	US-08-485-393-3	Sequence 3, Appli
339	96	1.5	4149	2	US-08-737-715-1	Sequence 1, Appli
340	96	1.5	4723	3	US-09-023-655-1137	Sequence 1137, Ap
341	95.8	1.5	1398	2	US-08-604-989A-9	Sequence 9, Appli
342	95.8	1.5	1521	2	US-08-604-989A-10	Sequence 10, Appl
343	95.8	1.5	1713	3	US-09-741-154-1	Sequence 1, Appli
344	95.8	1.5	1713	3	US-10-187-900-1	Sequence 1, Appli
345	95.8	1.5	1942	2	US-08-604-989A-11	Sequence 11, Appl
346	95.8	1.5	2000	3	US-08-426-509A-1	Sequence 1, Appli
347	95.8	1.5	2000	3	US-08-232-545-1	Sequence 1, Appli
348	95.8	1.5	2000	3	US-09-977-261-1	Sequence 1, Appli
349	95.8	1.5	2000	6	PCT-US95-05008-1	Sequence 1, Appli
350	95.4	1.5	3398	6	PCT-US95-08493-12	Sequence 12, Appl
351	95.2	1.5	1374	3	US-09-949-016-2639	Sequence 2639, Ap
352	95.2	1.5	2827	3	US-08-492-723-1	Sequence 1, Appli
353	95.2	1.5	2940	2	US-08-286-305A-8	Sequence 8, Appli
354	95.2	1.5	2940	2	US-08-441-104A-8	Sequence 8, Appli
355	95.2	1.5	2940	2	US-08-440-816A-8	Sequence 8, Appli
356	95.2	1.5	2940	3	US-09-417-381A-8	Sequence 8, Appli
357	95.2	1.5	4626	2	US-08-306-691B-22	Sequence 22, Appl
358	95.2	1.5	4626	6	PCT-US93-06251-27	Sequence 27, Appl
359	94.8	1.5	738	2	US-08-604-989A-8	Sequence 8, Appli
360	94.8	1.5	2153	3	US-09-949-016-4896	Sequence 4896, Ap
361	94.8	1.5	2187	3	US-09-023-655-1267	Sequence 1267, Ap
362	94.8	1.5	2187	3	US-09-470-881-4	Sequence 4, Appli
363	94.8	1.5	3608	3	US-09-016-434-1408	Sequence 1408, Ap
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ALIGNMENTS

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; Sequence 1, Application US/09769987
; Patent No. 6660488
; GENERAL INFORMATION:
;  APPLICANT: Matsui, Toshimitsu
;  APPLICANT:  Aaronson, Stuart A.
;  APPLICANT:  Pierce, Jacalyn H.
;  TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
;  FILE REFERENCE: 14014.0266U2
;  CURRENT APPLICATION NUMBER: US/09/769,987
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 08/460,656
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: US 08/439,095
;  PRIOR FILING DATE: 1995-05-11
;  PRIOR APPLICATION NUMBER: US 07/915,884
;  PRIOR FILING DATE: 1992-07-20
;  PRIOR APPLICATION NUMBER: US 07/308,282
;  PRIOR FILING DATE: 1989-02-09
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6412
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. 6660488e =
;   OTHER INFORMATION: synthetic construct
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;   LOCATION: (139)...(3406)
US-09-769-987-1

  Query Match             99.8%;  Score 6399.4;  DB 3;  Length 6412;
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  Matches 6411;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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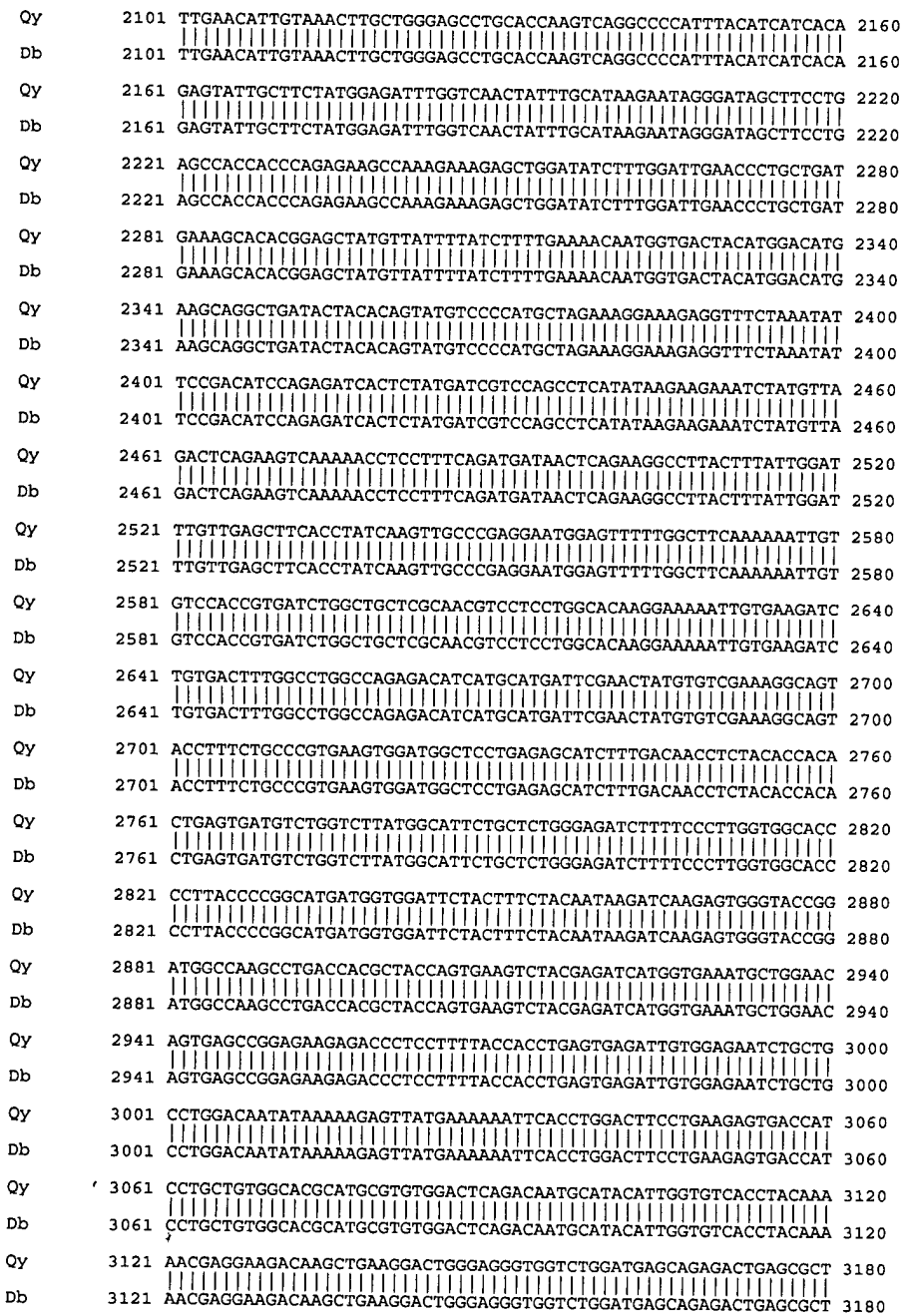
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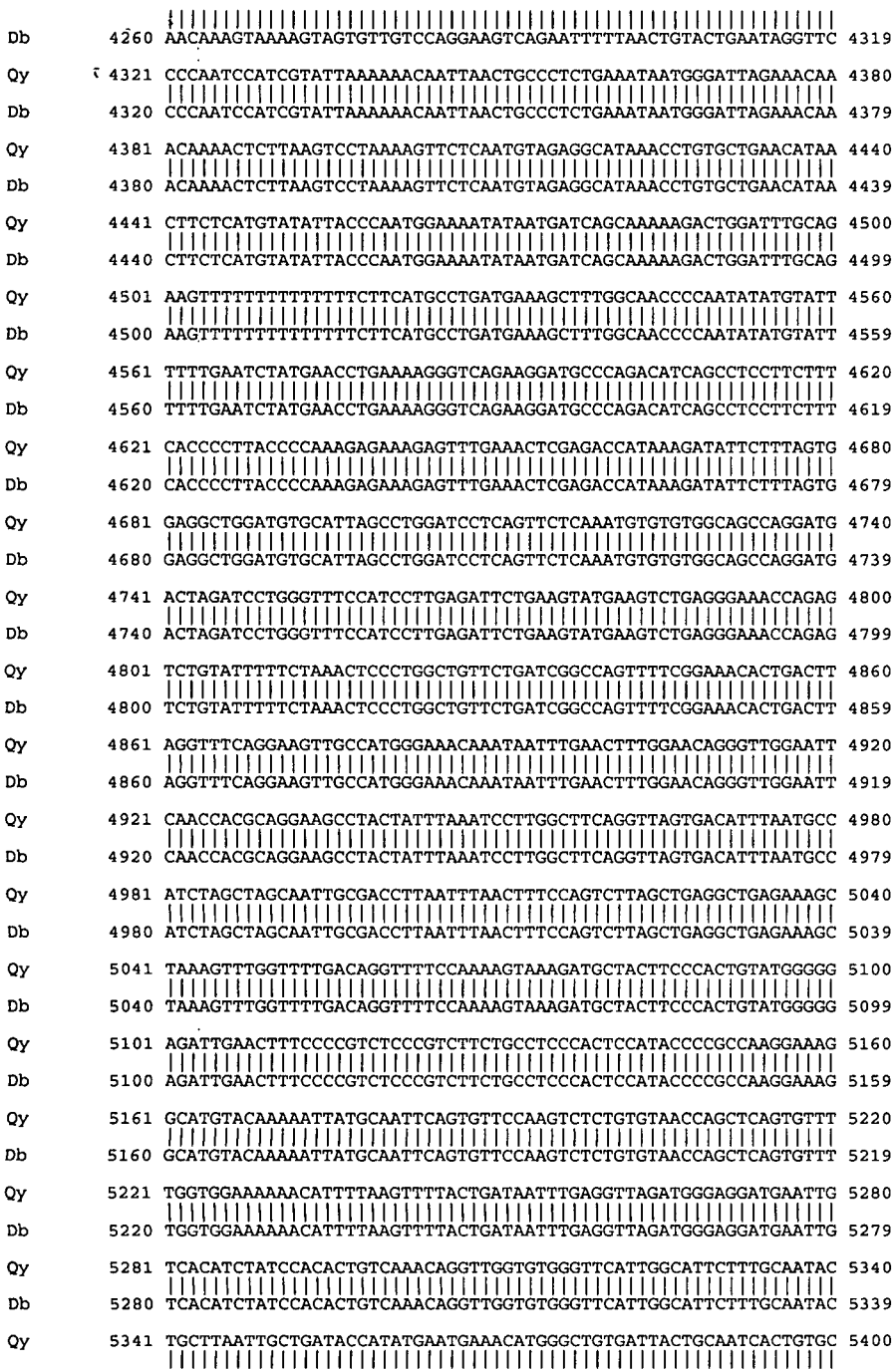
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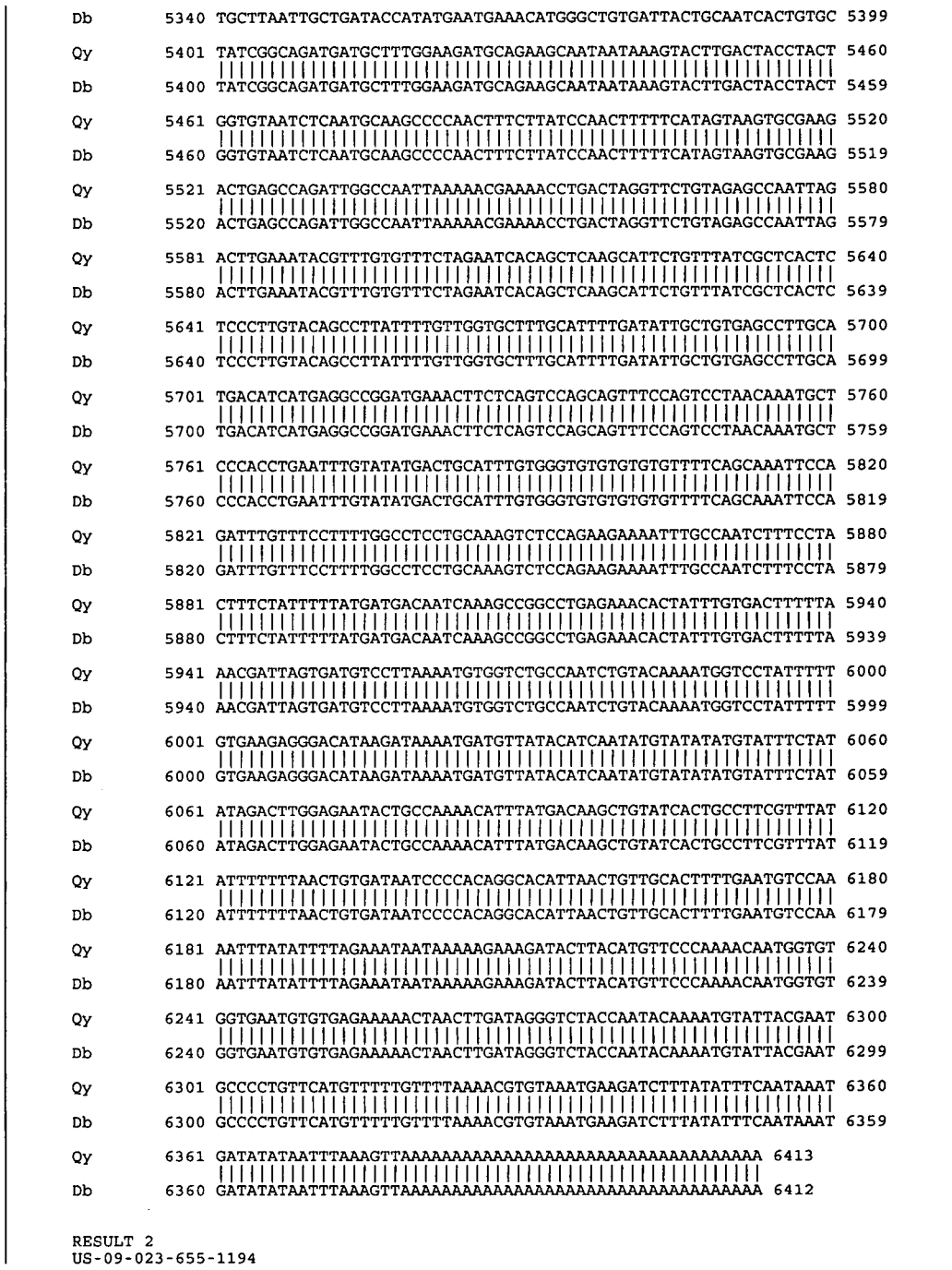
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RESULT 2
US-09-023-655-1194

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; Sequence 1194, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1194:
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;      LENGTH:  6378 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g189733
US-09-023-655-1194

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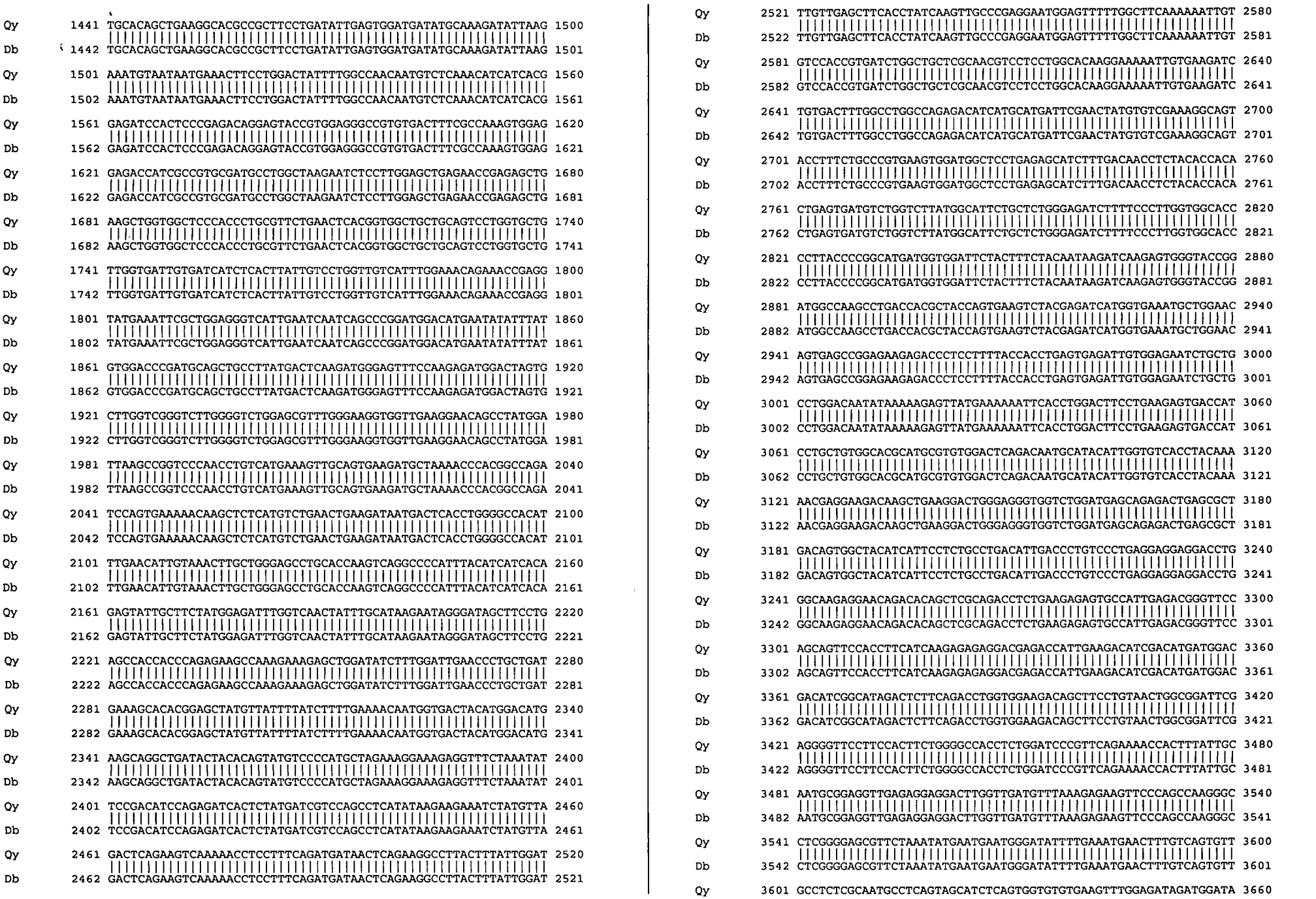
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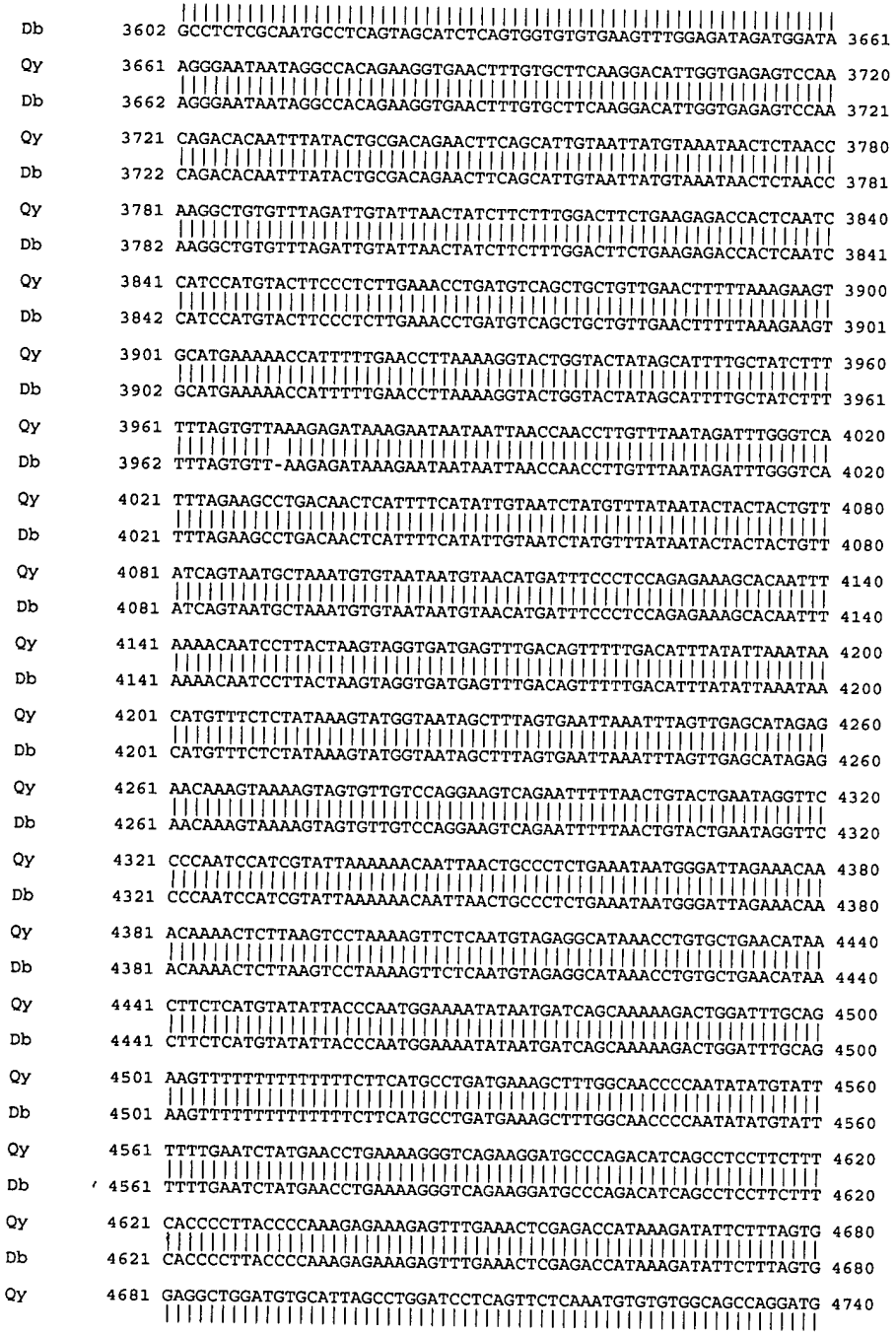
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Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
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Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Db 3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
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Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 3
US-09-919-497-40
; Sequence 40, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-40

Query Match 99.2%; Score 6364.4; DB 3; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801

Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTTAT 1861

Qy       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921

Qy       1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981

Qy       1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041

Qy       2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101

Qy       2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161

Qy       2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221

Qy       2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281

Qy       2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341

Qy       2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401

Qy       2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461

Qy       2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521

Qy       2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581

Qy       2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641

Qy       2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701

Qy       2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761

Qy       2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821

Qy       2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881

Qy       2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941

Qy       2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001

Qy       3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061

Qy       3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121

Qy       3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181

Qy       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241

Qy       3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301

Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361

Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421
Qy       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db       3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481
Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db       3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db       3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601
Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db       3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
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Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db       3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db       3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy       3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db       3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy       3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db       3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
Qy       3961 TTTAGTGTTAAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db       3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Qy       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Qy       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Qy       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Db       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Qy       4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Db       4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Qy       4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
Db       4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Db       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Db       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Db       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Db       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Db       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Db       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             |||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 4
US-09-949-016-832
; Sequence 832, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 832
;   LENGTH: 6378
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-832

  Query Match             99.2%;  Score 6364.4;  DB 3;  Length 6378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;
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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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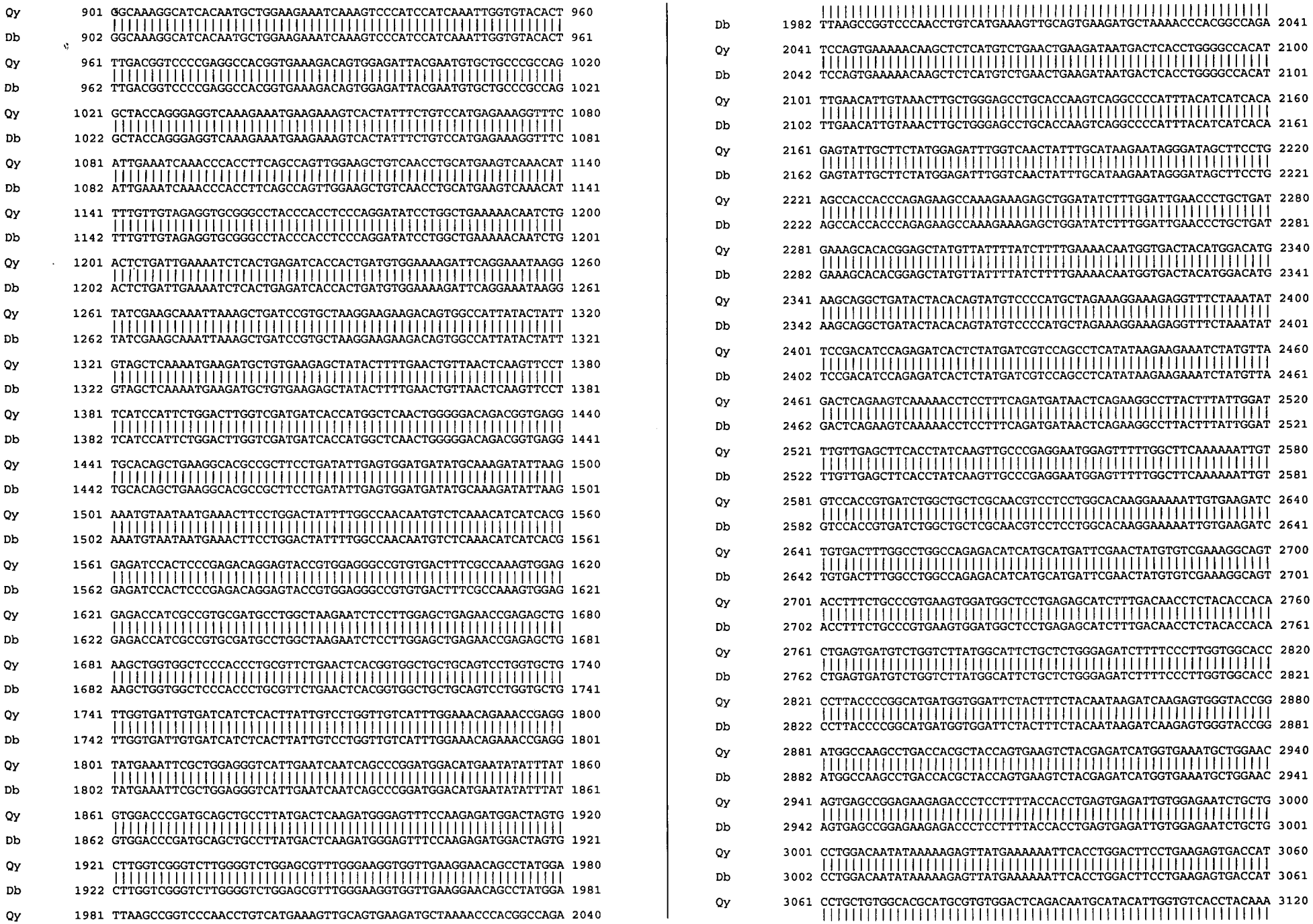
Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901
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Db       3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
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Db       3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db       3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
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Db       3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301
Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
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Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db       3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db       3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601
Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db       3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db       3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721
Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db       3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db       3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy       3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db       3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy       3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db       3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
Qy       3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db       3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Qy       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Qy       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Qy       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy       4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
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Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 5
US-08-462-728-1
; Sequence 1, Application US/08462728
; Patent No. 6043211
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,728
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..3398
US-08-462-728-1

Query Match 74.5%; Score 4777; DB 3; Length 6373;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4880; Conservative 0; Mismatches 20; Indels 11; Gaps 8;

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Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

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Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Qy       248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Db       538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

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Db       598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
Db       658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db       838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
Db      1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db      1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
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Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
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Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
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Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457
Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517
Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577
Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
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Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697
Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
Db      2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757
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Db      2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817
Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
Db      2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877
Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
Db      2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937
Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
Db      2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997
Qy      3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
Db      2998 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057
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Db      3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117
Qy      3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
Db      3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177
Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
Db      3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237
Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
Db      3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297
Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
Db      3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357
Qy      3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
Db      3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417
Qy      3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
Db      3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477
Qy      3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Db      3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537
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Db      3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597
Qy      3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
Db      3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657
Qy      3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
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Qy      3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
Db      3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837
Qy      3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
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Db      4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076
Qy      4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
Db      4077 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAATTTAAAAAC 4136
Qy      4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
Db      4137 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4196
Qy      4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Qy      4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
Db      4257 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4316
Qy      4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
Db      4317 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4376
Qy      4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
Db      4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436
Qy      4446 CATGTATATTACCCAATGGAAAATATAATGATCAGC-AAAAAGACTGGATTTGCAGAAGT 4504
Db      4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCAAAAGACTGGATTTGCAGAAGT 4496
Qy      4505 TTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTT 4564
Db      4497 TTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTT 4556
Qy      4565 GAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTCAC 4623
Db      4557 GAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTCAC 4616
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Qy       4624 CCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAG 4683
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Db       4617 CCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAG 4676

Qy       4684 GCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACT 4743
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Db       4677 GCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGACT 4735

Qy       4744 AGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCT 4803
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Db       4736 AGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCT 4795

Qy       4804 GTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGG 4863
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Db       4796 GTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTAGG 4855

Qy       4864 TTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
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Db       4856 TTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4906
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RESULT 6
US-08-461-917-1
; Sequence 1, Application US/08461917
; Patent No. 6372438
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..3398
US-08-461-917-1

Query Match 74.5%; Score 4777; DB 3; Length 6373;

Best Local Similarity 99.4%; Pred. No. 0;
Matches 4880; Conservative 0; Mismatches 20; Indels 11; Gaps 8;

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Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

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Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
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Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
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Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
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Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
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Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy       1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
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Db       1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy       1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
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Qy       1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy       1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy       1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy       1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy       1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy       1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy       2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
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Db       2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy       2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy       2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy       2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy       2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy       2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy       2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy       2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy       2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy       2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy       2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy       2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757

Qy       2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817

Qy       2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877

Qy       2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy       2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
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Qy       3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
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Db       2998 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057

Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
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Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy       3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
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Db       3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237
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Qy       3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
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Qy       3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357

Qy       3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
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Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
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Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
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Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657

Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
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Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777

Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
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Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956

Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016

Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
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Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
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Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
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Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
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Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Db       4317 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4376

Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
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Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCAGC-AAAAAGACTGGATTTGCAGAAGT 4504
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Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCAAAAGACTGGATTTGCAGAAGT 4496

Qy       4505 TTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTT 4564
             |||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||
Db       4497 TTTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTT 4556

Qy       4565 GAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTCAC 4623
             |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db       4557 GAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTCAC 4616

Qy       4624 CCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAG 4683
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Db       4617 CCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAG 4676

Qy       4684 GCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACT 4743
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Db       4677 GCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGACT 4735

Qy       4744 AGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCT 4803
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Db       4736 AGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCT 4795

Qy       4804 GTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGG 4863
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Db       4796 GTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTAGG 4855

Qy       4864 TTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
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Db       4856 TTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4906
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RESULT 7
US-08-464-436-1
; Sequence 1, Application US/08464436
; Patent No. 6514723
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,436
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.

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;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6373 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3398
US-08-464-436-1

  Query Match             74.5%;  Score 4777;  DB 3;  Length 6373;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   11;  Gaps    8;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

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Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

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Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
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Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Db        718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

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Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
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Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
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Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
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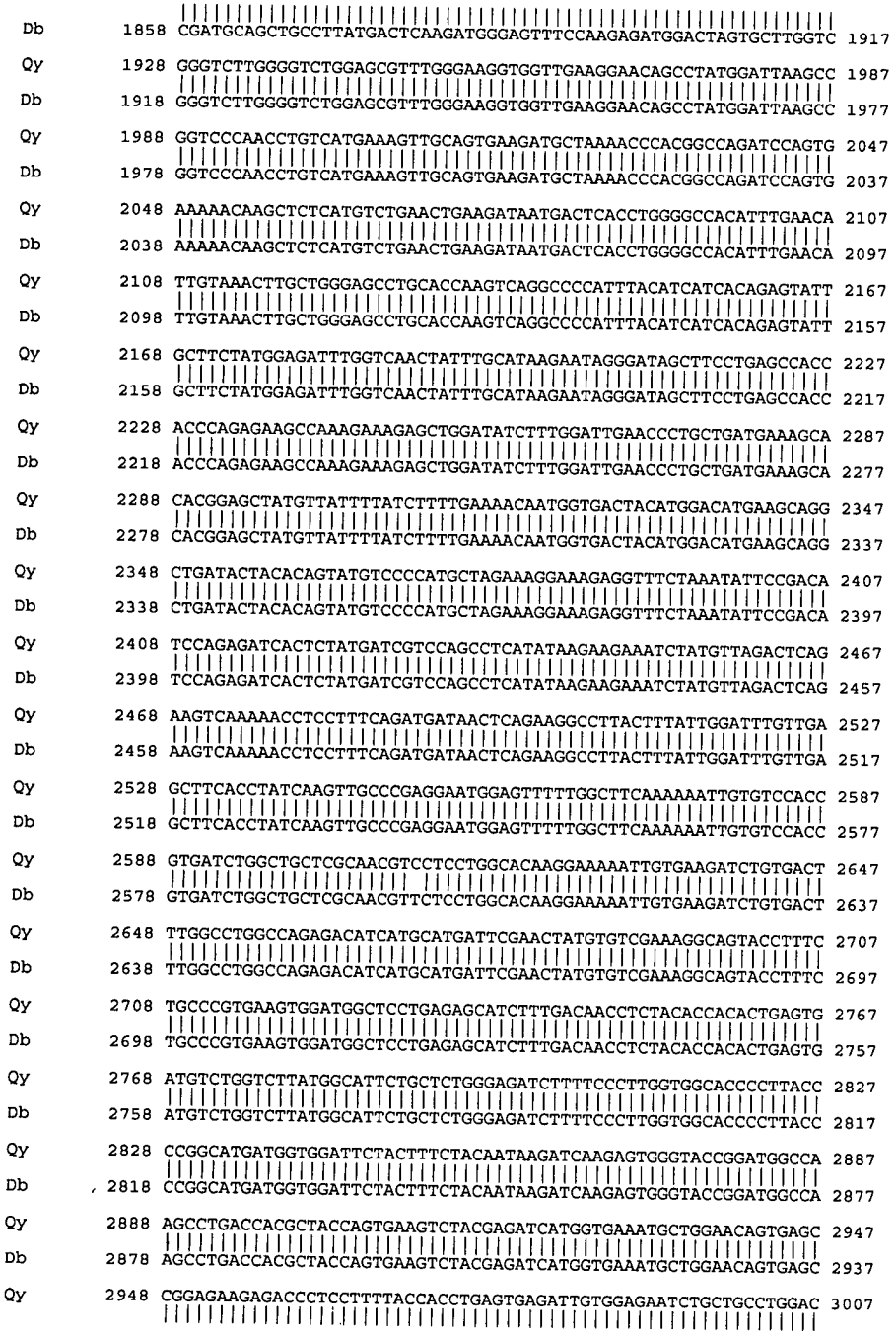
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RESULT 8
US-08-464-436-1
; Sequence 1, Application US/08464436
; Patent No. 6642022
;   GENERAL INFORMATION:
;        APPLICANT: WILLIAMS, Lewis T.
;                   ESCOBEDO, Jaime A.
;        TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew
;             STREET: One Market, Steuart Street Tower, 20th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,436
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/309,322
;             FILING DATE: 10-FEB-1989
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dow, Karen B.
;             REGISTRATION NUMBER: 29,684
;             REFERENCE/DOCKET NUMBER: 2307K-267-2-3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6373 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
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;             NAME/KEY:  CDS
;             LOCATION:  129..3398
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US-08-464-436-1

  Query Match             74.5%;  Score 4777;  DB 3;  Length 6373;
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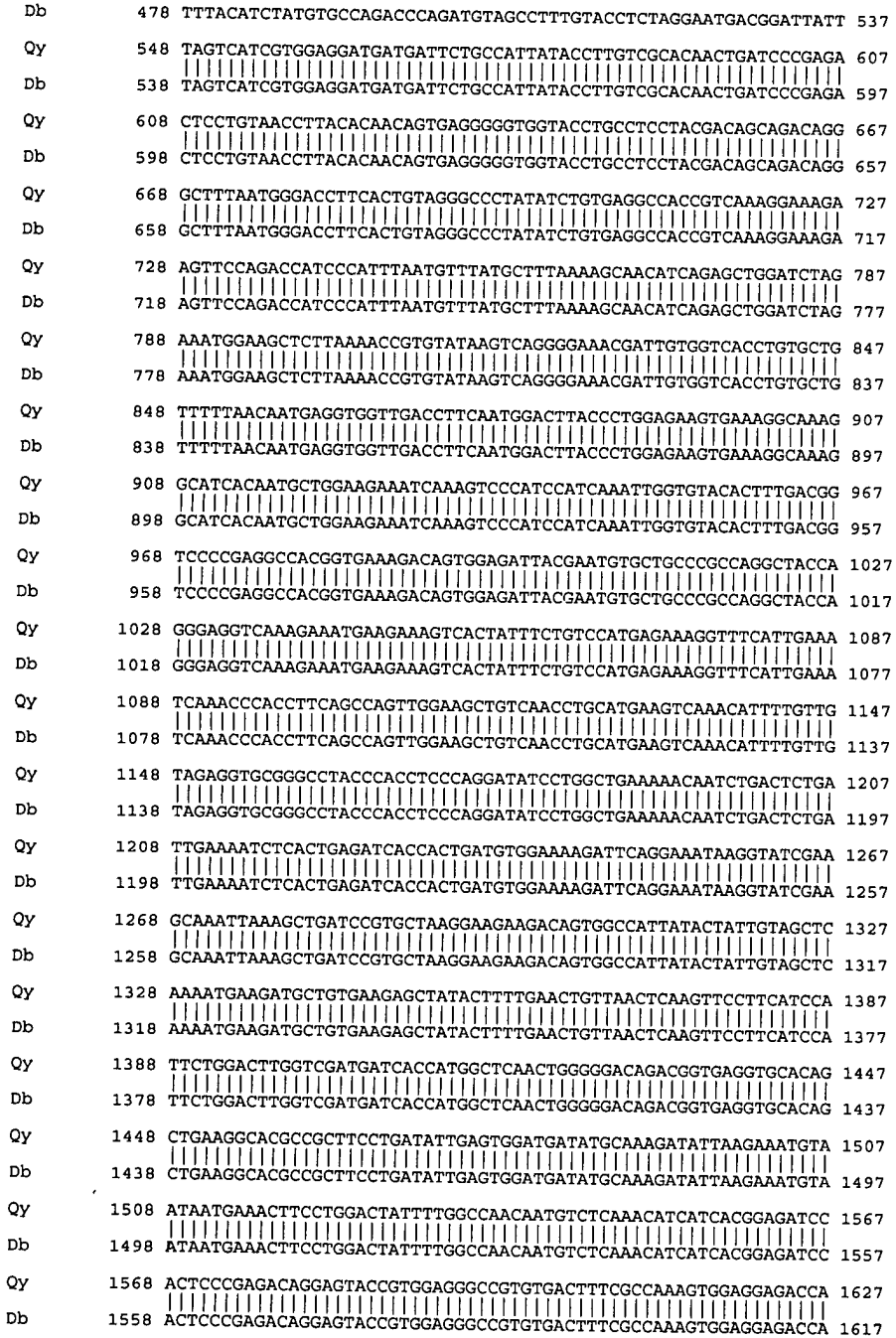
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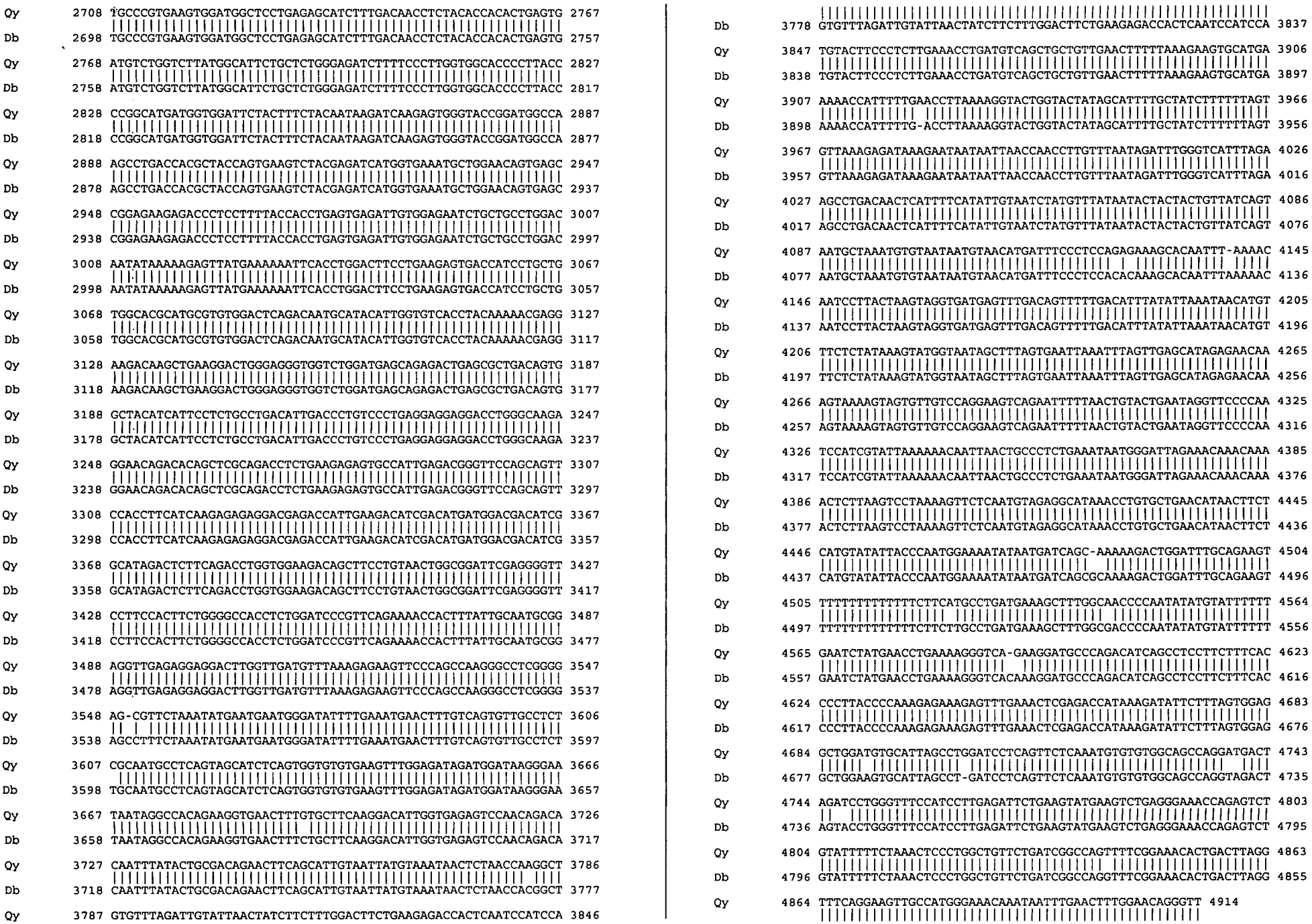
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Db 1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497
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RESULT 9
US-08-168-917-5
; Sequence 5, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6375 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
;      OTHER INFORMATION:  /note= "nucleotide number 1 of this
;      OTHER INFORMATION:  sequence is identical to the nucleotide number 1
;      OTHER INFORMATION:  of the previous 4100 long sequence"
US-08-168-917-5

  Query Match             74.3%;  Score 4765.6;  DB 2;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  |||||||| ||||||||||||||  |   |||||||
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Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

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Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
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Db        538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

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Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

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Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467

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Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
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Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
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Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
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Db       4137 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4196

Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
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Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
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RESULT 10
US-08-460-510-5
; Sequence 5, Application US/08460510
; Patent No. 5872218
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,510
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6375 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo Sapiens
;       STRAIN:  lambda gt10
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  129..3395
;       OTHER INFORMATION:  /note= "nucleotide number 1 of this
;       OTHER INFORMATION:  sequence is identical to the nucleotide number 1
;       OTHER INFORMATION:  of the previous 4100 long sequence"
US-08-460-510-5

  Query Match             74.3%;  Score 4765.6;  DB 2;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              ||||||||||||||||||||||  ||||||||| ||||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

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Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
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Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
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Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
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Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
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Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
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Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

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Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

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Db       1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy       1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
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Db       1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917
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Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
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Db       4257 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4316

Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Db       4317 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4376

Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
             ||| |||||||||||||||||||||||||||||  ||| ||||||||||||||||||||
Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496

Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
              || |||||||||||||| |||||||||||||||||| |||||||||||||||||||||
Db       4497 TTNTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4556

Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
             |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db       4557 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4616

Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4617 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4676

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
             |||||||| |||||||||||| |||||||||||||||||||||||||||||  ||
Db       4677 AGGCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGA 4735

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
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Db       4736 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4795

Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
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Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
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Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908


RESULT 11
US-08-460-490-5
; Sequence 5, Application US/08460490
; Patent No. 5891652
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,490
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6375 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
;      OTHER INFORMATION:  /note= "nucleotide number 1 of this
;      OTHER INFORMATION:  sequence is identical to the nucleotide number 1
;      OTHER INFORMATION:  of the previous 4100 long sequence"
US-08-460-490-5

  Query Match             74.3%;  Score 4765.6;  DB 2;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  ||||||||| |||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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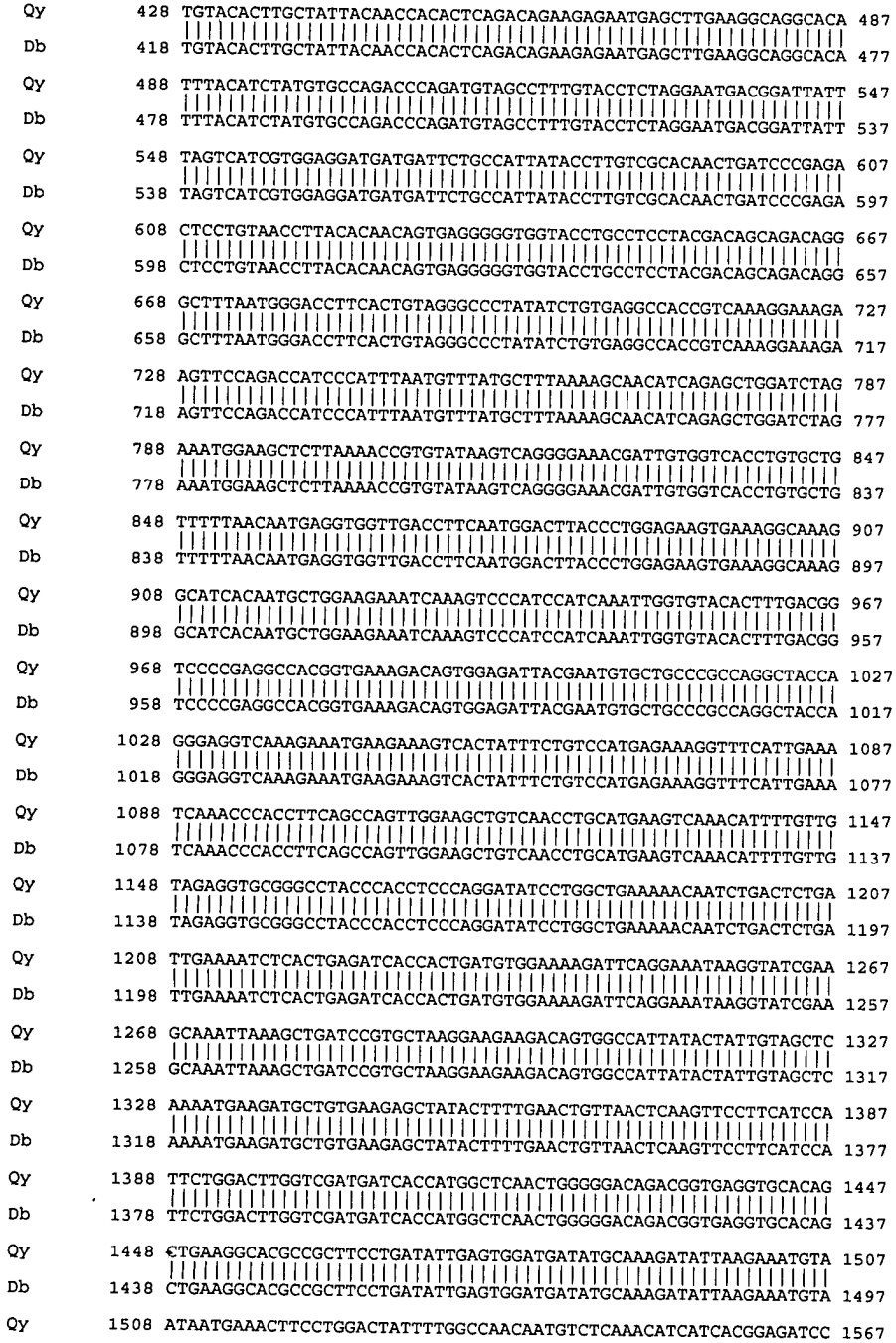
Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417
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Qy 428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
Db 418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477
Qy 488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
Db 478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537
Qy 548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
Db 538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597
Qy 608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
Db 598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657
Qy 668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
Db 658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717
Qy 728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy 788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
Db 778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837
Qy 848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db 838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897
Qy 908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
Db 898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957
Qy 968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
Db 958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017
Qy 1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
Db 1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077
Qy 1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db 1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137
Qy 1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
Db 1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197
Qy 1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
Db 1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257
Qy 1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
Db 1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317
Qy 1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db 1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377
Qy 1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db 1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437
Qy 1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
Db 1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497
Qy 1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
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Qy 1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
Db 1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617
Qy 1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db 1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677
Qy 1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
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Db 1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857
Qy 1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
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Qy 1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
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Qy 1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db 1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037
Qy 2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db 2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097
Qy 2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db 2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157
Qy 2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
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Qy 2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
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Qy 2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db 2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337
Qy 2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
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Qy 2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
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Qy 2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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Qy 2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647

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Db       2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy       2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707

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Db       2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy       2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007

Db       2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

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Db       2998 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057

Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127

Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

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Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247

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Db       4257 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4316

Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385

Db       4317 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4376

Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445

Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503

Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496

Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562

Db       4497 TTNTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4556

Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621

Db       4557 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4616

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Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801

Db       4736 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4795
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Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908


RESULT 12
PCT-US92-00730-5
; Sequence 5, Application PC/TUS9200730
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00730
;      FILING DATE:  19920128
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6375 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
;      OTHER INFORMATION:  /note= "nucleotide number 1 of this
;      OTHER INFORMATION:  sequence is identical to the nucleotide number 1
;      OTHER INFORMATION:  of the previous 4100 long sequence"
PCT-US92-00730-5

  Query Match             74.3%;  Score 4765.6;  DB 6;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              ||||||||||||||||||||||  |||||||||| |||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
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Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137
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Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
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Db      1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
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Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
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Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
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Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
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Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
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Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757

Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817

Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877

Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

Qy      3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2998 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057

Qy      3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy      3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237

Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297

Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357
Qy       3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417
Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477
Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537
Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597
Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657
Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
Db       3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717
Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777
Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837
Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897
Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956
Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016
Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076
Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
Db       4077 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAATTTAAAAAC 4136
Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
Db       4137 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4196
Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
Db       4197 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4256
Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
Db       4257 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4316
Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
Db       4317 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4376
Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496
Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
Db       4497 TTNTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4556
Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
Db       4557 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4616
Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
Db       4617 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4676
Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
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Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
Db       4736 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4795
Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855
Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908
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RESULT 13
PCT-US92-00862-5
; Sequence 5, Application PC/TUS9200862
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Lewis T.
;    APPLICANT:  Escobedo, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00862
;      FILING DATE:  19920131
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,141
;      FILING DATE:  02-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  2307U-267-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:' 6375 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
;      OTHER INFORMATION:  /note= "nucleotide number 1 of this
;      OTHER INFORMATION:  sequence is identical to the nucleotide
;      OTHER INFORMATION:  number 1 of the previous 4100 long
;      OTHER INFORMATION:  sequence."
PCT-US92-00862-5

  Query Match             74.3%;  Score 4765.6;  DB 6;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  |||||||| ||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
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Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
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Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
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Db        538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
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Db        838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy       1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy       1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy       1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy       1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy       1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy       1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
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Db       1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy       1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
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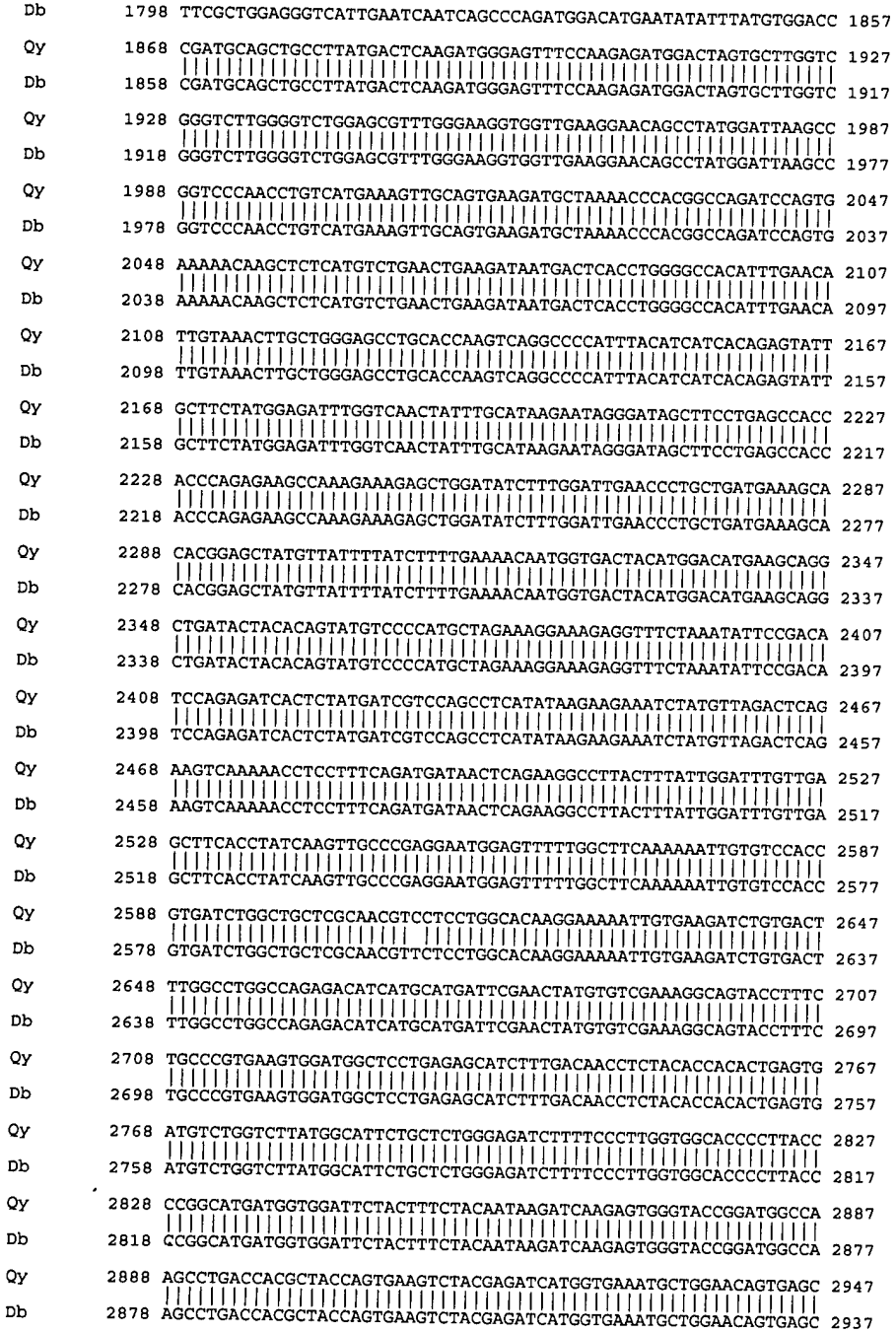
Qy       1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
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Db       1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

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Qy       1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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Db 1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857
Qy 1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
Db 1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917
Qy 1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
Db 1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977
Qy 1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db 1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037
Qy 2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
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Qy 2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
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Qy 3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
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Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
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Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

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Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Db       4197 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4256

Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
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Db       4257 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4316

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Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
             |||||||||||||||||||||||||||||||||  ||| ||||||||||||||||||||
Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496

Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
             || |||||||||||||||| |||||||||||||||||| |||||||||||||||||||||
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             |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db       4557 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4616

Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4617 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4676

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
             |||||||| |||||||||||| ||||||||||||||||||||||||||||||||  ||
Db       4677 AGGCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGA 4735

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4736 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4795

Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908


RESULT 14
US-08-168-917-3
; Sequence 3, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4100 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
US-08-168-917-3

  Query Match             63.0%;  Score 4037.2;  DB 2;  Length 4100;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 4089;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    4;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  ||||||||| ||||||||||||||| |   |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357
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Qy       368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
Db       358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy       428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
Db       418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy       488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
Db       478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy       548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
Db       538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy       608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
Db       598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
Db       658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
Db       718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db       838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
Db       898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
Db      1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db      1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
Db      1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4100 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo Sapiens
;       STRAIN:  lambda gt10
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  129..3395
US-08-460-510-3

  Query Match             63.0%;  Score 4037.2;  DB 2;  Length 4100;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 4089;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    4;

Qy        10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
             ||||||||||||||||||||||  |||||||| ||||||||||||||  |   |||||||
Db         1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy        68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy       128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy       188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy       248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy       308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy       368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy       428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy       488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy       548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy       608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917
Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977
Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037
Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097
Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157
Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217
Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277
Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337
Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397
Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457
Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517
Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577
Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637
Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697
Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
Db      2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757
Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
Db      2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817
Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
Db      2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877
Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
Db      2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937
Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
Db      2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

Qy      3008 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
Db      2998 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057
Qy      3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
Db      3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117
Qy      3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
Db      3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177
Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
Db      3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237
Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
Db      3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297
Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
Db      3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357
Qy      3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
Db      3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417
Qy      3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
Db      3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477
Qy      3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
Db      3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537
Qy      3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
Db      3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597
Qy      3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
Db      3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657
Qy      3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
Db      3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717
Qy      3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
Db      3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777
Qy      3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
Db      3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837
Qy      3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
Db      3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897
Qy      3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
Db      3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956
Qy      3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
Db      3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016
Qy      4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
Db      4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076
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Qy       4087 AATGCTAAATGTGTAATAATGTAA 4110
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Db       4077 AATGCTAAATGTGTAATAATGTAA 4100


RESULT 16
US-08-460-490-3
; Sequence 3, Application US/08460490
; Patent No. 5891652
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,490
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4100 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
US-08-460-490-3

  Query Match             63.0%;  Score 4037.2;  DB 2;  Length 4100;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 4089;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    4;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
              |||||||||||||||||||||  |||||||| ||||||||||||||  |  |||||||
Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy       1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy       1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257
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Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
             ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAAATTGTGAAGATCTGTGACT 2647
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757

Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817

Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877

Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

Qy      3008 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2998 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057

Qy      3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy      3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237

Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297

Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357

Qy      3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy      3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547

Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606

Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666

Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657

Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726

Db       3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717

Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786

Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777

Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846

Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906

Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897

Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966

Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956

Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026

Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016

Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086

Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

Qy       4087 AATGCTAAATGTGTAATAATGTAA 4110

Db       4077 AATGCTAAATGTGTAATAATGTAA 4100
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RESULT 17
PCT-US92-00730-3
; Sequence 3, Application PC/TUS9200730
;  GENERAL INFORMATION:
;     APPLICANT:  Wolf, David
;     APPLICANT:  Tomlinson, James E.
;     APPLICANT:  Fretto, Larry J.
;     APPLICANT:  Giese, Neill A.
;     APPLICANT:  Escobedo, Jaime A.
;     APPLICANT:  Williams, Lewis T.
;     TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;     TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  TOWNSEND and TOWNSEND
;       STREET:  Steuart Street Tower, 20th Floor \ One Market
;       STREET:  Plaza
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  US
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/00730
;       FILING DATE:  19920128
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ching, Edwin P.
;       REGISTRATION NUMBER:  34,090
;       REFERENCE/DOCKET NUMBER:  12418-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4100 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo Sapiens
;       STRAIN:  lambda gt10
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  129..3395
PCT-US92-00730-3

  Query Match             63.0%;  Score 4037.2;  DB 6;  Length 4100;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 4089;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    4;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67

Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127

Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187

Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247

Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307

Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367

Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427

Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487

Db        418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547

Db        478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy        548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607

Db        538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597
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Qy       608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
Db       598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
Db       658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
Db       718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
Db       838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
Db       898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
Db      1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
Db      1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy      1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
Db      1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
Db      1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
Db      1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
Db      1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy      1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
Db      1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy      1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
Db      2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757

Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
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Db       2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817

Qy       2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877

Qy       2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy       2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997

Qy       3008 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2998 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057

Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy       3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237

Qy       3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297

Qy       3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
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Db       3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357

Qy       3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
             || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657

Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717

Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777

Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897

Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956

Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016

Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

Qy       4087 AATGCTAAATGTGTAATAATGTAA 4110
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Db       4077 AATGCTAAATGTGTAATAATGTAA 4100
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RESULT 18
PCT-US92-00862-3
; Sequence 3, Application PC/TUS9200862
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Lewis T.
;    APPLICANT:  Escobedo, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00862
;      FILING DATE:  19920131
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,141
;      FILING DATE:  02-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  2307U-267-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4100 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;    IMMEDIATE SOURCE:
;      LIBRARY:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  129..3395
;      OTHER INFORMATION:
PCT-US92-00862-3
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Query Match 63.0%; Score 4037.2; DB 6; Length 4100;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 4089; Conservative 0; Mismatches 8; Indels 7; Gaps 4;

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Qy      10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
           ||||||||||||||||||||||  ||||||||| |||||||||||||| |   |||||||
Db       1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy      68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117

Qy     128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy     188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy     248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy     308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy     368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy     428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 477

Qy     488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 537

Qy     548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 597

Qy     608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy     668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy     728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 777

Qy     788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy     848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 897

Qy     908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy     968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy    1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy    1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy    1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy    1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy    1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy    1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy    1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1437

Qy    1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1497

Qy    1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy    1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy    1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677

Qy    1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1678 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1737

Qy    1748 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1807
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1738 TTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAA 1797

Qy    1808 TTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACC 1867
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy    1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy    1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy    1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy    2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy    2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
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Db       2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157
Qy       2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db       2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217
Qy       2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db       2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277
Qy       2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
Db       2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337
Qy       2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db       2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397
Qy       2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
Db       2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457
Qy       2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
Db       2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517
Qy       2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db       2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577
Qy       2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
Db       2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637
Qy       2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
Db       2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697
Qy       2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
Db       2698 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2757
Qy       2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
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Qy       2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
Db       2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877
Qy       2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
Db       2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937
Qy       2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
Db       2938 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 2997
Qy       3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
Db       2998 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057
Qy       3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
Db       3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117
Qy       3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
Db       3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177
Qy       3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
Db       3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237
Qy       3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
Db       3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297
Qy       3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
Db       3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357
Qy       3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417
Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477
Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537
Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597
Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
Db       3598 TGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3657
Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
Db       3658 TAATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3717
Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777
Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837
Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897
Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956
Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016
Qy       4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076
Qy       4087 AATGCTAAATGTGTAATAATGTAA 4110
Db       4077 AATGCTAAATGTGTAATAATGTAA 4100
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RESULT 19
US-08-180-195-35
; Sequence 35, Application US/08180195
; Patent No. 5567584
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE

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;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/180,195
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,510
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-08-180-195-35

  Query Match             59.9%;  Score 3838.8;  DB 2;  Length 4054;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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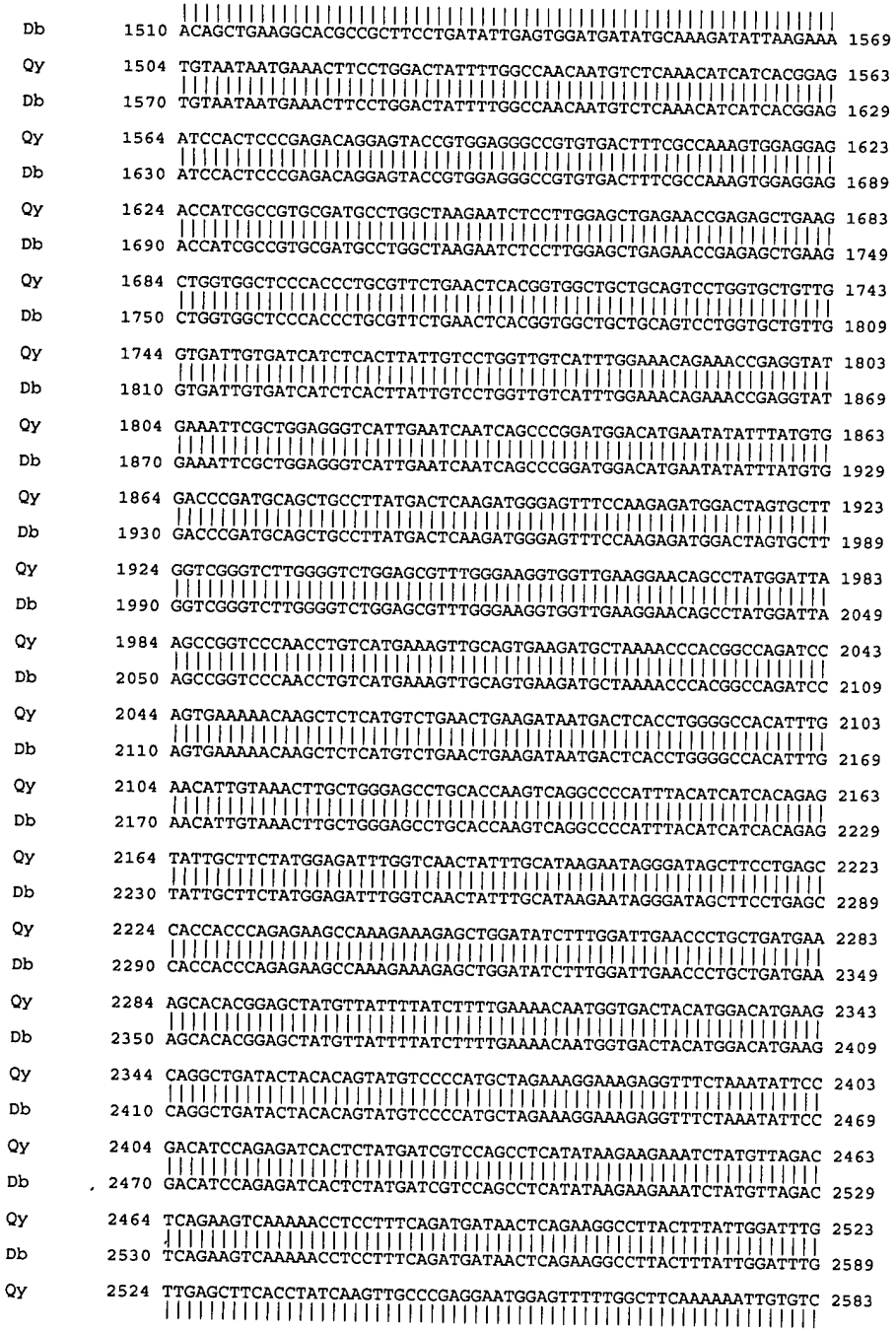
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RESULT 20
US-08-477-329-35
; Sequence 35, Application US/08477329
; Patent No. 5750375
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,329
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
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;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
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;      LOCATION:  205..3471
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US-08-477-329-35

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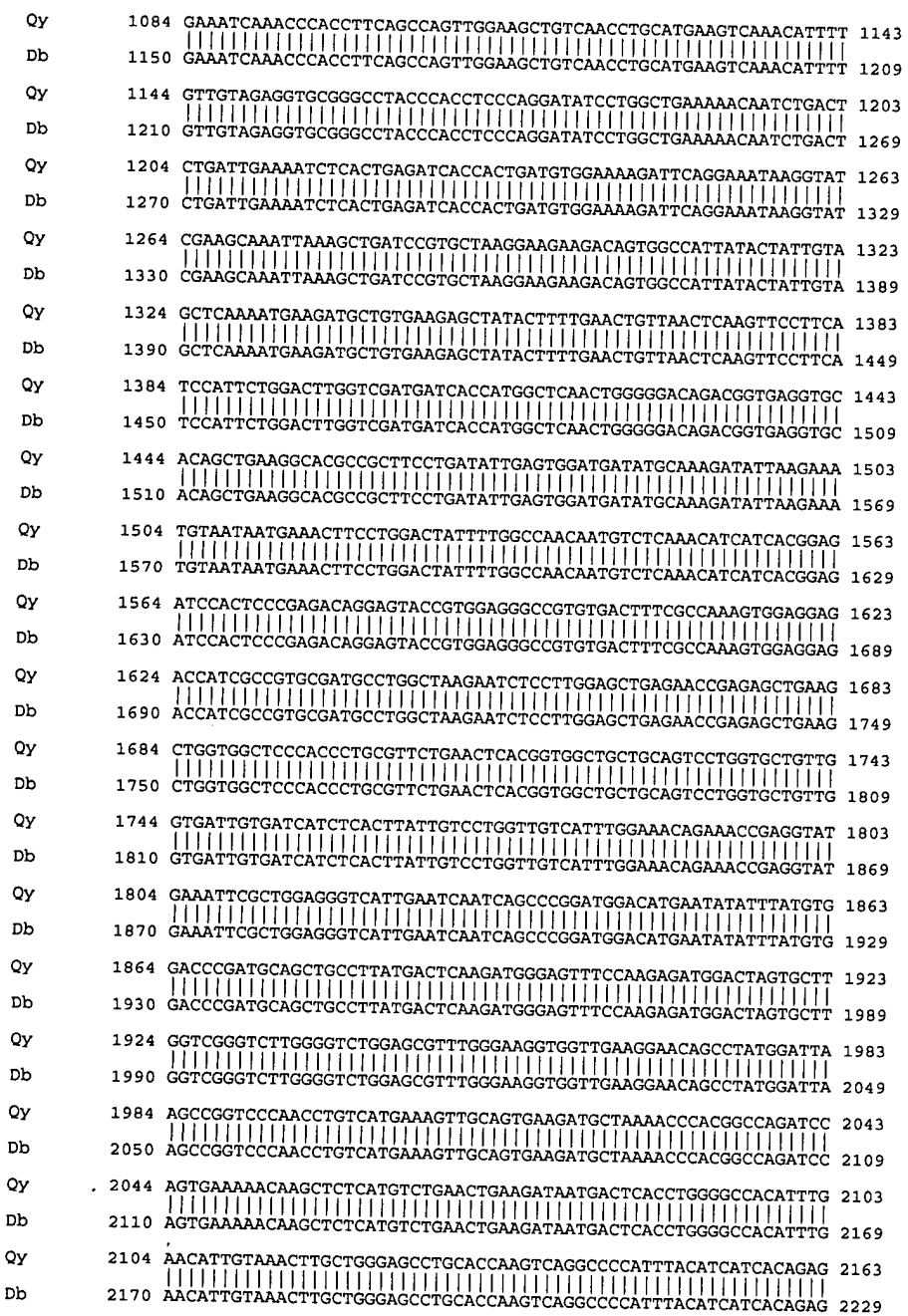
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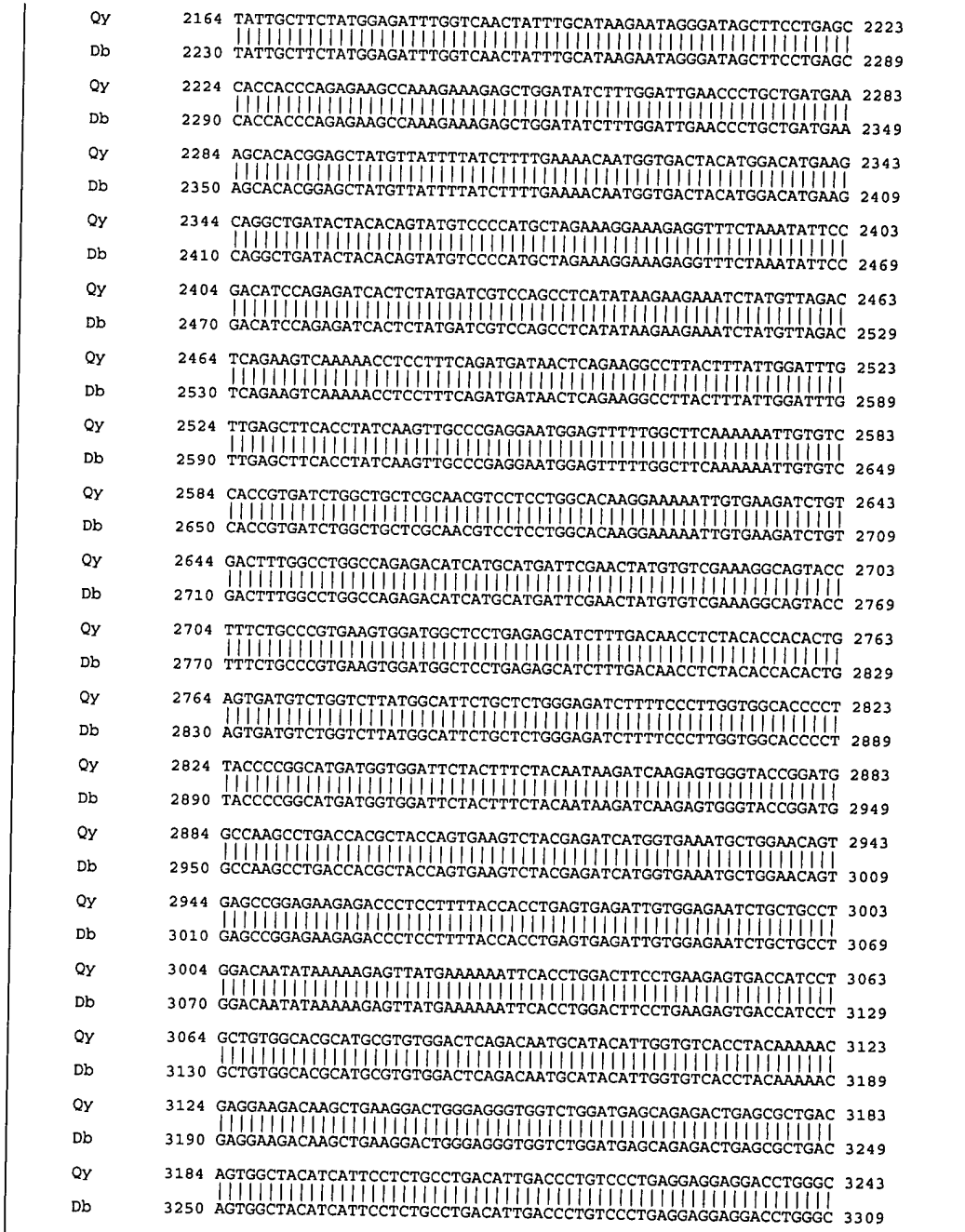
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Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149
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Qy 1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db 1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209
Qy 1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db 1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269
Qy 1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
Db 1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329
Qy 1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db 1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389
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Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

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Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

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Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053


RESULT 21
US-08-475-458-35
; Sequence 35, Application US/08475458
; Patent No. 5843725
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,458
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446D5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-08-475-458-35

  Query Match             59.9%;  Score 3838.8;  DB 2;  Length 4054;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

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Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

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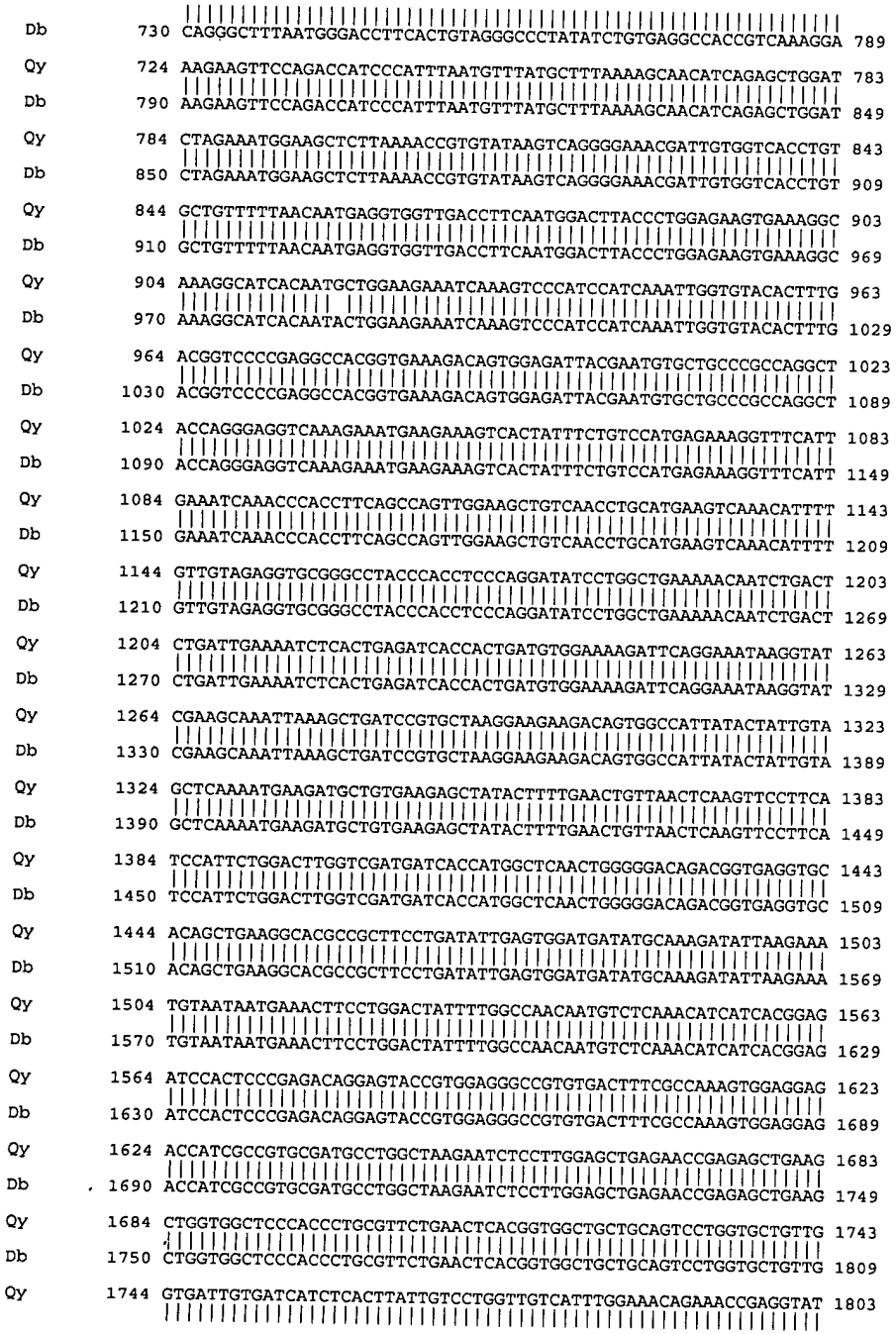
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Db        490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Qy        544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
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Db        610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy        604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
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Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Qy 724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
Db 790 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 849
Qy 784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
Db 850 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 909
Qy 844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
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Qy 904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
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Qy 964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Db 2650 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2709
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Qy 2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
Db 2770 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2829
Qy 2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
Db 2830 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2889
Qy 2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
Db 2890 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2949

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Qy       2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 3009

Qy       2944 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3069

Qy       3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3129

Qy       3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3189

Qy       3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Qy       3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
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Db       3310 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3369

Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Db       3370 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3429

Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

Qy       3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903
             || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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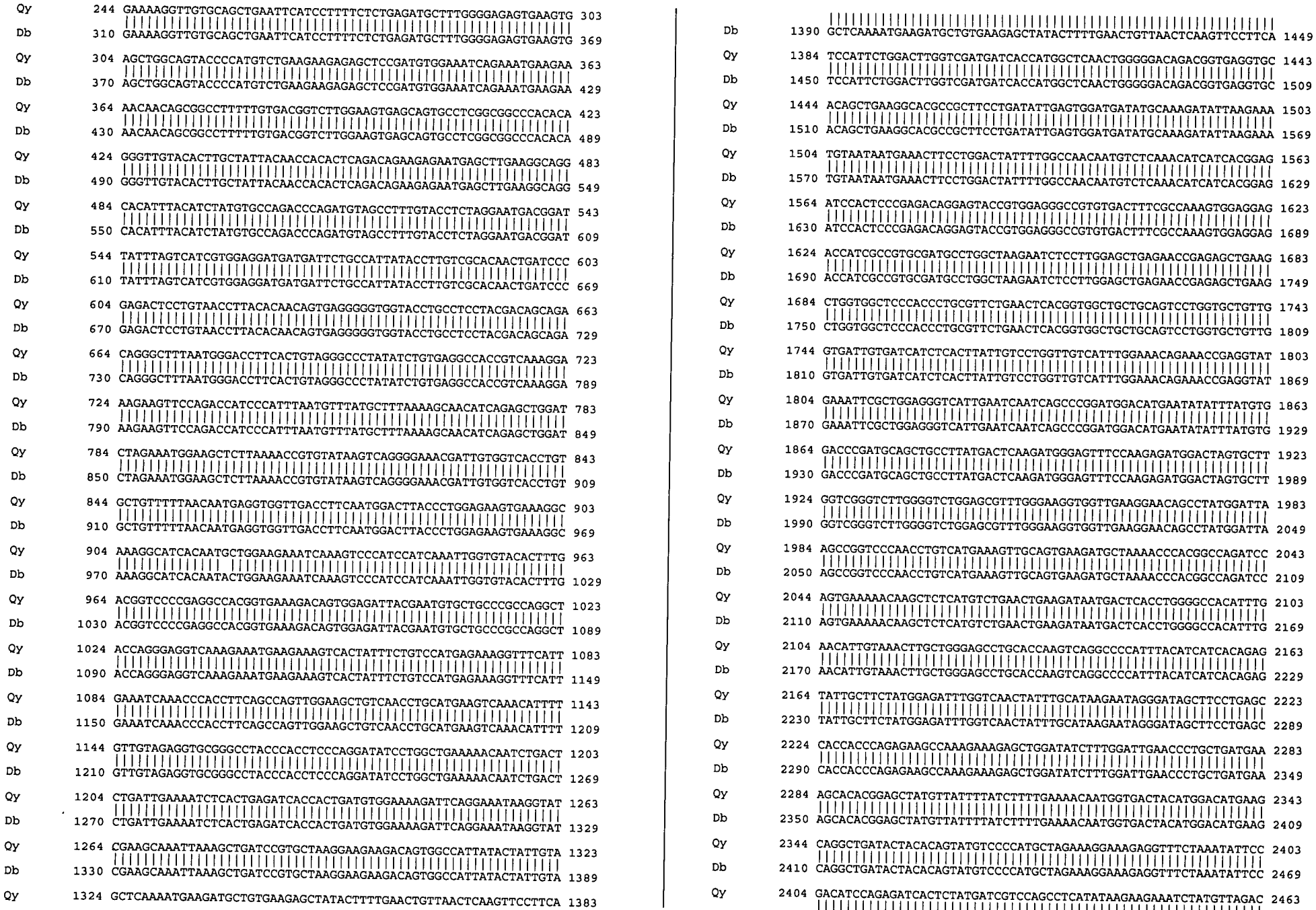
Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053


RESULT 22
US-08-980-400-35
; Sequence 35, Application US/08980400
; Patent No. 6018026
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/980,400
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,329
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-08-980-400-35

  Query Match           59.9%;  Score 3838.8;  DB 3;  Length 4054;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309
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Qy 244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
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Qy 304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
Db 370 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 429
Qy 364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
Db 430 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489
Qy 424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
Db 490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549
Qy 484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
Db 550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609
Qy 544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
Db 610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669
Qy 604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
Db 670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729
Qy 664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
Db 730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789
Qy 724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
Db 790 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 849
Qy 784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
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Qy 844 GCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
Db 910 GCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969
Qy 904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
Db 970 AAAGGCATCACAATACTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 1029
Qy 964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Qy 1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
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Db 1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209
Qy 1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db 1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269
Qy 1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
Db 1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329
Qy 1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db 1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389
Qy 1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
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Qy 1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
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Db 1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629
Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
Db 1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689
Qy 1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
Db 1690 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1749
Qy 1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
Db 1750 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1809
Qy 1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
Db 1810 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1869
Qy 1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
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Qy 1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
Db 1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989
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Qy 1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
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Qy 2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
Db 2110 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2169
Qy 2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
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Qy 2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
Db 2230 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2289
Qy 2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
Db 2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349
Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
Db 2350 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2409
Qy 2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
Db 2410 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2469
Qy 2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463

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Db       2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529

Qy       2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
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Qy       2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2644 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2703
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Qy       2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
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Db       2890 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2949

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Db       2950 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 3009

Qy       2944 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3069

Qy       3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3309

Qy       3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
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Db       3310 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3369

Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3370 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3429

Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Db       3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
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Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

Qy       3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903
             || |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053
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RESULT 23
US-09-583-459A-35
; Sequence 35, Application US/09583459A
; Patent No. 6291212
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,459A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4054 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: p-alpha-17B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..3471
; OTHER INFORMATION:
US-09-583-459A-35

Query Match 59.9%; Score 3838.8; DB 3; Length 4054;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3862; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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Qy       124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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Db       190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy       184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
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Qy       244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
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Db       310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy       304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Db       370 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 429

Qy       364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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Db       430 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489

Qy       424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
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Db       490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy       484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Db       550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

Qy       544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
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Db       610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy       604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
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Db       670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729

Qy       664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Db       730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789

Qy       724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
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Qy       784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
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Qy       844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
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Db       910 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969

Qy       904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
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Qy       964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Db      1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089

Qy      1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
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Qy      1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
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Db      1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209

Qy      1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
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Qy      1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
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Db      1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329

Qy      1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
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Db      1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389

Qy      1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
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Db      1390 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1449

Qy      1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1450 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1509

Qy      1444 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1503
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Db      1510 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1569

Qy      1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
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Db      1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629

Qy      1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
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Qy      1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
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Qy      1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
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Db      1750 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1809

Qy      1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
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Db      1810 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1869

Qy      1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
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Db      1870 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1929

Qy      1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
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Qy       1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
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Qy       2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
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Db       2110 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2169

Qy       2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
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Db       2170 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2229

Qy       2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
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Db       2230 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2289

Qy       2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
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Db       2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349

Qy       2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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Qy       2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
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Qy       2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Qy       2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
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Qy       3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
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Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
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Db       3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
             |||||||||||||||||||||||||||
Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053
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RESULT 24
US-09-583-210-35
; Sequence 35, Application US/09583210
; Patent No. 6291646

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;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,210
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-09-583-210-35

  Query Match           59.9%;  Score 3838.8;  DB 3;  Length 4054;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
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Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

Qy        244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
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Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Qy        364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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Db        430 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 489

Qy        424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
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Db        490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Db        550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

Qy        544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
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Db        610 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 669

Qy        604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
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Db        670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729

Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Db        730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789

Qy        724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
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Db        790 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 849

Qy        784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
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Db        850 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 909

Qy        844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
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Db        910 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
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Db        970 AAAGGCATCACAATACTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 1029

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Db       1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
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Db       1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
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Db       1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269

Qy       1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
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Db       1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329

Qy       1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389

Qy       1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
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Qy      1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
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Db      1450 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1509

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Db      1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629

Qy      1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
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Db      1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689

Qy      1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
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Db      1690 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1749

Qy      1684 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1743
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Db      1750 CTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTG 1809

Qy      1744 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1803
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Db      1810 GTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTAT 1869

Qy      1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
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Qy      1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
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Db      1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989

Qy      1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
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Db      1990 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 2049

Qy      1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
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Db      2050 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2109

Qy      2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2110 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2169

Qy      2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163
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Db      2170 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2229

Qy      2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223
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Db      2230 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2289

Qy      2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
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Db      2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349

Qy      2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
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Db      2350 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2409

Qy      2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
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Db      2410 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2469

Qy      2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
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Db      2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529

Qy      2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
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Db      2530 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2589

Qy      2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Db      2590 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2649

Qy      2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
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Db      2650 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2709

Qy      2644 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2703
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Db      2710 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2769

Qy      2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
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Db      2770 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2829

Qy      2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
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Db      2830 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2889

Qy      2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
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Db      2890 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2949

Qy      2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
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Qy      2944 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3003
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Db      3010 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3069

Qy      3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
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Db      3070 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3129

Qy      3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
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Db      3130 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3189

Qy      3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
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Db      3190 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3249

Qy      3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Db      3250 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3309

Qy      3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
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Qy      3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Db      3370 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3429

Qy      3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
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Db      3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy      3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Db      3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy      3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Db      3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy      3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
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Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

Qy       3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903
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Qy       3904 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 3963
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Db       3968 TGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTT 4027

Qy       3964 AGTGTTAAAGAGATAAAGAATAATAA 3989
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Db       4028 AGTGTTAAAGAGATAAAGAATAATAA 4053
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RESULT 25
US-09-583-449A-35
; Sequence 35, Application US/09583449A
; Patent No. 6300099
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/583,449A
;      FILING DATE:  30-MAY-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,510
;      FILING DATE:  27-DEC-1990
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-09-583-449A-35

  Query Match             59.9%;  Score 3838.8;  DB 3;  Length 4054;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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Db        190 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 249

Qy        184 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 243
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Db        250 ACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAAT 309

Qy        244 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 303
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Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

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Qy        424 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 483
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Db        490 GGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGG 549

Qy        484 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 543
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Db        550 CACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGAT 609

Qy        544 TATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCC 603
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Qy        604 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 GAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGA 729

Qy        664 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 723
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Db        730 CAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGA 789

Qy        724 AAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGAT 783
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Qy        784 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 843
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Db        850 CTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGT 909

Qy        844 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 903
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Db        910 GCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGC 969

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963

Db        970 AAAGGCATCACAATACTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 1029

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023

Db       1030 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1089

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083

Db       1090 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1149

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Db       1150 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1209

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203

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Qy       1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323

Db       1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389

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Db       1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989

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Db       1990 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 2049

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Db       3250 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3309

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Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Db       3730 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3789

Qy       3724 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3783
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Db       3850 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3909

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RESULT 26
US-09-435-059-35
; Sequence 35,.Application US/09435059
; Patent No. 6323323
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/435,059
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/477,329
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4054 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      CLONE:  p-alpha-17B
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  205..3471
;      OTHER INFORMATION:
US-09-435-059-35

  Query Match             59.9%;  Score 3838.8;  DB 3;  Length 4054;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3862;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

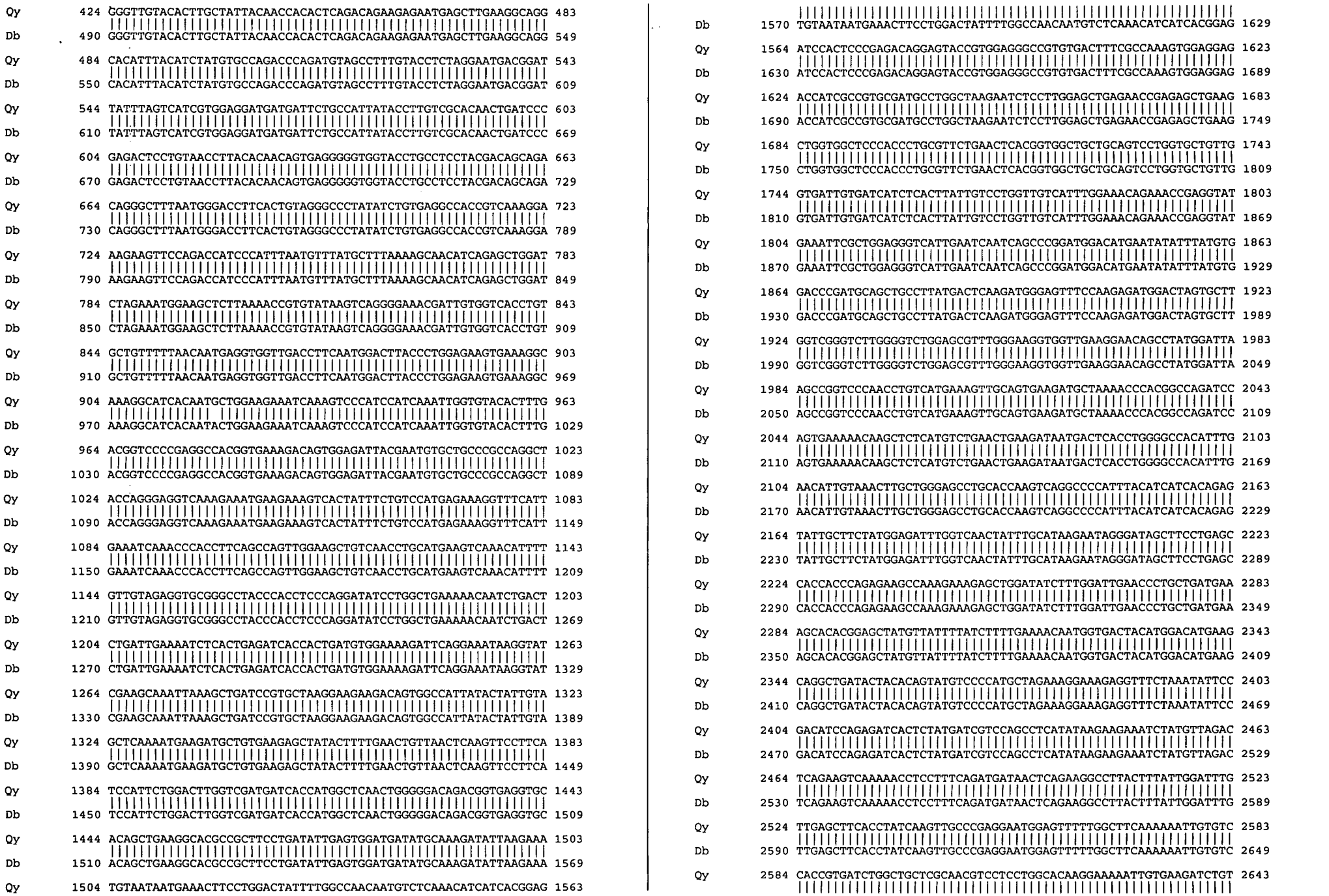
Qy        124 AAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTC 183
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Db        310 GAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTG 369

Qy        304 AGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAA 363
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Qy 1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db 1210 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1269
Qy 1204 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1263
Db 1270 CTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTAT 1329
Qy 1264 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1323
Db 1330 CGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTA 1389
Qy 1324 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1383
Db 1390 GCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCA 1449
Qy 1384 TCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGC 1443
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Qy 1444 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1503
Db 1510 ACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAA 1569
Qy 1504 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1563
Db 1570 TGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAG 1629
Qy 1564 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1623
Db 1630 ATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAG 1689
Qy 1624 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1683
Db 1690 ACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAG 1749
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Qy 1804 GAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTG 1863
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Qy 1864 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1923
Db 1930 GACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTT 1989
Qy 1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
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Qy 1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
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Db 2170 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2229
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Db 2230 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2289
Qy 2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283
Db 2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349
Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
Db 2350 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2409
Qy 2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
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Qy 2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
Db 2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529
Qy 2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
Db 2530 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2589
Qy 2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Qy 2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643

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Db       2710 GACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACC 2769

Qy       2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
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Db       2770 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2829

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Db       2830 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2889

Qy       2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
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Qy       2884 GCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGT 2943
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Db       3010 GAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCT 3069

Qy       3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
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Db       3070 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3129

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Qy       3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
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Qy       3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Db       3370 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3429

Qy       3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
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Qy       3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Db       3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy       3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Db       3550 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3609

Qy       3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Db       3610 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3669

Qy       3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy       3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Db       3790 ACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAG 3849

Qy       3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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RESULT 27
US-09-866-510-1
; Sequence 1, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3267)
US-09-866-510-1

Query Match 51.0%; Score 3270; DB 3; Length 3270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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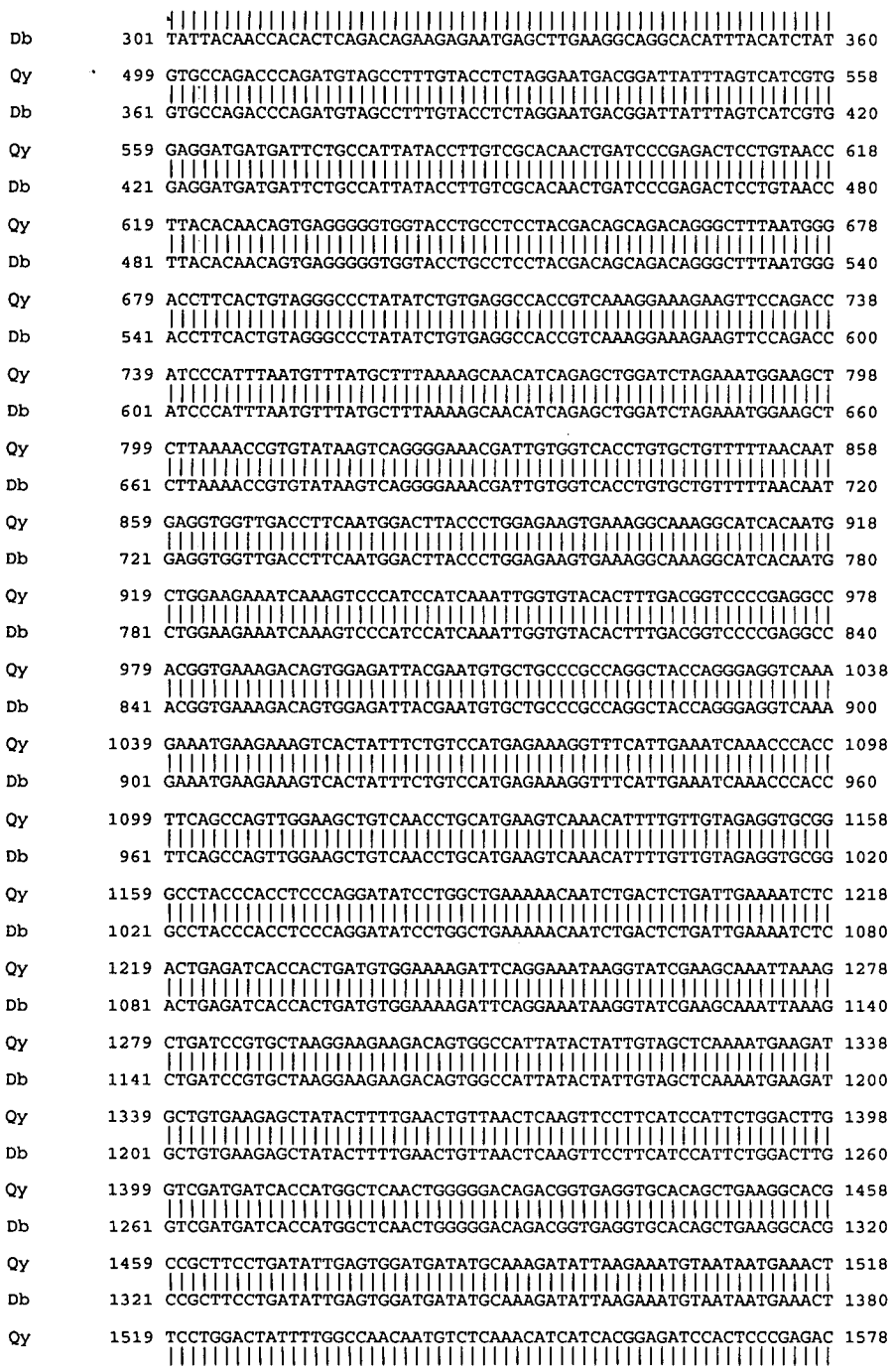
Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
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Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
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Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
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Db 361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420
Qy 559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
Db 421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480
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Db 1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200
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Db 2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100
Qy 2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
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Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270
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RESULT 28
US-09-866-510-3
; Sequence 3, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-3

  Query Match           51.0%;  Score 3268.4;  DB 3;  Length 3270;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3269;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy       1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy       1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
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Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCTTATGACTCAAGATGGAAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

Qy       2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
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Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100

Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
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Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Db       2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460

Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Db       2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
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Db       2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580

Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
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Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
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Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
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Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120
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Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
             ||||||||||||||||||||||||||||||
Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270


RESULT 29
US-09-866-510-7
; Sequence 7, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 3270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-7

  Query Match           51.0%;  Score 3268.4;  DB 3;  Length 3270;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3269;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
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Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
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Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
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Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
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Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
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Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
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Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
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Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
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Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
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Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
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Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
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Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
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Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
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Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
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Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
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Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
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Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
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Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
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Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
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Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
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Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
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Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
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Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
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Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
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Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

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Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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RESULT 30
US-09-866-510-9
; Sequence 9, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3267)
US-09-866-510-9

Query Match 51.0%; Score 3268.4; DB 3; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3269; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
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Qy      199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy      559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy      619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
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Qy      679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
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Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy      859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

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Qy     1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
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Qy     1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy     1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

Qy     2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy     2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy     2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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Qy     2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
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Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
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Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460

Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCATGAAG 2580

Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270


RESULT 31
US-09-866-510-5
; Sequence 5, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 3270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-5

  Query Match            50.9%;  Score 3266.8;  DB 3;  Length 3270;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3268;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600
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Qy      739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy      799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy      859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy      919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy      979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy      1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy      1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy      1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy      1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy      1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy      1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy      1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

Qy      2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy      2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
             |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 CTGGGAGCCTGCATGAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy      2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100

Qy      2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy      2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy      2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy      2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy      2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

Qy      2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460

Qy      2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy      2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580

Qy      2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy      2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy      2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy      2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
                ||||||||||||||||||||||||||||||
Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270


RESULT 32
US-09-628-188A-2
; Sequence 2, Application US/09628188A
; Patent No. 6566075
;   GENERAL INFORMATION:
;        APPLICANT: ESCOBEDO, Jaime A.
;                   WILLIAMS, Lewis T.
;        TITLE OF INVENTION: METHODS FOR DETECTING HUMAN
;                            PLATELET-DERIVED GROWTH FACTOR RECEPTOR AGONISTS
;                            AND ANTAGONISTS
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
;             STREET: P.O. Box 1404
;             CITY: Alexandria
;             STATE: Virginia
;             COUNTRY: United States
;             ZIP: 22313-1404
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/628,188A
;             FILING DATE: 28-Jul-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/240,294
;             FILING DATE: 19-MAY-1994
;             APPLICATION NUMBER: US 08/031,082
;             FILING DATE: 15-MAR-1993
;             APPLICATION NUMBER: US 07/771,829
;             FILING DATE: 07-OCT-1991
;             APPLICATION NUMBER: US 07/309,322
;             FILING DATE: 10-FEB-1989
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McGowan, Malcolm K.
;             REGISTRATION NUMBER: 39,300
;             REFERENCE/DOCKET NUMBER: 028723-266
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (703) 836-6620
;             TELEFAX: (703) 836-2021
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3199 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  2..3199
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-628-188A-2

  Query Match           49.5%;  Score 3176.8;  DB 3;  Length 3199;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3192;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy        240 AAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGA 299
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Db          1 AAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGA 60

Qy        300 AGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGA 359
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGA 120

Qy        360 AGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCA 419
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        121 AGAAAACAACAGCGGCCTTTCTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCA 180

Qy        420 CACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGG 479
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGG 240

Qy        480 CAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGAC 539
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGAC 300

Qy        540 GGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGA 599
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGA 360

Qy        600 TCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAG 659
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAG 420

Qy        660 CAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAA 719
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAA 480

Qy        720 AGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCT 779
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCT 540

Qy        780 GGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCAC 839
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCAC 600

Qy        840 CTGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAA 899
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAA 660

Qy        900 AGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACAC 959
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACAC 720
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Qy      960 TTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCA 1019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCA 780

Qy     1020 GGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTT 1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTT 840

Qy     1080 CATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACA 1139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACA 900

Qy     1140 TTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCT 1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCT 960

Qy     1200 GACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAG 1259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAG 1020

Qy     1260 GTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTAT 1319
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GTATCGAAGCAAATTAAAGCTGATCCGTGCTAACCAAGAAGACAGTGGCCATTATACTAT 1080

Qy     1320 TGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCC 1379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCC 1140

Qy     1380 TTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAG 1439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAG 1200

Qy     1440 GTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAA 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAA 1260

Qy     1500 GAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCAC 1559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCAC 1320

Qy     1560 GGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGA 1619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGA 1380

Qy     1620 GGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCT 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 GGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCT 1440

Qy     1680 GAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCT 1739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 GAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCT 1500

Qy     1740 GTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAG 1799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAG 1560

Qy     1800 GTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTA 1859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTA 1620

Qy     1860 TGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGT 1919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 TGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGT 1680

Qy     1920 GCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGG 1979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGG 1740

Qy     1980 ATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAG 2039
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 ATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAACATGCTAAAACCCACGGCCAG 1800

Qy     2040 ATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACA 2099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 ATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACA 1860

Qy     2100 TTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCAC 2159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 TTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCAC 1920

Qy     2160 AGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCT 2219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 AGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCT 1980

Qy     2220 GAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGA 2279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 GAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGA 2040

Qy     2280 TGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACAT 2339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 TGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACAT 2100

Qy     2340 GAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATA 2399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 GAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATA 2160

Qy     2400 TTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTT 2459
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Db     2161 TTCCGACGTCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTT 2220

Qy     2460 AGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGA 2519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 AGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGA 2280

Qy     2520 TTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTG 2579
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Db     2281 TTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTG 2340

Qy     2580 TGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGAT 2639
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Db     2341 TGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGAT 2400

Qy     2640 CTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAG 2699
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Db     2401 CTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGTTCTATGTGTCGAAAGGCAG 2460

Qy     2700 TACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCAC 2759
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 TACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCAC 2520

Qy     2760 ACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCAC 2819
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Db     2521 ACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCAC 2580

Qy     2820 CCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCG 2879
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Db     2581 CCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCG 2640

Qy     2880 GATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAA 2939
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 GATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAA 2700

Qy     2940 CAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCT 2999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701 CAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCT 2760

Qy     3000 GCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCA 3059
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Db     2761 GCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCA 2820

Qy     3060 TCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAA 3119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821 TCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAA 2880

Qy     3120 AAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGC 3179
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Db       2881 AAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGC 2940

Qy       3180 TGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCT 3239
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCT 3000

Qy       3240 GGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTC 3299
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTC 3060

Qy       3300 CAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGA 3359
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 CAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGA 3120

Qy       3360 CGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTC 3419
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 CGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTC 3180

Qy       3420 GAGGGGTTCCTTCCACTTCT 3439
              || ||||||||||||||||
Db       3181 GA-GGGTTCCTTCCACTTCT 3199


RESULT 33
US-09-949-016-12574
; Sequence 12574, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12574
;   LENGTH: 72843
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(72843)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12574

  Query Match             48.4%;  Score 3106.4;  DB 3;  Length 72843;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3121;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
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Db      67724 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 67783

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67784 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 67843

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
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Db      67844 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 67903

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
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Db      67904 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 67963

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67964 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 68023

Qy       3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68024 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 68083

Qy       3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68084 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 68143

Qy       3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68144 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 68203

Qy       3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68204 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 68263

Qy       3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68264 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 68323

Qy       3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68324 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 68383

Qy       3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
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Db      68384 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 68443

Qy       3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
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Db      68444 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 68503

Qy       4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
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Db      68504 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 68563

Qy       4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68564 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 68623

Qy       4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68624 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 68683

Qy       4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      68684 TATGGTAATAGCTTTAGTGAATCAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 68743

Qy       4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68744 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 68803

Qy       4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68804 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 68863

Qy       4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68864 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 68923

Qy       4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68924 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 68982

Qy       4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      68983 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 69042

Qy       4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      69043 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 69102
Qy       4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697
Db      69103 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 69162
Qy       4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
Db      69163 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 69222
Qy       4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
Db      69223 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 69282
Qy       4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
Db      69283 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 69342
Qy       4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937
Db      69343 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 69402
Qy       4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997
Db      69403 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 69462
Qy       4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057
Db      69463 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 69522
Qy       5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
Db      69523 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 69582
Qy       5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177
Db      69583 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 69642
Qy       5178 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237
Db      69643 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 69702
Qy       5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297
Db      69703 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 69762
Qy       5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357
Db      69763 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 69822
Qy       5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 5417
Db      69823 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 69882
Qy       5418 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 5477
Db      69883 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 69942
Qy       5478 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 5537
Db      69943 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 70002
Qy       5538 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 5597
Db      70003 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 70062
Qy       5598 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 5657
Db      70063 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 70122
Qy       5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717
Db      70123 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 70182
Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
Db      70183 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 70242
Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
Db      70243 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 70302
Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
Db      70303 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 70362
Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
Db      70363 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 70422
Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
Db      70423 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 70482
Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
Db      70483 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 70542
Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
Db      70543 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 70602
Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
Db      70603 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 70662
Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
Db      70663 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 70722
Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
Db      70723 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 70782
Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
Db      70783 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 70842
Qy       6378 TAAAAAAA 6385
Db      70843 TATACTAA 70850
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RESULT 34
US-09-949-016-13439
; Sequence 13439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13439
;   LENGTH: 40505
;   TYPE: DNA
;   ORGANISM: Human
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(40505)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13439

  Query Match            33.3%;  Score 2135.2;  DB 3;  Length 40505;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 2148;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38355 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 38414

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38415 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 38474

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38475 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 38534

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38535 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 38594

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38595 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 38654

Qy       3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
             |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db      38655 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 38714

Qy       3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38715 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 38774

Qy       3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38775 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 38834

Qy       3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38835 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 38894

Qy       3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38895 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 38954

Qy       3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38955 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 39014

Qy       3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39015 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 39074

Qy       3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39075 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 39134

Qy       4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39135 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 39194

Qy       4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39195 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 39254

Qy       4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39255 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 39314

Qy       4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      39315 TATGGTAATAGCTTTAGTGAATCAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 39374

Qy       4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39375 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 39434

Qy       4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39435 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 39494

Qy       4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39495 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 39554

Qy       4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      39555 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 39613

Qy       4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39614 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 39673

Qy       4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39674 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 39733

Qy       4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39734 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 39793

Qy       4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39794 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 39853

Qy       4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39854 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 39913

Qy       4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39914 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 39973

Qy       4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39974 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 40033

Qy       4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40034 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 40093

Qy       4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40094 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 40153

Qy       5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40154 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 40213

Qy       5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40214 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 40273

Qy       5178 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40274 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 40333

Qy       5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40334 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 40393
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Qy       5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357
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Db      40394 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 40453

Qy       5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAG 5409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40454 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAG 40505


RESULT 35
US-09-949-016-1697
; Sequence 1697, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1697
;   LENGTH: 2768
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-1697

  Query Match             32.5%;  Score 2085.2;  DB 3;  Length 2768;
  Best Local Similarity   82.0%;  Pred. No. 0;
  Matches 2680;  Conservative    0;  Mismatches   88;  Indels  502;  Gaps    4;

Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

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Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
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Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
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Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
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Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
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Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
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Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

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Db         901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
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Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
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Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
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Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
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Db       1810 GTCATGAAAGTTGCAGTGAAGATGCTAAAAC------------------------------ 1840

Qy       2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118

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Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298

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Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
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Db       1942 CAC------------------------------------------------------- 1944

Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Db       1945 --------------------------TCTGGGTGTTGGTGTGTCCACCGTGATCTGGCT 1977

Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Db       2038 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2097

Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
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Db       2158 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTATGGGCCTGACATTGCTGCTTATT 2217

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Db       2218 TGGGCTGTTCTGAAACACCACTGGAAGGAAAATG------------------TGTTCTT 2258

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             | | |       ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 TCAAGCCCCAGGATCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2318

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Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
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RESULT 36
US-09-866-510-11
; Sequence 11, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
US-09-866-510-11

Query Match 27.6%; Score 1767; DB 3; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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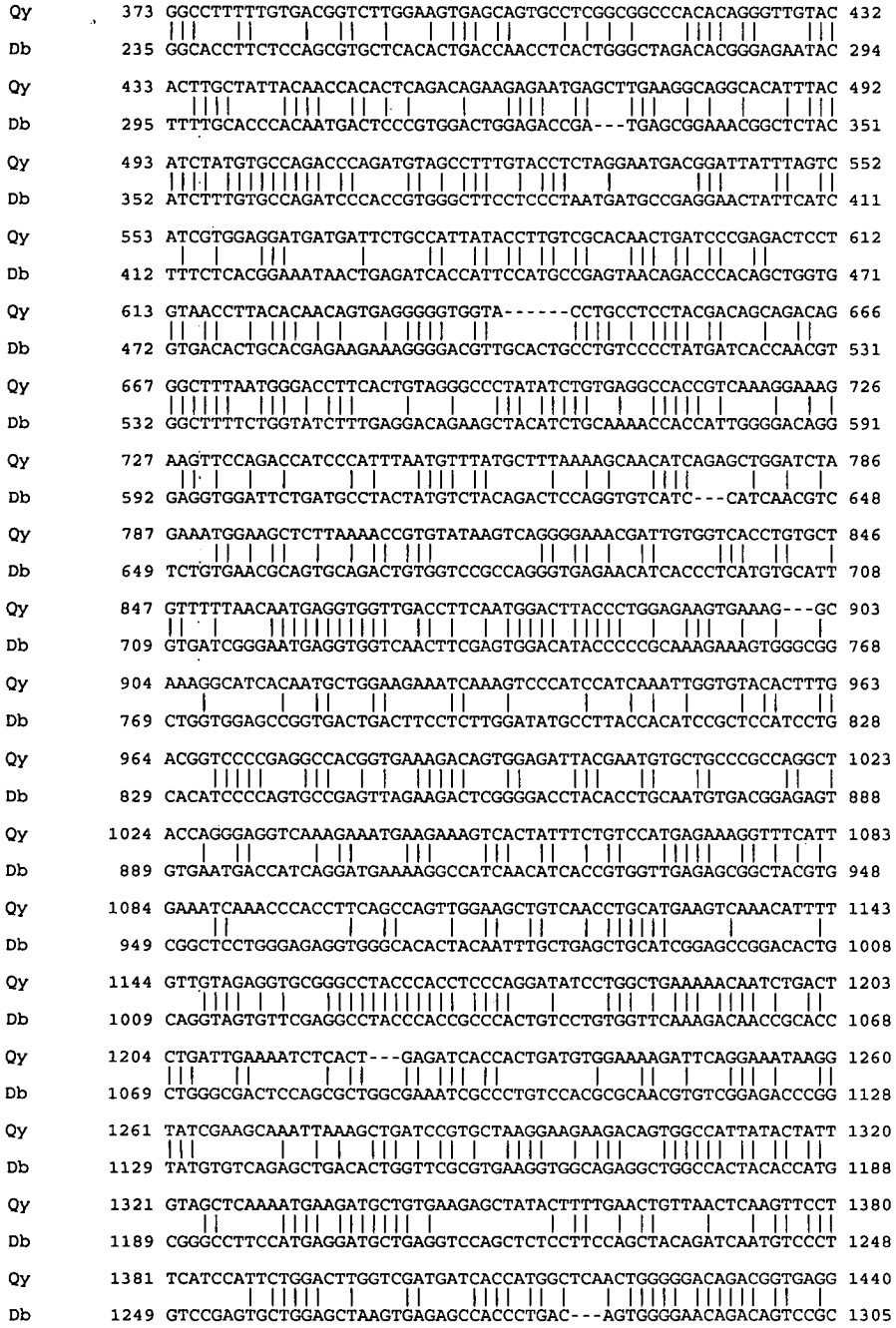
Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

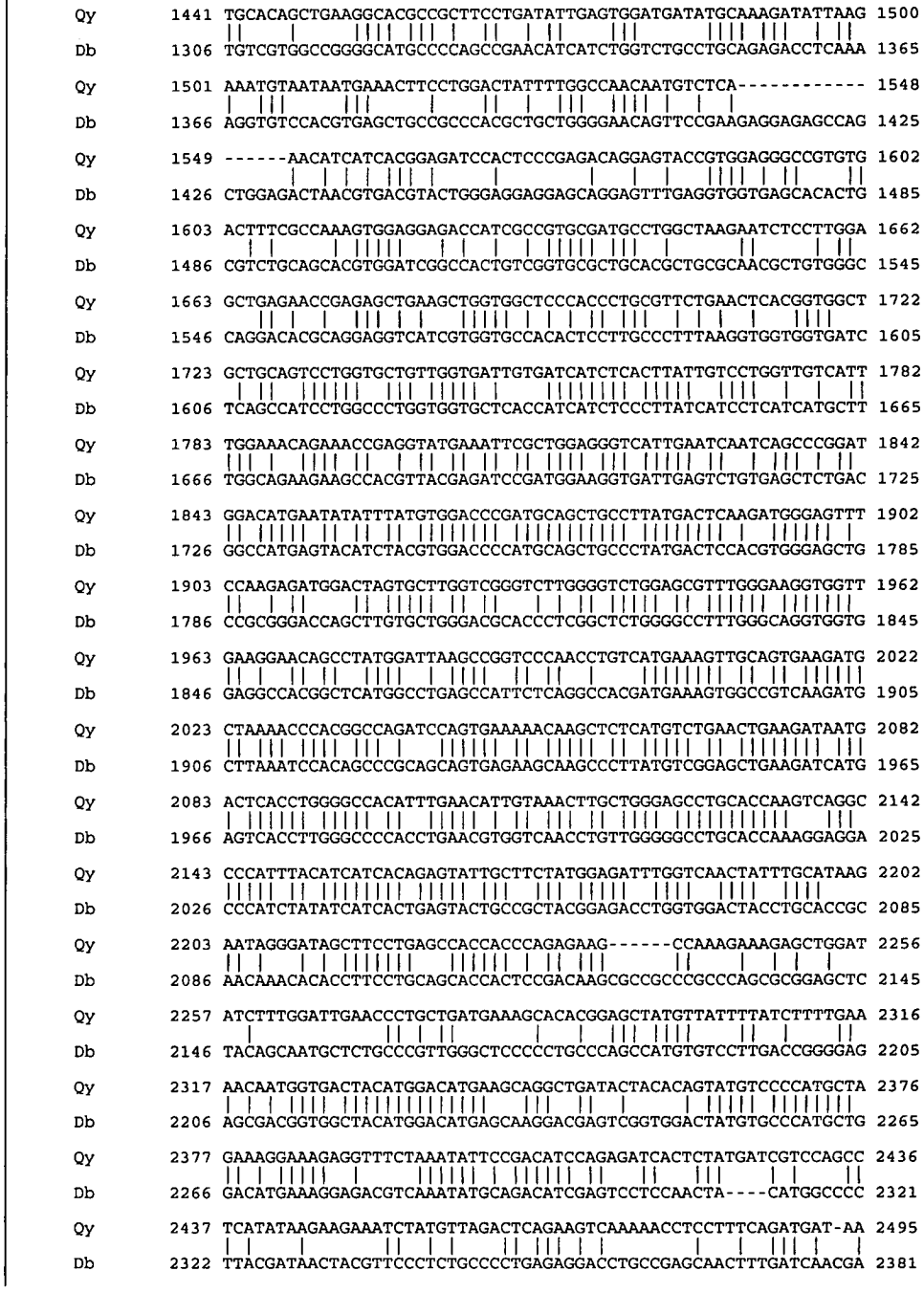
Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCA 1905
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RESULT 37
US-09-866-510-21
; Sequence 21, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3318)
US-09-866-510-21

Query Match 10.4%; Score 667.6; DB 3; Length 3321;
Best Local Similarity 55.5%; Pred. No. 9.1e-137;

Matches 1516; Conservative 0; Mismatches 1164; Indels 50; Gaps 10;





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Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
             ||   ||  || |  |   ||||  |  || ||||||| ||| || || |||   || ||
Db       2382 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2441

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
             ||||||| |||| || || || || |||||| | || ||||| ||| | ||||| ||| |
Db       2442 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2501

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
              |||| ||  | || ||||||||||||||||||||||||  |||||||||||  ||
Db       2502 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2561

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
              ||||| ||  | || |||||||| |||||| |||| ||||||||||||||| |||||
Db       2562 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTATGAAGTGGATGGCTCCGGAGAG 2621

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
              |||||| ||| |||||||||||| ||||| || || ||||| | || || ||||||||
Db       2622 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2681

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
              |||||||||  || | |||||||||||||||||  |   ||   || |     |||||
Db       2682 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2741

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
              ||||   |||||  | || ||||| |||||| |||||| ||| ||  ||  ||  ||||
Db       2742 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2801

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
              |||||||||  ||| |||||| |     ||   ||||   | ||| |||| | ||| ||
Db       2802 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 2861

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
              |     | || | ||||  ||| ||   | |   || |||||||  ||  |  |  |  |
Db       2862 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 2921

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
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Db       2922 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 2951
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RESULT 38
US-08-168-917-1
; Sequence 1, Application US/08168917
; Patent No. 5686572
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor \ One Market
;      STREET:  Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/168,917
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/650,793
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  12418-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3504
US-08-168-917-1

  Query Match             10.4%;  Score 667.6;  DB 2;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||     |  ||  |    | ||| ||    | | | |    |||| ||   |||
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
              ||||    ||||  || | |    |  ||||  ||  |||  | |  |   | |||
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||| ||    || | |||  | |||   |       |||    ||  ||
Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              |  |  |||        |   || || || ||    ||| || ||
Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | ||| | |   | ||||  ||        ||||  | ||||  ||   | ||
Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||     |   |  ||| |||||  |  |||||  |    | | |
Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

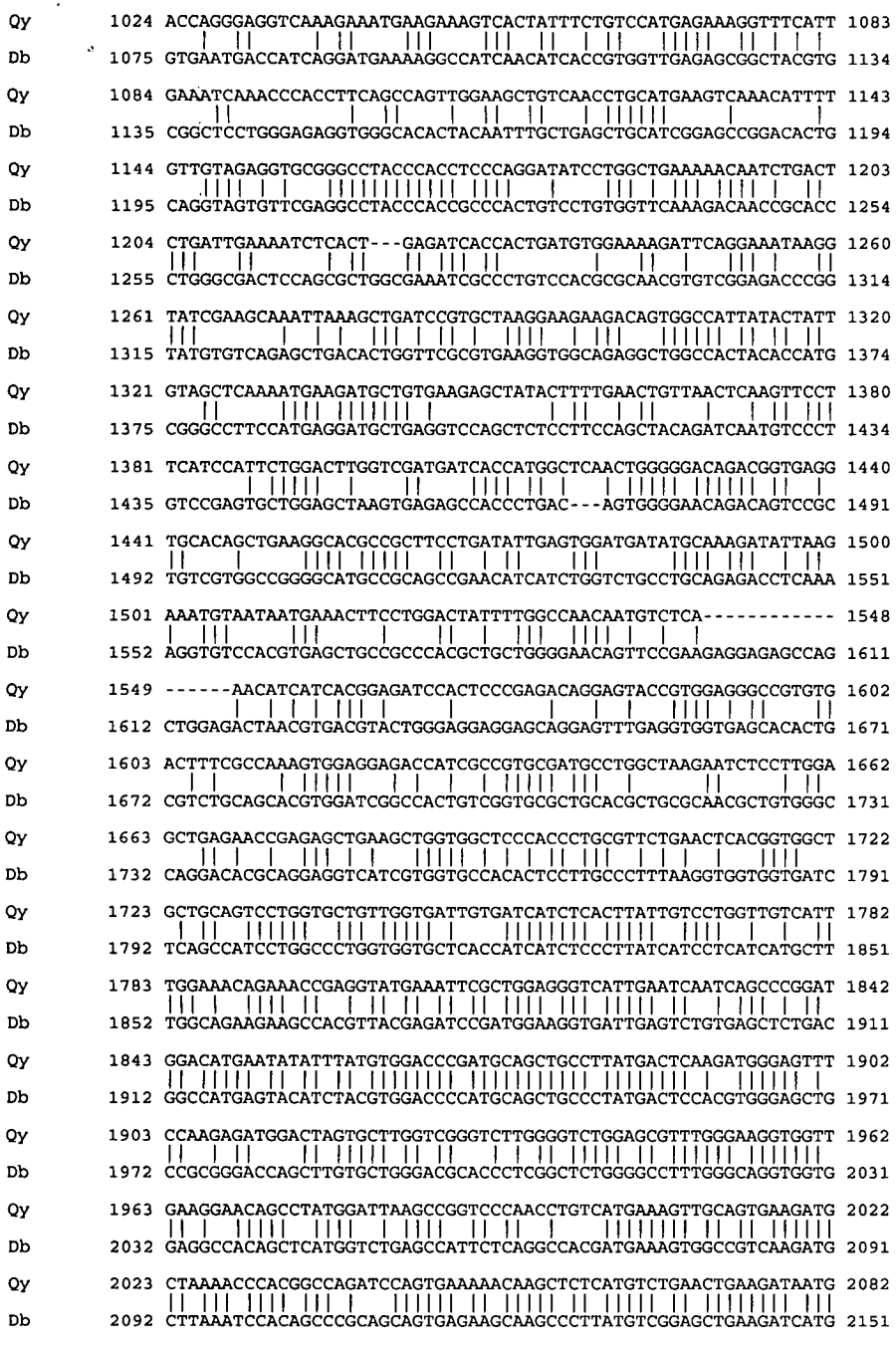
Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  |  |     | |  |||| ||      |  |  ||||      |  |  |
Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

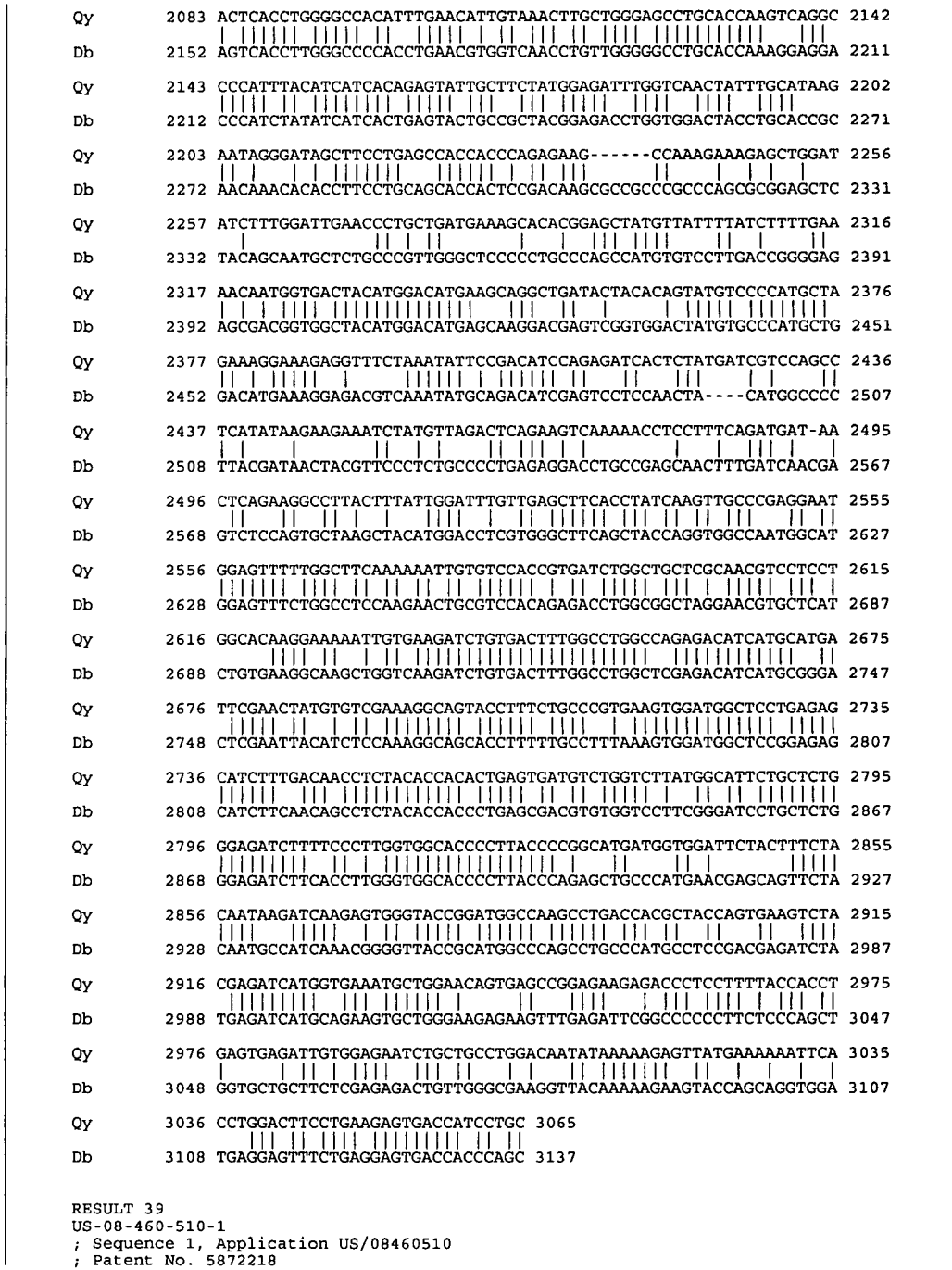
Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
              || | ||  |  | || |||          || || |  ||     |||  ||   |
Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |  ||||| |||||  || |  | ||||| |||||  |  |||  | |  |
Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
              |     |  ||  ||  ||  |     |  | | |  |  |||  ||
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
              |||||  |||  | |  |||||  ||   |||  ||  ||      ||  |
Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074
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RESULT 39
US-08-460-510-1
; Sequence 1, Application US/08460510
; Patent No. 5872218

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;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,510
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3504
US-08-460-510-1

  Query Match           10.4%;  Score 667.6;  DB 2;  Length 5427;
  Best Local Similarity  55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy       373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
Db       421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy       433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
Db       481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy       493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
Db       538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy       553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
Db       598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy       613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
Db       658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy       667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
Db       718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy       727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
Db       778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy       787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
Db       835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy       847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
Db       895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy       904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
Db       955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy       964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db       1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db       1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db       1255 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1314

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db       1315 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1374

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db       1375 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1434

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db       1435 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1491

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db       1492 TGTCGTGGCCGGGGCATGCCGCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1551

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
Db       1552 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1611

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
Db       1612 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1671

Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
Db       1672 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1731

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
Db       1732 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1791
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Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
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Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
Db       1852 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 1911

Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
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Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
Db       1972 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2031

Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
Db       2032 GAGGCCACAGCTCATGGTCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2091

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082
Db       2092 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 2151

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142
Db       2152 AGTCACCTTGGGCCCCACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGA 2211

Qy       2143 CCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAG 2202
Db       2212 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2271

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256
Db       2272 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2331

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316
Db       2332 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2391

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376
Db       2392 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2451

Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
Db       2452 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2507

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
Db       2508 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2567

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
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Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
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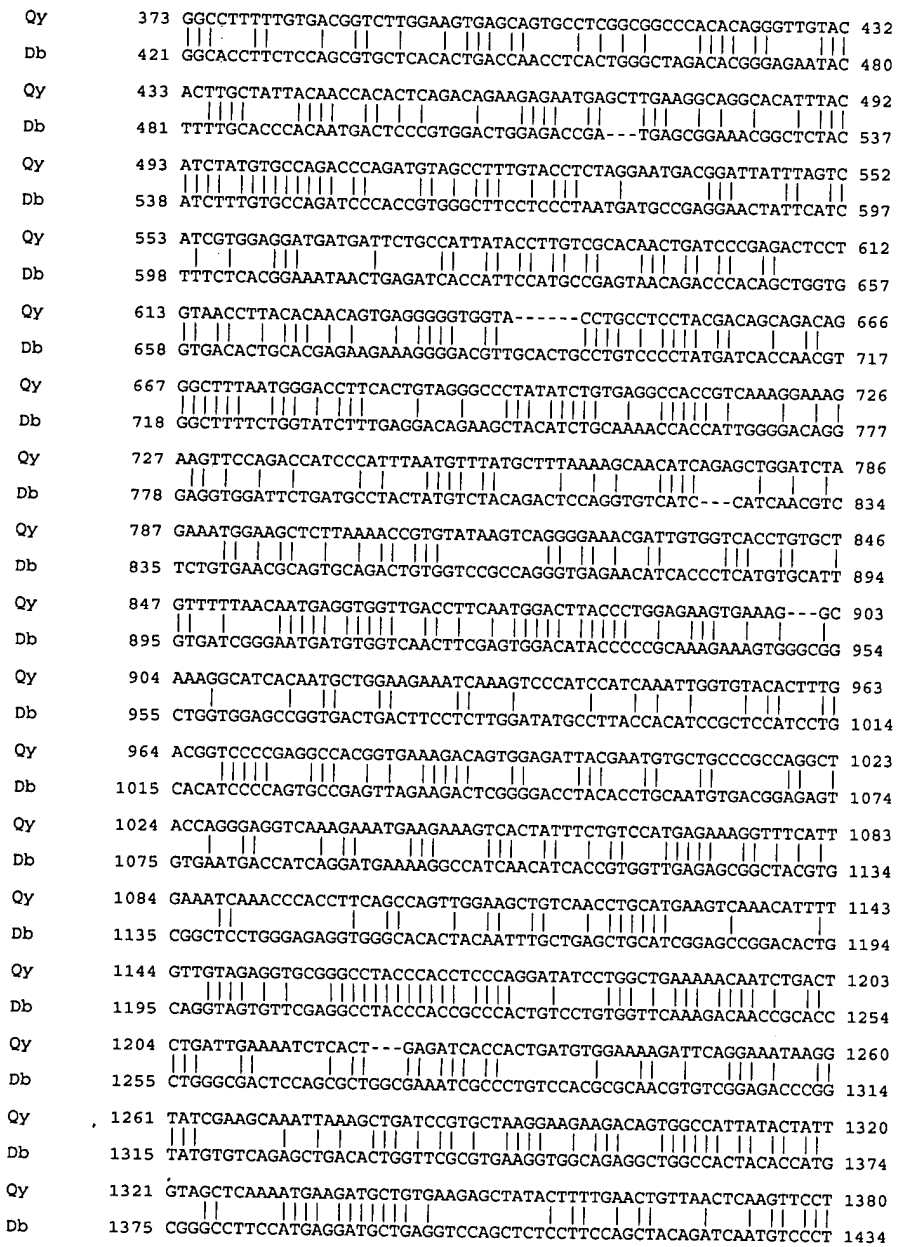
Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

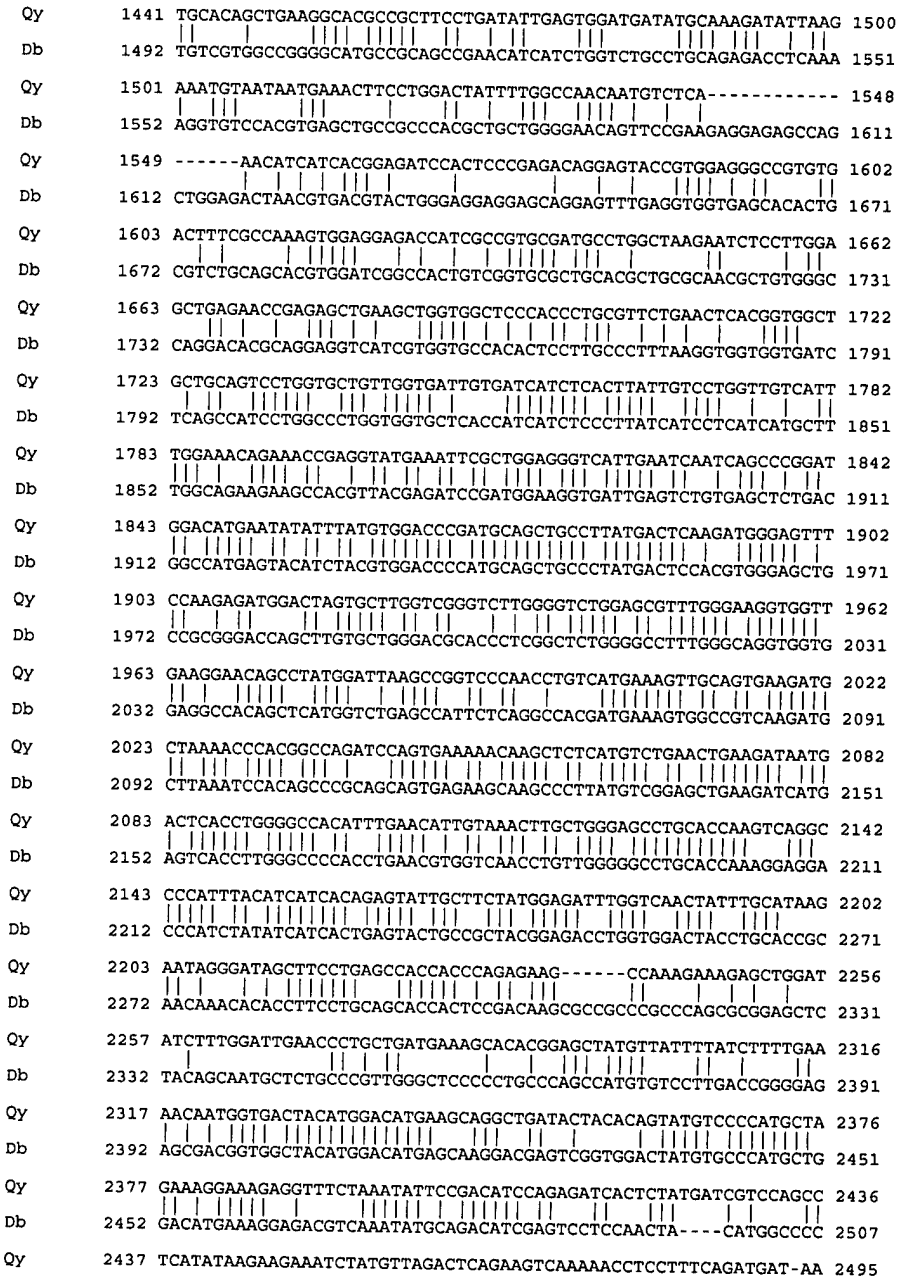
Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137
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RESULT 40
US-08-460-490-1
; Sequence 1, Application US/08460490
; Patent No. 5891652
;  GENERAL INFORMATION:
;    APPLICANT:  Wolf, David
;    APPLICANT:  Tomlinson, James E.
;    APPLICANT:  Fretto, Larry J.
;    APPLICANT:  Giese, Neill A.
;    APPLICANT:  Escobedo, Jaime A.
;    APPLICANT:  Williams, Lewis T.
;    TITLE OF INVENTION:  DOMAINS OF EXTRACELLULAR REGION OF HUMAN
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW
;      STREET:  One Market Plaza, Steuart Street Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,490
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  012418-001420
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3504
US-08-460-490-1
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Query Match 10.4%; Score 667.6; DB 2; Length 5427;
Best Local Similarity 55.5%; Pred. No. 1.1e-136;
Matches 1516; Conservative 0; Mismatches 1164; Indels 50; Gaps 10;





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Db       2508 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2567

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555

Db       2568 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2627

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615

Db       2628 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2687

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675

Db       2688 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2747

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735

Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795

Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855

Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915

Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975

Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137


RESULT 41
US-08-462-728-3
; Sequence 3, Application US/08462728
; Patent No. 6043211
;  GENERAL INFORMATION:
;    APPLICANT:  WILLIAMS, Lewis T.
;    APPLICANT:  ESCOBEDO, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:. Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,728
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3507
US-08-462-728-3

  Query Match            10.4%;  Score 667.6;  DB 3;  Length 5427;
  Best Local Similarity  55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552

Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612

Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666

Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726

Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786

Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846

Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903

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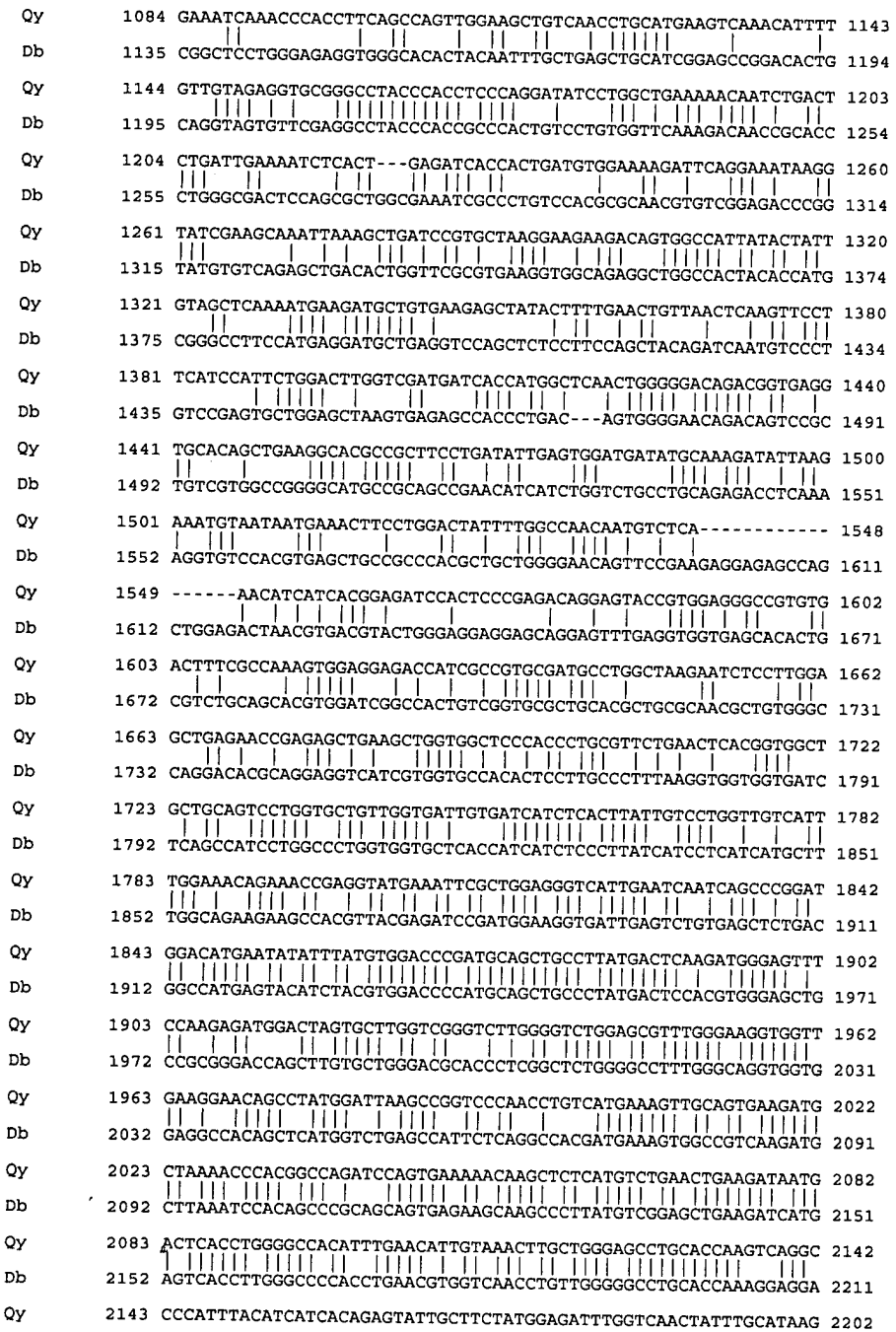
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

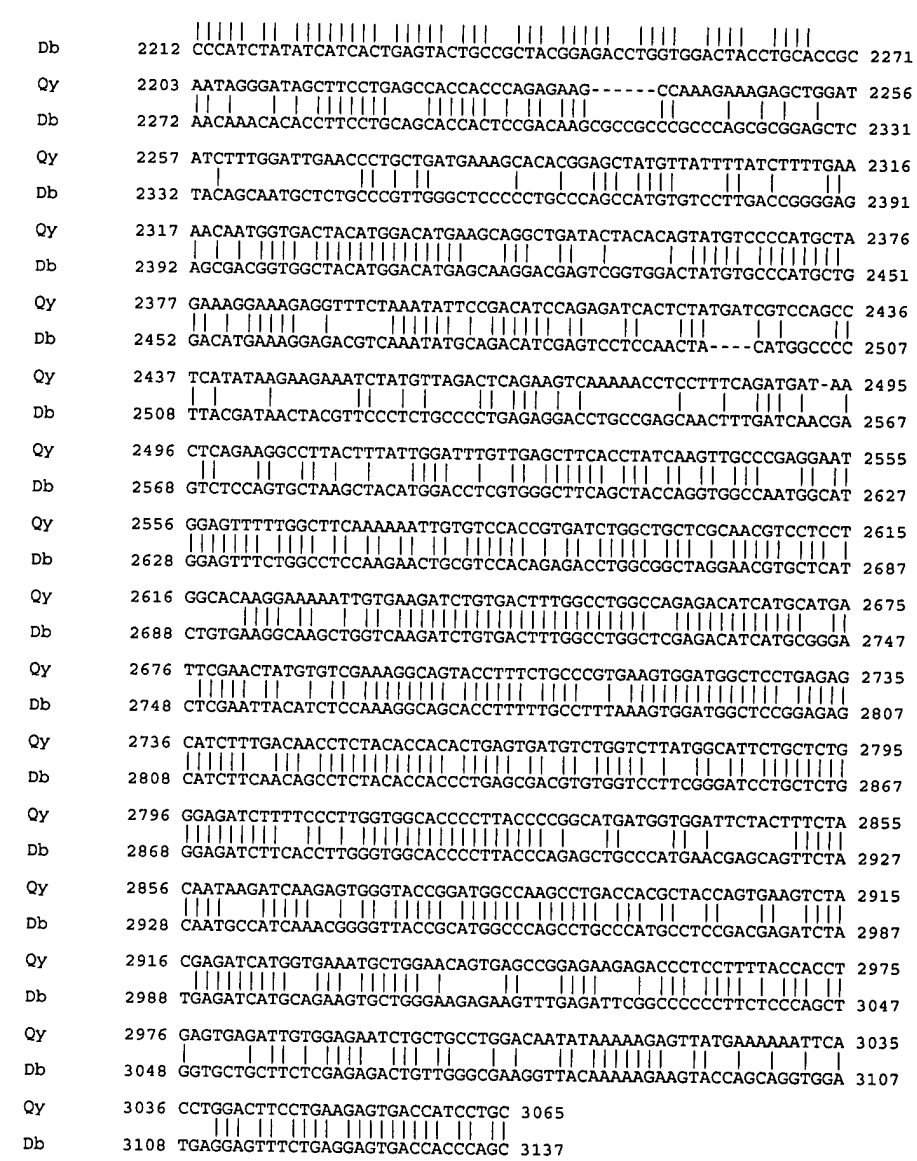
Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023

Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083

Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134
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RESULT 42
US-08-461-917-3
; Sequence 3, Application US/08461917
; Patent No. 6372438
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market, Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,917
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,414
;      FILING DATE:  02-FEB-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Karen B.
;      REGISTRATION NUMBER:  29,684
;      REFERENCE/DOCKET NUMBER:  2307K-267-2-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/326-2400
;      TELEFAX:  415/326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3507
US-08-461-917-3

  Query Match             10.4%;  Score 667.6;  DB 3;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
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Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
              ||||    ||||  || | |    |  ||||  ||   ||| | |   | |||
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
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Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              |  |   |||       |      ||  || || || ||   ||| || ||  ||
Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | ||| | |   | ||||  ||        |||| | |||| ||   |  ||
Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||    |   |   ||| |||||  |  |||||    |  | |
Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  |  |     | |   |||| ||      |  | |   ||||     |  | |
Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
              || | ||  |  | || |||          || || |  ||     |||  ||   |
Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |   ||||| |||||  || |  | ||||| |||||  |  |||  |  |   |
Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
              |     |  ||  ||   ||  |     |  | | |  | ||   ||
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
              |||||  |||  | |  |||||  ||   |||  ||   ||       || |
Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
              |  ||    | ||   |||   |||  ||  | ||  |||||  || | | |
Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
              ||          | ||    | ||  ||  | ||||||    |       |
Db       1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
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Db       1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              |||  ||      | ||  || ||| ||         |   ||  |  ||| |  ||
Db       1255 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1314

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              |||      |  | |  ||| | || |  ||||  | |||  ||||||  || || ||
Db       1315 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1374

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||      |||| |||||||  |          | ||  | ||    |  | ||| |||
Db       1375 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1434

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
                | |||||  |    ||    |||| || |   | |||||  ||||||  ||  |
Db       1435 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1491

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||    |    |||| |||||  ||  | ||   |||     |||| |||  | ||
Db       1492 TGTCGTGGCCGGGGCATGCCGCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1551

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
              |  |||      |||      ||  |  |||  |||| |  |  |
Db       1552 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1611

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
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Db       1612 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1671

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Db       1672 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1731

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
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Db       1732 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1791

Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
              | ||  ||||||  ||| ||||| |    |||||||| |||||  ||||  |  |  ||
Db       1792 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 1851

Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
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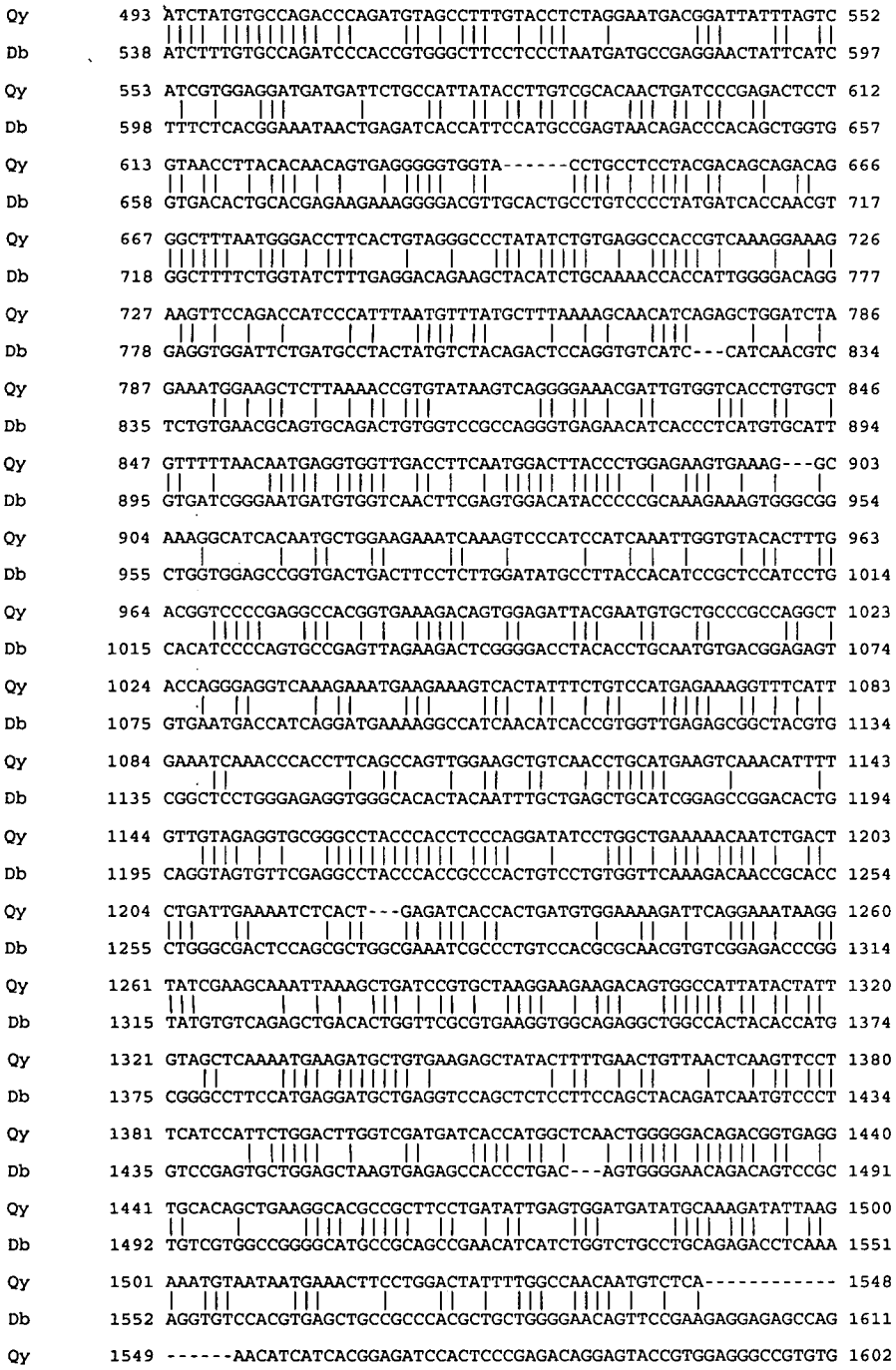
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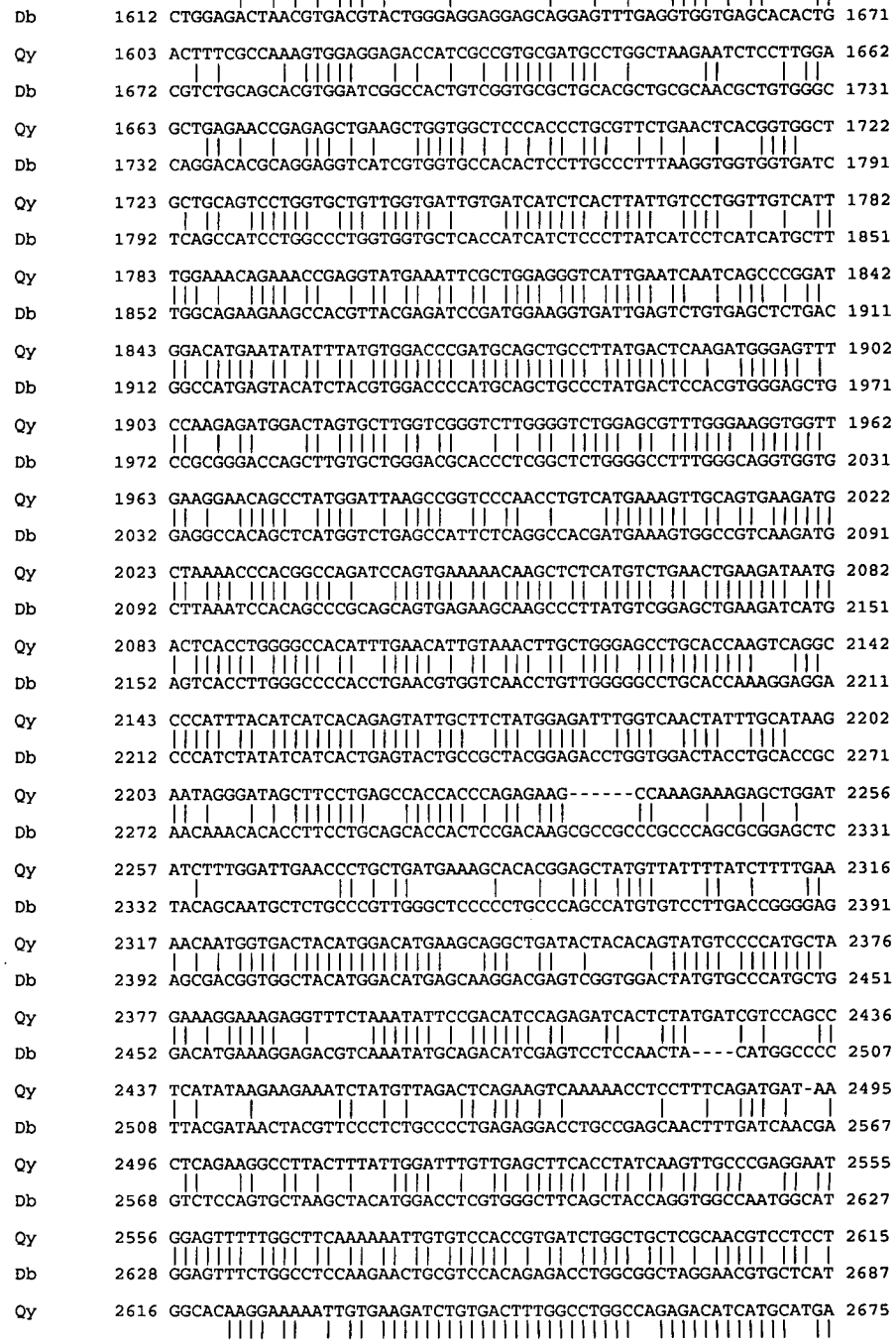
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Db       1972 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2031
Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
Db       2032 GAGGCCACAGCTCATGGTCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2091
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Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
Db       2452 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2507
Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
Db       2508 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2567
Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
Db       2568 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2627
Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
Db       2628 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2687
Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
Db       2688 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2747
Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807
Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867
Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927
Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987
Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047
Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107
Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137
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RESULT 43
US-08-464-436-3
; Sequence 3, Application US/08464436
; Patent No. 6514723
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: ESCOBEDO, Jaime A.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,436
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/309,322
; FILING DATE: 10-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3507
US-08-464-436-3

Query Match 10.4%; Score 667.6; DB 3; Length 5427;
Best Local Similarity 55.5%; Pred. No. 1.1e-136;
Matches 1516; Conservative 0; Mismatches 1164; Indels 50; Gaps 10;

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Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480
Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537
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Db       2688 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2747

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735

Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795

Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855

Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915

Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975

Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137


RESULT 44
US-08-464-436-3
; Sequence 3, Application US/08464436
; Patent No. 6642022
;   GENERAL INFORMATION:
;        APPLICANT: WILLIAMS, Lewis T.
;                   ESCOBEDO, Jaime A.
;        TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew
;             STREET: One Market, Steuart Street Tower, 20th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/464,436
;             FILING DATE: 05-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/309,322
;             FILING DATE: 10-FEB-1989
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dow, Karen B.
;             REGISTRATION NUMBER: 29,684
;             REFERENCE/DOCKET NUMBER: 2307K-267-2-3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5427 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  187..3507
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-464-436-3

  Query Match            10.4%;  Score 667.6;  DB 3;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552

Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612

Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666

Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726

Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786

Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846

Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903

Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963

Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023

Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083

Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143

Db       1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

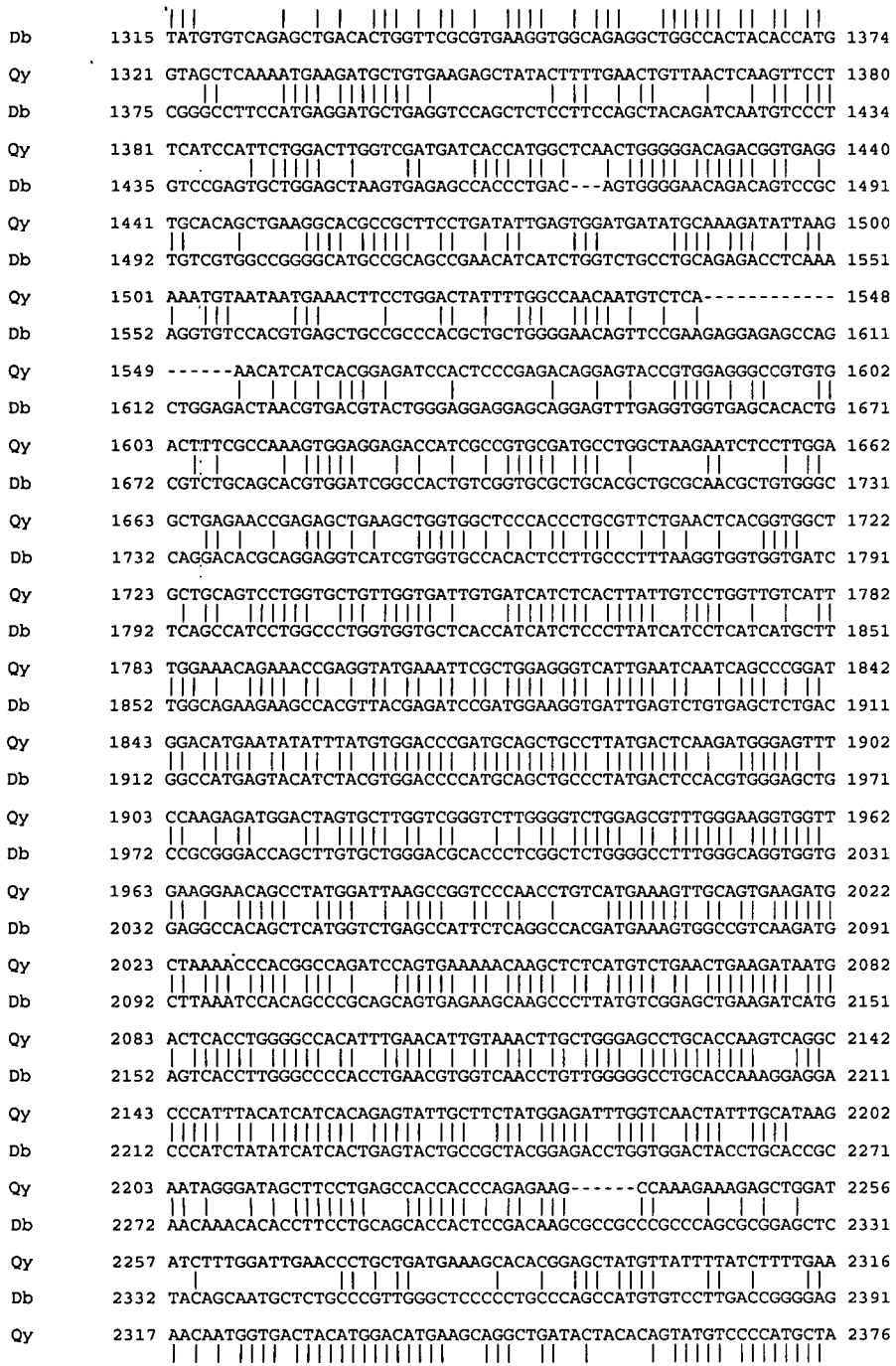
Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203

Db       1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260

Db       1255 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1314

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
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RESULT 45
PCT-US92-00730-1
; Sequence 1, Application PC/TUS9200730
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Steuart Street Tower, 20th Floor \ One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US92/00730
;       FILING DATE:  19920128
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ching, Edwin P.
;       REGISTRATION NUMBER:  34,090
;       REFERENCE/DOCKET NUMBER:  12418-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 326-2400
;       TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5427 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo Sapiens
;       STRAIN:  lambda gt10
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  187..3504
PCT-US92-00730-1

  Query Match             10.4%;  Score 667.6;  DB 6;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy       373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
Db       421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy       433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
Db       481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy       493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
Db       538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy       553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
Db       598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy       613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
Db       658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy       667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
Db       718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy       727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
Db       778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy       787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
Db       835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy       847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
Db       895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy       904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963

Db       955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy       964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
Db      1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy      1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db      1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy      1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db      1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

Qy      1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db      1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy      1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
Db      1255 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1314

Qy      1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db      1315 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1374

Qy      1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db      1375 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1434

Qy      1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db      1435 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1491

Qy      1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db      1492 TGTCGTGGCCGGGGCATGCCGCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1551

Qy      1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA---------- 1548
Db      1552 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1611

Qy      1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
Db      1612 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1671

Qy      1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
Db      1672 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1731

Qy      1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
Db      1732 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1791

Qy      1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
Db      1792 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 1851

Qy      1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
Db      1852 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 1911

Qy      1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
Db      1912 GGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGGAGCTG 1971

Qy      1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
Db      1972 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2031

Qy      1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
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Db       2032 GAGGCCACAGCTCATGGTCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2091

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082

Db       2092 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 2151

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142

Db       2152 AGTCACCTTGGGCCCCACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGA 2211

Qy       2143 CCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAG 2202

Db       2212 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2271

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256

Db       2272 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2331

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316

Db       2332 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2391

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376

Db       2392 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2451

Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436

Db       2452 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2507

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495

Db       2508 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2567

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555

Db       2568 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2627

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615

Db       2628 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2687

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675

Db       2688 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2747

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735

Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795

Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855

Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915

Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975

Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137
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RESULT 46
PCT-US92-00862-1
; Sequence 1, Application PC/TUS9200862
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Lewis T.
;    APPLICANT:  Escobedo, Jaime A.
;    TITLE OF INVENTION:  PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND
;      STREET:  Steuart Street Tower, 20th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00862
;      FILING DATE:  19920131
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/151,141
;      FILING DATE:  02-FEB-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/309,322
;      FILING DATE:  10-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  2307U-267-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5427 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  lambda gt10
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  187..3504
;      OTHER INFORMATION:
PCT-US92-00862-1

  Query Match           10.4%;  Score 667.6;  DB 6;  Length 5427;
  Best Local Similarity  55.5%;  Pred. No. 1.1e-136;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

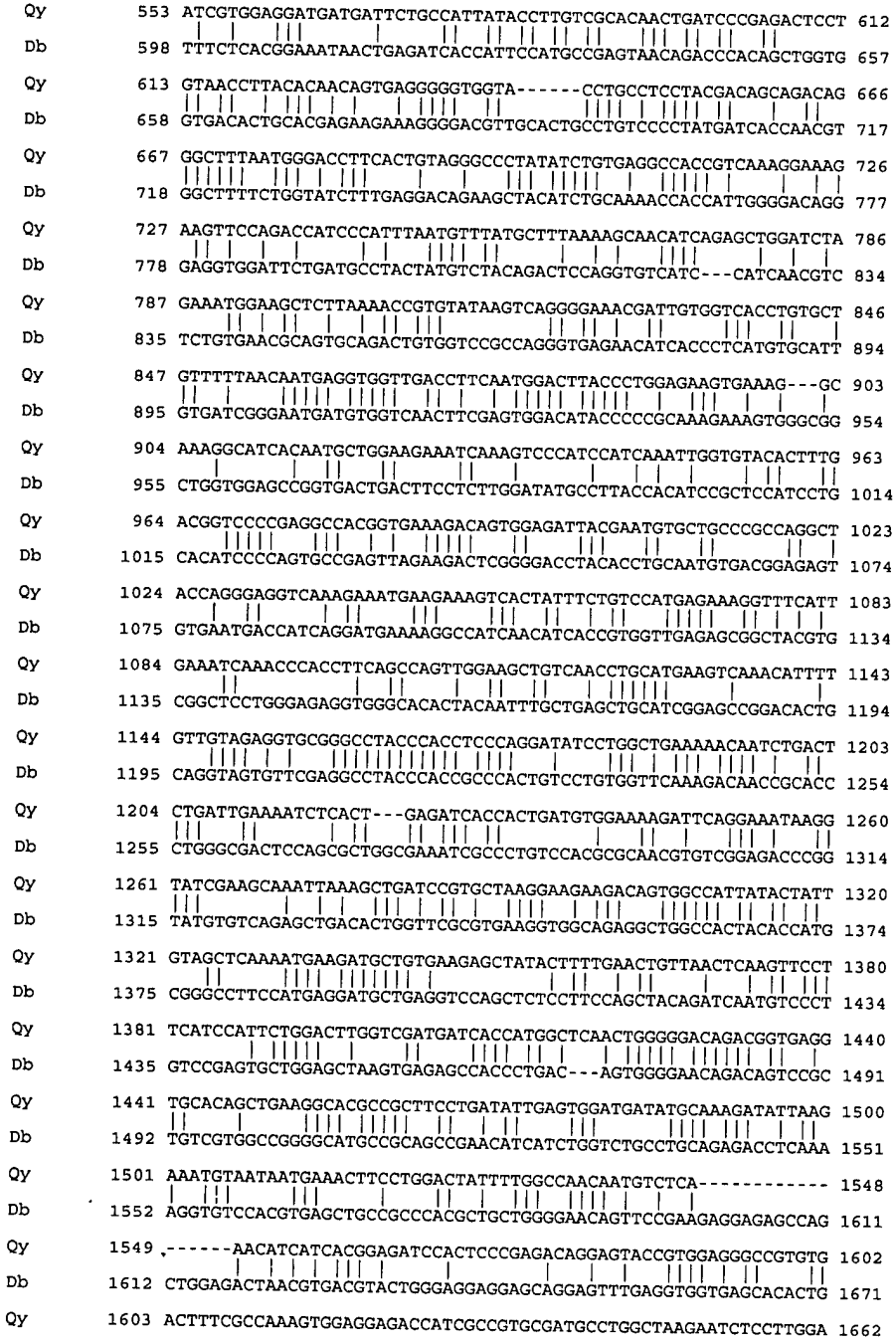
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

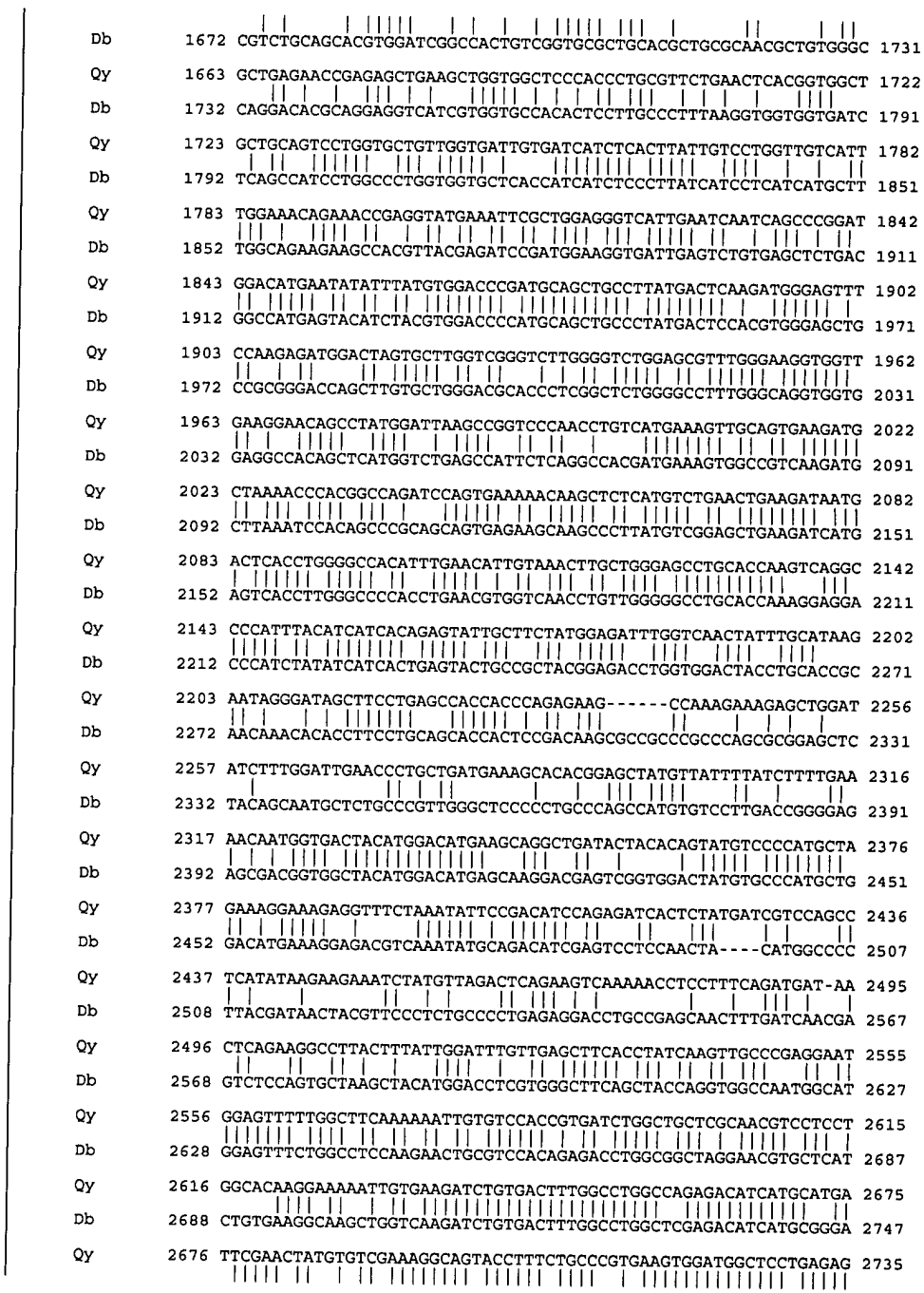
Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552

Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597
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Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795

Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855

Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915

Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975

Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137


RESULT 47
US-09-866-510-13
; Sequence 13, Application US/09866510
; Patent No. 6667173
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 3321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3270)
US-09-866-510-13

  Query Match           10.4%;  Score 666;  DB 3;  Length 3321;
  Best Local Similarity  55.5%;  Pred. No. 2.1e-136;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

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Db        352 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 411

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612

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Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903

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Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023

Db        829 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 888

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083

Db        889 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 948

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143

Db        949 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1008

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203

Db        1009 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1068

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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380

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Db        1249 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1305

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500

Db        1306 TGTCGTGGCCGGGGCATGCCCCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1365

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548

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Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662

Db        1486 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1545

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Db       1546 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1605
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Db       1606 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 1665
Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
Db       1666 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 1725
Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
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Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
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Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316
Db       2146 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2205
Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376
Db       2206 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2265
Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
Db       2266 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2321
Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
Db       2322 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2381
Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
Db       2382 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2441
Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
Db       2442 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2501
Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
Db       2502 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2561
Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
Db       2562 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2621
Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
Db       2622 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2681
Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
Db       2682 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2741
Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
Db       2742 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2801
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Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
Db       2862 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 2921
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RESULT 48
US-08-180-195-1
; Sequence 1, Application US/08180195
; Patent No. 5567584
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;    TITLE OF INVENTION:  AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;    TITLE OF INVENTION:  FUSIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/180,195
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,510
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/146,877
;      FILING DATE:  22-JAN-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/347,291
;      FILING DATE:  02-MAY-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki J.D., David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4465 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      DEVELOPMENTAL STAGE:  Adult
;      TISSUE TYPE:  Skin
;      CELL TYPE:  fibroblasts
;    IMMEDIATE SOURCE:
;      CLONE:  pR-rX1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  354..3671
;      OTHER INFORMATION:
US-08-180-195-1

  Query Match            10.4%;  Score 666;  DB 2;  Length 4465;
  Best Local Similarity  55.5%;  Pred. No. 2.3e-136;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||     |  ||  |   | ||| ||    | | | |    |||| ||     |||
Db        588 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 647

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
              ||||    ||||  || | |    |   ||||  ||  ||| | |   |   | |||
Db        648 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 704

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||||  ||     || | |||   | |||    |       |||    ||  ||
Db        705 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 764

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              |  |  |||       |     ||  || || || ||  ||| || ||  ||
Db        765 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 824

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | ||| | |   | ||||  ||       |||| | |||| ||   |  ||
Db        825 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 884

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||     |   |   ||| |||||  |  |||||  |     | | |
Db        885 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 944

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
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Db        945 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 1001

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Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
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Db       1062 GTGATCGGGAATGAGGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 1121

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Db       1122 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1181

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
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Db       1182 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1241

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
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Db       1242 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1301

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Db       1302 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1361

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
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Db       1362 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1421

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Db       1422 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1481

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              |||        |  | |  ||| | || |  ||||  | |||   ||||| || || ||
Db       1482 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1541

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
                 ||     |||| |||||| | |  | ||  | ||    |  | || |||
Db       1542 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1601

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
                   | |||||  |    ||    |||| || |   | ||||| |||||| ||  |
Db       1602 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1658

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||    |    |||| ||| |  ||  | ||    |||       |||| |||  | ||
Db       1659 TGTCGTGGCCGGGGCATGCCCCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1718

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
              | |||    |||    |  ||  |  |||  |||| | |  |
Db       1719 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1778

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
                    | | | | |||  |       |   |  |  |  |||| | ||    ||
Db       1779 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1838

Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
              | |     | |||||   | |  |  | ||||| |||  |      ||      | ||
Db       1839 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1898

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
              || |  |  ||| | |   ||||| | | | || |||  | | |  |  ||||
Db       1899 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1958

Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
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Db       1959 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 2018

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RESULT 49
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; Sequence 1, Application US/08477329
; Patent No. 5750375
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OE SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,329
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4465 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      DEVELOPMENTAL STAGE:  Adult
;      TISSUE TYPE:  Skin
;      CELL TYPE:  fibroblasts
;    IMMEDIATE SOURCE:
;      CLONE:  pR-rX1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  354..3671
;      OTHER INFORMATION:
US-08-477-329-1

  Query Match           10.4%;  Score 666;  DB 2;  Length 4465;
  Best Local Similarity  55.5%;  Pred. No. 2.3e-136;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

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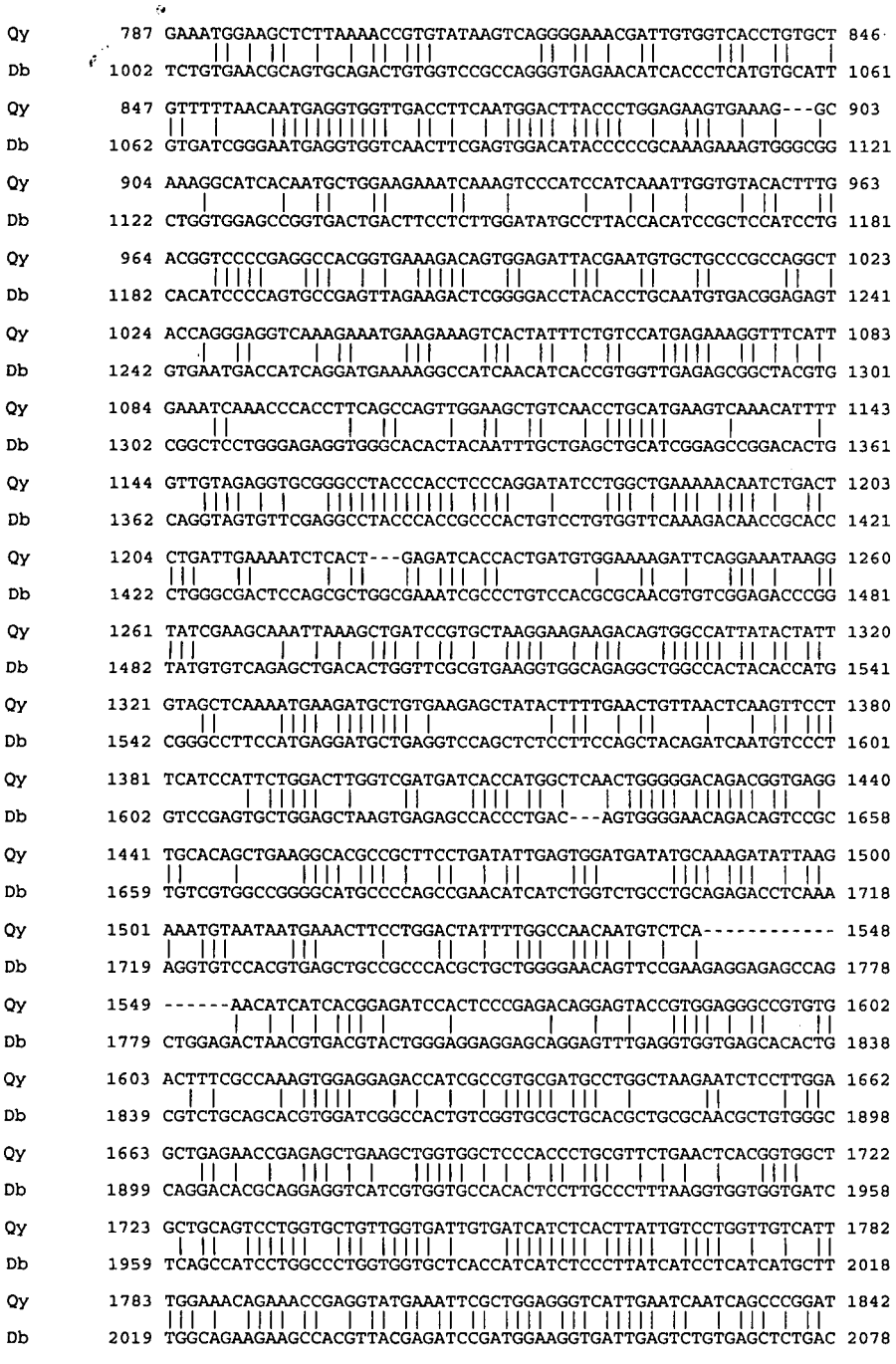
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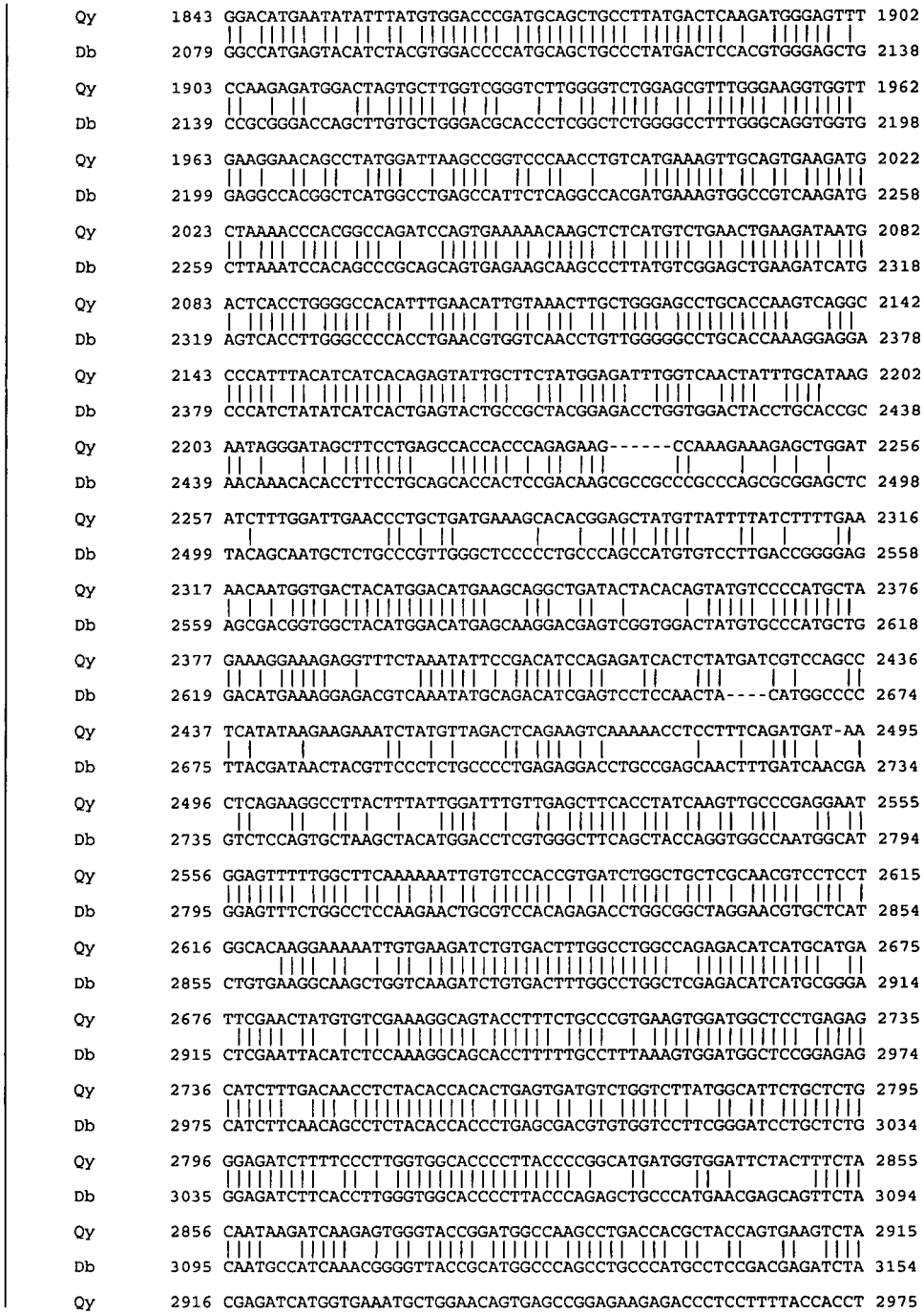
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Db       3155 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3214

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Db       3215 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3274

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

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; Sequence 1, Application US/08475458
; Patent No. 5843725
;  GENERAL INFORMATION:
;    APPLICANT:  Sledziewski Ph.D., Andrzej Z
;    APPLICANT:  Bell, Lillian A.
;    APPLICANT:  Kindsvogel Ph.D., Wayne R.
;    TITLE OF INVENTION:  METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,458
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  990008.446D5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-622-4900
;      TELEFAX:  206-682-6031
;      TELEX:  3723836
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4465 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      DEVELOPMENTAL STAGE:  Adult
;      TISSUE TYPE:  Skin
;      CELL TYPE:  fibroblasts
;    IMMEDIATE SOURCE:
;      CLONE:  pR-rX1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  354..3671
;      OTHER INFORMATION:
US-08-475-458-1

  Query Match          10.4%;  Score 666;  DB 2;  Length 4465;
  Best Local Similarity  55.5%;  Pred. No. 2.3e-136;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

Db        588 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 647

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        648 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 704

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Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726

Db        885 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 944

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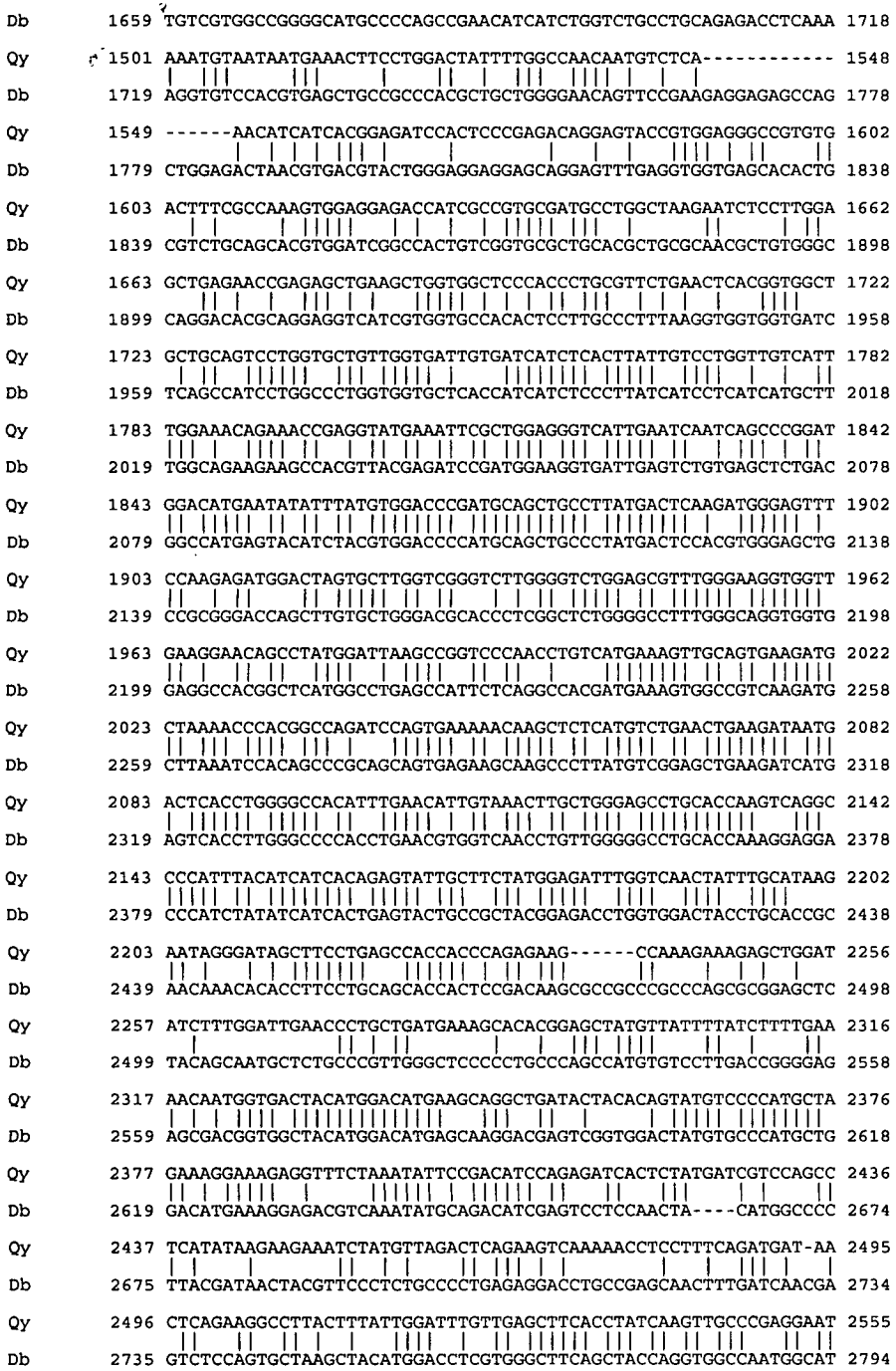
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SUMMARIES

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3	6373.2	99.4	6428	3	US-09-814-353-21714	Sequence 21714, A
4	6364.4	99.2	6378	3	US-09-919-497-40	Sequence 40, Appl
5	6364.4	99.2	6378	3	US-09-873-367C-709	Sequence 709, App
6	6364.4	99.2	6378	3	US-09-968-007A-386	Sequence 386, App
7	6364.4	99.2	6378	7	US-10-641-643-1194	Sequence 1194, Ap
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13	6364.4	99.2	6633	6	US-10-159-563-124	Sequence 124, App
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26	3268.4	51.0	3270	3	US-09-866-510-9	Sequence 9, Appli
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45	666	10.4	3321	3	US-09-866-510-13	Sequence 13, Appl
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47	666	10.4	5570	6	US-10-007-926A-209	Sequence 209, App
48	666	10.4	5570	6	US-10-101-510-28	Sequence 28, Appl
49	666	10.4	5570	7	US-10-641-643-1193	Sequence 1193, Ap
50	666	10.4	5570	9	US-10-505-680-581	Sequence 581, App
51	666	10.4	5598	6	US-10-159-563-297	Sequence 297, App
52	666	10.4	5598	9	US-10-926-806-5	Sequence 5, Appli
53	666	10.4	5622	5	US-10-084-817-164	Sequence 164, App
54	666	10.4	6315	8	US-10-723-860-5421	Sequence 5421, Ap
55	664.6	10.4	5602	9	US-10-450-763-20744	Sequence 20744, A
56	664.4	10.4	3321	3	US-09-866-510-15	Sequence 15, Appl
57	664.4	10.4	3321	3	US-09-866-510-19	Sequence 19, Appl
58	662.8	10.3	3321	3	US-09-866-510-17	Sequence 17, Appl
c 59	649.6	10.1	650	4	US-09-925-065A-81823	Sequence 81823, A
60	620.4	9.7	5110	9	US-10-764-420-1716	Sequence 1716, Ap
61	539.4	8.4	1176	7	US-10-641-643-1404	Sequence 1404, Ap
62	526.4	8.2	528	7	US-10-384-339C-44	Sequence 44, Appl
63	514.8	8.0	572	6	US-10-264-049-1303	Sequence 1303, Ap
64	475	7.4	475	7	US-10-242-535A-42528	Sequence 42528, A
65	475	7.4	475	7	US-10-085-783A-42528	Sequence 42528, A
c 66	453.4	7.1	492	8	US-10-696-639-2694	Sequence 2694, Ap
67	439.4	6.9	475	3	US-09-918-995-12960	Sequence 12960, A
68	434.2	6.8	477	3	US-09-918-995-13107	Sequence 13107, A
69	418	6.5	561	7	US-10-242-535A-17064	Sequence 17064, A
70	418	6.5	561	7	US-10-085-783A-17064	Sequence 17064, A
71	406.2	6.3	506	3	US-09-814-353-18307	Sequence 18307, A
72	404.8	6.3	490	7	US-10-242-535A-18834	Sequence 18834, A
73	404.8	6.3	490	7	US-10-085-783A-18834	Sequence 18834, A
74	404	6.3	477	3	US-09-918-995-25649	Sequence 25649, A
75	403.6	6.3	477	3	US-09-918-995-12415	Sequence 12415, A
76	391.8	6.1	427	8	US-10-696-639-2693	Sequence 2693, Ap
c 77	391	6.1	629	7	US-10-152-319A-1270	Sequence 1270, Ap
78	390.8	6.1	6390	9	US-10-450-763-15469	Sequence 15469, A
79	390.8	6.1	6390	9	US-10-450-763-20740	Sequence 20740, A
80	366	5.7	366	7	US-10-242-535A-11171	Sequence 11171, A
81	366	5.7	366	7	US-10-085-783A-11171	Sequence 11171, A
82	366	5.7	392	7	US-10-242-535A-31618	Sequence 31618, A
83	366	5.7	392	7	US-10-085-783A-31618	Sequence 31618, A
84	360.4	5.6	420	7	US-10-242-535A-53159	Sequence 53159, A
85	360.4	5.6	420	7	US-10-085-783A-53159	Sequence 53159, A
86	357.8	5.6	465	6	US-10-062-674-1570	Sequence 1570, Ap
87	344.4	5.4	5098	5	US-10-192-867-1	Sequence 1, Appli
88	335.2	5.2	369	7	US-10-242-535A-25491	Sequence 25491, A
89	335.2	5.2	369	7	US-10-085-783A-25491	Sequence 25491, A
90	331.6	5.2	2931	6	US-10-457-954-1	Sequence 1, Appli
91	331.6	5.2	5084	3	US-09-967-768A-277	Sequence 277, App
92	331.6	5.2	5084	3	US-09-954-531-1383	Sequence 1383, Ap
93	331.6	5.2	5084	5	US-10-192-867-3	Sequence 3, Appli
94	331.6	5.2	5084	5	US-10-175-523-185	Sequence 185, App
95	331.6	5.2	5084	6	US-10-295-027-707	Sequence 707, App
96	331.6	5.2	5084	7	US-10-641-643-1335	Sequence 1335, Ap

	97	331.6	5.2	5084	9	US-10-843-641A-2450 Sequence 2450, Ap
	98	331.6	5.2	5084	9	US-10-843-641A-6422 Sequence 6422, Ap
	99	331.6	5.2	5084	10	US-11-099-266-185 Sequence 185, App
	100	330.6	5.2	341	7	US-10-242-535A-50384 Sequence 50384, A
	101	330.6	5.2	341	7	US-10-085-783A-50384 Sequence 50384, A
	102	322.8	5.0	2919	9	US-10-758-422-64 Sequence 64, Appl
	103	320.6	5.0	500	7	US-10-242-535A-16333 Sequence 16333, A
	104	320.6	5.0	500	7	US-10-085-783A-16333 Sequence 16333, A
	105	319.6	5.0	3952	9	US-10-823-142A-1 Sequence 1, Appli
	106	319	5.0	320	7	US-10-242-535A-51588 Sequence 51588, A
	107	319	5.0	320	7	US-10-085-783A-51588 Sequence 51588, A
	108	309.4	4.8	355	7	US-10-242-535A-50349 Sequence 50349, A
	109	309.4	4.8	355	7	US-10-085-783A-50349 Sequence 50349, A
	110	303.2	4.7	3475	8	US-10-741-600-828 Sequence 828, App
	111	303.2	4.7	4225	8	US-10-741-600-827 Sequence 827, App
	112	302.6	4.7	2982	6	US-10-457-954-7 Sequence 7, Appli
	113	302.6	4.7	2982	7	US-10-052-482-138 Sequence 138, App
	114	302.6	4.7	3475	7	US-10-052-482-137 Sequence 137, App
	115	302.6	4.7	3501	3	US-09-919-408-3 Sequence 3, Appli
	116	302.6	4.7	3501	3	US-09-872-136-3 Sequence 3, Appli
	117	302.6	4.7	3501	8	US-10-639-603-3 Sequence 3, Appli
	118	302.6	4.7	3501	10	US-11-030-539-3 Sequence 3, Appli
	119	299.6	4.7	3270	7	US-10-210-130-97 Sequence 97, Appl
	120	299.4	4.7	3120	3	US-09-982-610-22 Sequence 22, Appl
	121	295.8	4.6	2958	3	US-09-942-711-25 Sequence 25, Appl
	122	295.8	4.6	2958	9	US-10-653-147-25 Sequence 25, Appl
	123	294	4.6	302	7	US-10-242-535A-1966 Sequence 1966, Ap
	124	294	4.6	302	7	US-10-085-783A-1966 Sequence 1966, Ap
	125	290.8	4.5	2958	3	US-09-942-711-23 Sequence 23, Appl
	126	290.8	4.5	2958	9	US-10-653-147-23 Sequence 23, Appl
	127	290.8	4.5	2982	3	US-09-942-711-22 Sequence 22, Appl
	128	290.8	4.5	2982	9	US-10-653-147-22 Sequence 22, Appl
	129	289.2	4.5	3986	8	US-10-741-600-742 Sequence 742, App
	130	289.2	4.5	3993	8	US-10-741-600-743 Sequence 743, App
	131	288.2	4.5	2949	3	US-09-942-711-24 Sequence 24, Appl
	132	288.2	4.5	2949	9	US-10-653-147-24 Sequence 24, Appl
	133	288	4.5	3985	8	US-10-723-860-2313 Sequence 2313, Ap
	134	288	4.5	3992	3	US-09-944-807-9 Sequence 9, Appli
	135	288	4.5	3992	6	US-10-007-926A-292 Sequence 292, App
	136	288	4.5	3992	8	US-10-874-015-9 Sequence 9, Appli
	137	288	4.5	3992	9	US-10-450-763-15470 Sequence 15470, A
	138	288	4.5	4008	6	US-10-101-510-544 Sequence 544, App
	139	286.4	4.5	2979	7	US-10-052-482-135 Sequence 135, App
	140	286.4	4.5	3426	7	US-10-052-482-134 Sequence 134, App
	141	286.4	4.5	3453	3	US-09-919-408-1 Sequence 1, Appli
	142	286.4	4.5	3453	3	US-09-872-136-1 Sequence 1, Appli
	143	286.4	4.5	3453	8	US-10-639-603-1 Sequence 1, Appli
	144	286.4	4.5	3453	10	US-11-030-539-1 Sequence 1, Appli
	145	280.8	4.4	2978	3	US-09-942-711-21 Sequence 21, Appl
	146	280.8	4.4	2978	9	US-10-653-147-21 Sequence 21, Appl
c	147	266.2	4.2	534	6	US-10-029-386-3014 Sequence 3014, Ap
c	148	265.2	4.1	272	6	US-10-029-386-16714 Sequence 16714, A
	149	263	4.1	4240	8	US-10-723-860-6517 Sequence 6517, Ap
	150	260.4	4.1	467	3	US-09-814-353-5636 Sequence 5636, Ap
	151	260.4	4.1	467	3	US-09-814-353-11923 Sequence 11923, A
	152	246.4	3.8	400	7	US-10-242-535A-10815 Sequence 10815, A
	153	246.4	3.8	400	7	US-10-085-783A-10815 Sequence 10815, A
	154	243.6	3.8	1911	7	US-10-384-339C-45 Sequence 45, Appl
	155	235.4	3.7	1400	10	US-11-060-756-809 Sequence 809, App
	156	235.4	3.7	1400	10	US-11-060-756-5081 Sequence 5081, Ap
	157	234.6	3.7	600	10	US-11-060-756-135 Sequence 135, App
	158	234.6	3.7	600	10	US-11-060-756-4407 Sequence 4407, Ap
	159	234.2	3.7	600	10	US-11-060-756-1057 Sequence 1057, Ap
	160	234.2	3.7	600	10	US-11-060-756-5329 Sequence 5329, Ap
c	161	227.4	3.5	539	3	US-09-796-692-8255 Sequence 8255, Ap
c	162	227.4	3.5	539	5	US-10-040-862-8255 Sequence 8255, Ap
c	163	227.4	3.5	539	6	US-10-057-475B-8255 Sequence 8255, Ap
c	164	227.4	3.5	539	6	US-10-154-884B-8255 Sequence 8255, Ap
c	165	227.4	3.5	539	8	US-10-764-324-8255 Sequence 8255, Ap
c	166	225.8	3.5	608	3	US-09-796-692-8132 Sequence 8132, Ap
c	167	225.8	3.5	608	5	US-10-040-862-8132 Sequence 8132, Ap
c	168	225.8	3.5	608	6	US-10-057-475B-8132 Sequence 8132, Ap
c	169	225.8	3.5	608	6	US-10-154-884B-8132 Sequence 8132, Ap
c	170	225.8	3.5	608	8	US-10-764-324-8132 Sequence 8132, Ap
	171	224.4	3.5	248	7	US-10-242-535A-18262 Sequence 18262, A
	172	224.4	3.5	248	7	US-10-085-783A-18262 Sequence 18262, A
	173	221.6	3.5	4113	6	US-10-081-126-1 Sequence 1, Appli
	174	221.6	3.5	4450	7	US-10-326-048-3 Sequence 3, Appli
	175	221.6	3.5	4450	8	US-10-781-581-221 Sequence 221, App
	176	220	3.4	3277	6	US-10-252-157-455 Sequence 455, App
	177	220	3.4	3897	7	US-10-384-339C-96 Sequence 96, Appl
	178	220	3.4	4111	3	US-09-375-248-1 Sequence 1, Appli
	179	220	3.4	4111	7	US-10-661-740-1 Sequence 1, Appli
	180	220	3.4	4195	3	US-09-765-534B-1 Sequence 1, Appli
	181	220	3.4	4195	5	US-10-262-538-31 Sequence 31, Appl
	182	220	3.4	4195	8	US-10-774-802-1 Sequence 1, Appli
	183	220	3.4	4195	8	US-10-669-176-31 Sequence 31, Appl
	184	220	3.4	4416	5	US-10-201-386-1 Sequence 1, Appli
	185	220	3.4	4416	7	US-10-792-480-1 Sequence 1, Appli
	186	220	3.4	4416	7	US-10-792-461-1 Sequence 1, Appli
	187	220	3.4	4425	3	US-09-982-610-31 Sequence 31, Appl
	188	220	3.4	4425	7	US-10-641-643-889 Sequence 889, App
	189	220	3.4	4795	3	US-09-765-534B-3 Sequence 3, Appli
	190	220	3.4	4795	8	US-10-774-802-3 Sequence 3, Appli
	191	220	3.4	5390	6	US-10-090-183-5 Sequence 5, Appli
	192	220	3.4	5406	3	US-09-919-408-5 Sequence 5, Appli
	193	220	3.4	5406	3	US-09-872-136-5 Sequence 5, Appli
	194	220	3.4	5406	8	US-10-639-603-5 Sequence 5, Appli
	195	220	3.4	5406	10	US-11-030-539-5 Sequence 5, Appli
	196	220	3.4	5470	3	US-09-766-678-1 Sequence 1, Appli
	197	220	3.4	5470	3	US-09-967-655-10 Sequence 10, Appl
	198	220	3.4	5470	9	US-10-799-782-1 Sequence 1, Appli
c	199	220	3.4	6827	3	US-09-982-610-17 Sequence 17, Appl
	200	220	3.4	9108	3	US-09-982-610-45 Sequence 45, Appl
	201	216	3.4	993	6	US-10-391-416-4 Sequence 4, Appli
	202	216	3.4	1035	6	US-10-391-416-3 Sequence 3, Appli
	203	215.6	3.4	5789	6	US-10-402-365-1 Sequence 1, Appli
	204	215	3.4	600	10	US-11-060-756-3614 Sequence 3614, Ap
	205	215	3.4	600	10	US-11-060-756-7886 Sequence 7886, Ap
	206	215	3.4	4017	6	US-10-090-183-3 Sequence 3, Appli
	207	215	3.4	4017	7	US-10-384-339C-95 Sequence 95, Appl
	208	215	3.4	4017	9	US-10-926-806-7 Sequence 7, Appli
	209	213.4	3.3	7680	3	US-09-953-318-3 Sequence 3, Appli
	210	213.4	3.3	7680	6	US-10-021-660-16 Sequence 16, Appl
	211	213.4	3.3	7680	6	US-10-393-590-77 Sequence 77, Appl
	212	213.4	3.3	7680	6	US-10-393-567-77 Sequence 77, Appl
	213	213.4	3.3	7680	6	US-10-394-087-77 Sequence 77, Appl
	214	213.4	3.3	7680	6	US-10-446-373-3 Sequence 3, Appli
	215	213.4	3.3	7680	6	US-10-172-118-711 Sequence 711, App
	216	213.4	3.3	7680	7	US-10-211-462-214 Sequence 214, App
	217	213.4	3.3	7680	7	US-10-342-887-711 Sequence 711, App
	218	213.4	3.3	7680	7	US-10-621-116-25 Sequence 25, Appl
	219	213.4	3.3	7680	9	US-10-848-755A-102 Sequence 102, App
	220	213.4	3.3	7680	9	US-10-450-763-6090 Sequence 6090, Ap
	221	211.4	3.3	1400	10	US-11-060-756-1537 Sequence 1537, Ap
	222	211.4	3.3	1400	10	US-11-060-756-5809 Sequence 5809, Ap
	223	204.2	3.2	6055	3	US-09-953-318-10 Sequence 10, Appl
	224	204.2	3.2	6055	6	US-10-446-373-10 Sequence 10, Appl
	225	200.6	3.1	201	7	US-10-741-601-3293 Sequence 3293, Ap
	226	200.6	3.1	201	7	US-10-741-601-3294 Sequence 3294, Ap
	227	200.6	3.1	201	7	US-10-741-601-3295 Sequence 3295, Ap
	228	200.6	3.1	201	7	US-10-741-601-3296 Sequence 3296, Ap
	229	200.6	3.1	201	7	US-10-741-601-3297 Sequence 3297, Ap
	230	200.6	3.1	201	7	US-10-741-601-3298 Sequence 3298, Ap
	231	200.6	3.1	201	7	US-10-741-601-3299 Sequence 3299, Ap
	232	200.6	3.1	201	7	US-10-741-601-3300 Sequence 3300, Ap
	233	200.6	3.1	201	7	US-10-741-601-3301 Sequence 3301, Ap
	234	200.6	3.1	201	7	US-10-741-601-3302 Sequence 3302, Ap
	235	200.6	3.1	201	7	US-10-741-601-3303 Sequence 3303, Ap
	236	200.6	3.1	201	7	US-10-741-601-3304 Sequence 3304, Ap
	237	200.6	3.1	201	7	US-10-741-601-3305 Sequence 3305, Ap
	238	200.6	3.1	201	7	US-10-741-601-3306 Sequence 3306, Ap
	239	200.6	3.1	201	7	US-10-741-601-3308 Sequence 3308, Ap
	240	200.6	3.1	201	7	US-10-741-601-3309 Sequence 3309, Ap
	241	200.6	3.1	201	7	US-10-741-601-16135 Sequence 16135, A
	242	200.6	3.1	201	7	US-10-741-601-16137 Sequence 16137, A

243	200.6	3.1	201	7	US-10-741-601-16140	Sequence 16140, A
244	200.6	3.1	201	7	US-10-741-601-16148	Sequence 16148, A
245	200.6	3.1	201	7	US-10-741-601-16200	Sequence 16200, A
246	200.6	3.1	201	8	US-10-741-600-12125	Sequence 12125, A
247	200.6	3.1	201	8	US-10-741-600-12126	Sequence 12126, A
248	200.6	3.1	201	8	US-10-741-600-12127	Sequence 12127, A
249	200.6	3.1	201	8	US-10-741-600-12128	Sequence 12128, A
250	200.6	3.1	201	8	US-10-741-600-12129	Sequence 12129, A
251	200.6	3.1	201	8	US-10-741-600-12130	Sequence 12130, A
252	200.6	3.1	201	8	US-10-741-600-12131	Sequence 12131, A
253	200.6	3.1	201	8	US-10-741-600-12132	Sequence 12132, A
254	200.6	3.1	201	8	US-10-741-600-12133	Sequence 12133, A
255	200.6	3.1	201	8	US-10-741-600-12134	Sequence 12134, A
256	200.6	3.1	201	8	US-10-741-600-12135	Sequence 12135, A
257	200.6	3.1	201	8	US-10-741-600-12136	Sequence 12136, A
258	200.6	3.1	201	8	US-10-741-600-12137	Sequence 12137, A
259	200.6	3.1	201	8	US-10-741-600-12138	Sequence 12138, A
260	200.6	3.1	201	8	US-10-741-600-12140	Sequence 12140, A
261	200.6	3.1	201	8	US-10-741-600-12141	Sequence 12141, A
262	200.6	3.1	201	8	US-10-741-600-45401	Sequence 45401, A
263	200.6	3.1	201	8	US-10-741-600-45403	Sequence 45403, A
264	200.6	3.1	201	8	US-10-741-600-45406	Sequence 45406, A
265	200.6	3.1	201	8	US-10-741-600-45414	Sequence 45414, A
266	200.6	3.1	201	8	US-10-741-600-45466	Sequence 45466, A
267	199.4	3.1	1704	6	US-10-327-414-7	Sequence 7, Appli
268	199.4	3.1	4044	7	US-10-384-339C-94	Sequence 94, Appl
269	199.4	3.1	4071	5	US-10-022-939-1	Sequence 1, Appli
270	199.4	3.1	4071	5	US-10-100-405A-1	Sequence 1, Appli
271	199.4	3.1	4071	6	US-10-327-414-5	Sequence 5, Appli
272	199.4	3.1	4071	6	US-10-090-183-1	Sequence 1, Appli
273	199.4	3.1	4071	7	US-10-384-339C-97	Sequence 97, Appl
274	199.4	3.1	5200	8	US-10-741-600-641	Sequence 641, App
275	199.4	3.1	5830	3	US-09-967-655-3	Sequence 3, Appli
276	199.4	3.1	5830	6	US-10-159-563-338	Sequence 338, App
277	199.4	3.1	5830	7	US-10-294-228-7	Sequence 7, Appli
278	199.4	3.1	5830	8	US-10-783-528-3	Sequence 3, Appli
279	199.4	3.1	5830	9	US-10-505-680-616	Sequence 616, App
280	199.4	3.1	5830	9	US-10-926-806-9	Sequence 9, Appli
281	199.4	3.1	5830	9	US-10-824-982-1	Sequence 1, Appli
282	199.4	3.1	5832	8	US-10-741-600-643	Sequence 643, App
283	199.4	3.1	5841	6	US-10-133-013-269	Sequence 269, App
284	198.2	3.1	504	3	US-09-911-904-130	Sequence 130, App
285	198	3.1	4230	5	US-10-262-538-29	Sequence 29, Appl
286	198	3.1	4230	8	US-10-669-176-29	Sequence 29, Appl
287	198	3.1	5832	5	US-10-116-802-18	Sequence 18, Appl
288	193.4	3.0	2184	3	US-09-728-952-82	Sequence 82, Appl
289	193.4	3.0	2184	7	US-10-302-812-45	Sequence 45, Appl
290	193.4	3.0	2184	8	US-10-775-920-55	Sequence 55, Appl
291	193.4	3.0	2421	3	US-09-997-722-114	Sequence 114, App
292	193.4	3.0	2421	7	US-10-384-339C-86	Sequence 86, Appl
293	193.4	3.0	2427	7	US-10-403-161-59	Sequence 59, Appl
294	193.4	3.0	2469	7	US-10-664-705-12	Sequence 12, Appl
295	193.4	3.0	2490	7	US-10-403-161-57	Sequence 57, Appl
296	193.4	3.0	2520	3	US-09-953-047-3	Sequence 3, Appli
297	193.4	3.0	2520	7	US-10-630-401-3	Sequence 3, Appli
298	193.4	3.0	2520	8	US-10-775-920-56	Sequence 56, Appl
299	193.4	3.0	2520	8	US-10-696-639-4	Sequence 4, Appli
300	193.4	3.0	3757	8	US-10-775-920-58	Sequence 58, Appl
301	193.4	3.0	4093	3	US-09-997-722-113	Sequence 113, App
302	193.4	3.0	4093	8	US-10-775-920-54	Sequence 54, Appl
303	193.4	3.0	4118	8	US-10-723-860-5997	Sequence 5997, Ap
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322	184.4	2.9	3328	7	US-10-283-975A-98	Sequence 98, Appl
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328	184.4	2.9	3726	3	US-09-925-302-271	Sequence 271, App
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ALIGNMENTS

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RESULT 1
US-09-769-987-1
; Sequence 1, Application US/09769987
; Patent No. US20020055129A1
; GENERAL INFORMATION:
;  APPLICANT: Matsui, Toshimitsu
;  APPLICANT:  Aaronson, Stuart A.
;  APPLICANT:  Pierce, Jacalyn H.
;  TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
;  FILE REFERENCE: 14014.0266U2
;  CURRENT APPLICATION NUMBER: US/09/769,987
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: US 08/460,656
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: US 08/439,095
;  PRIOR FILING DATE: 1995-05-11
;  PRIOR APPLICATION NUMBER: US 07/915,884
;  PRIOR FILING DATE: 1992-07-20
;  PRIOR APPLICATION NUMBER: US 07/308,282
;  PRIOR FILING DATE: 1989-02-09
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; SEQ ID NO 1
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;   ORGANISM: Artificial Sequence
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US-09-769-987-1

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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
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Qy        841 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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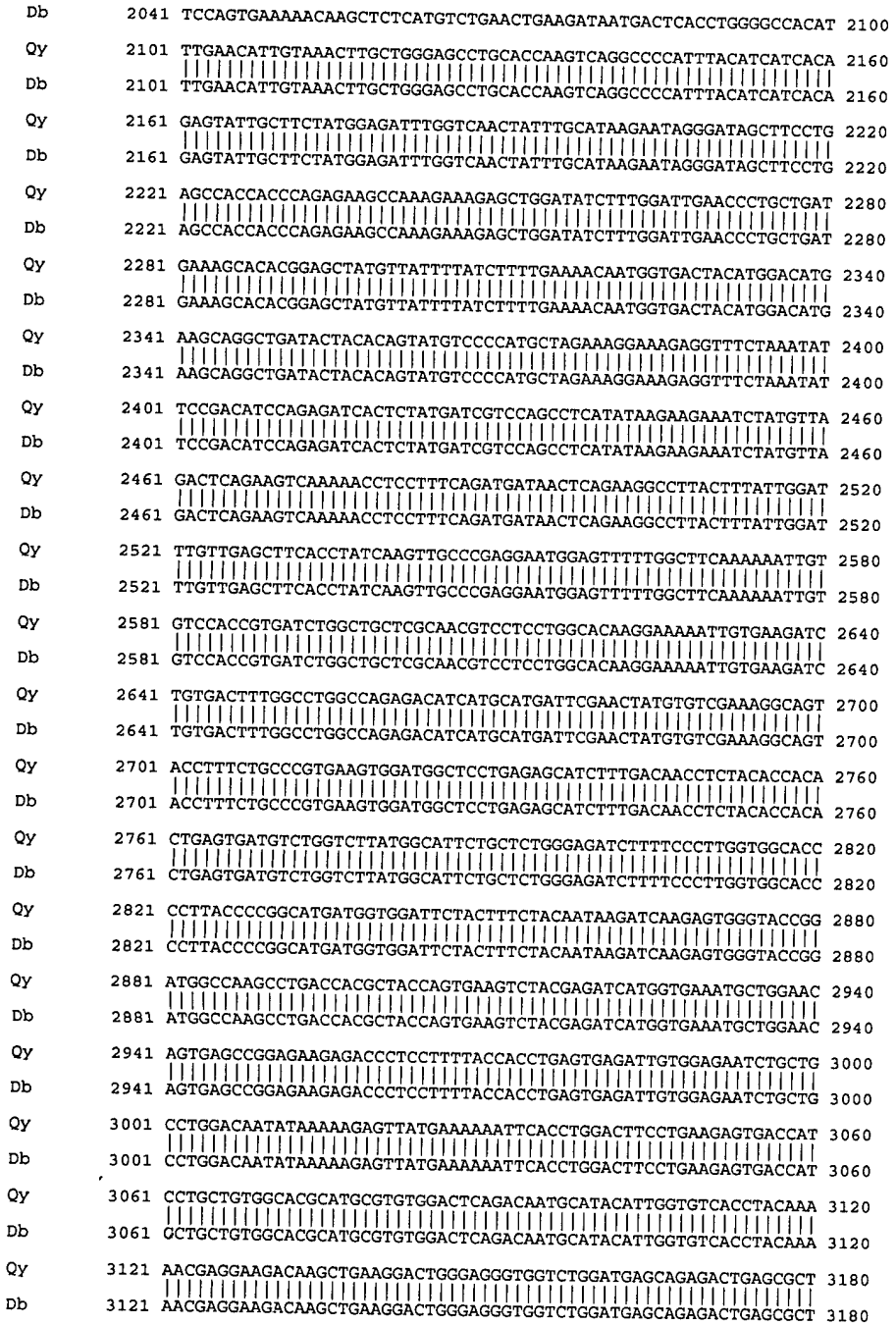
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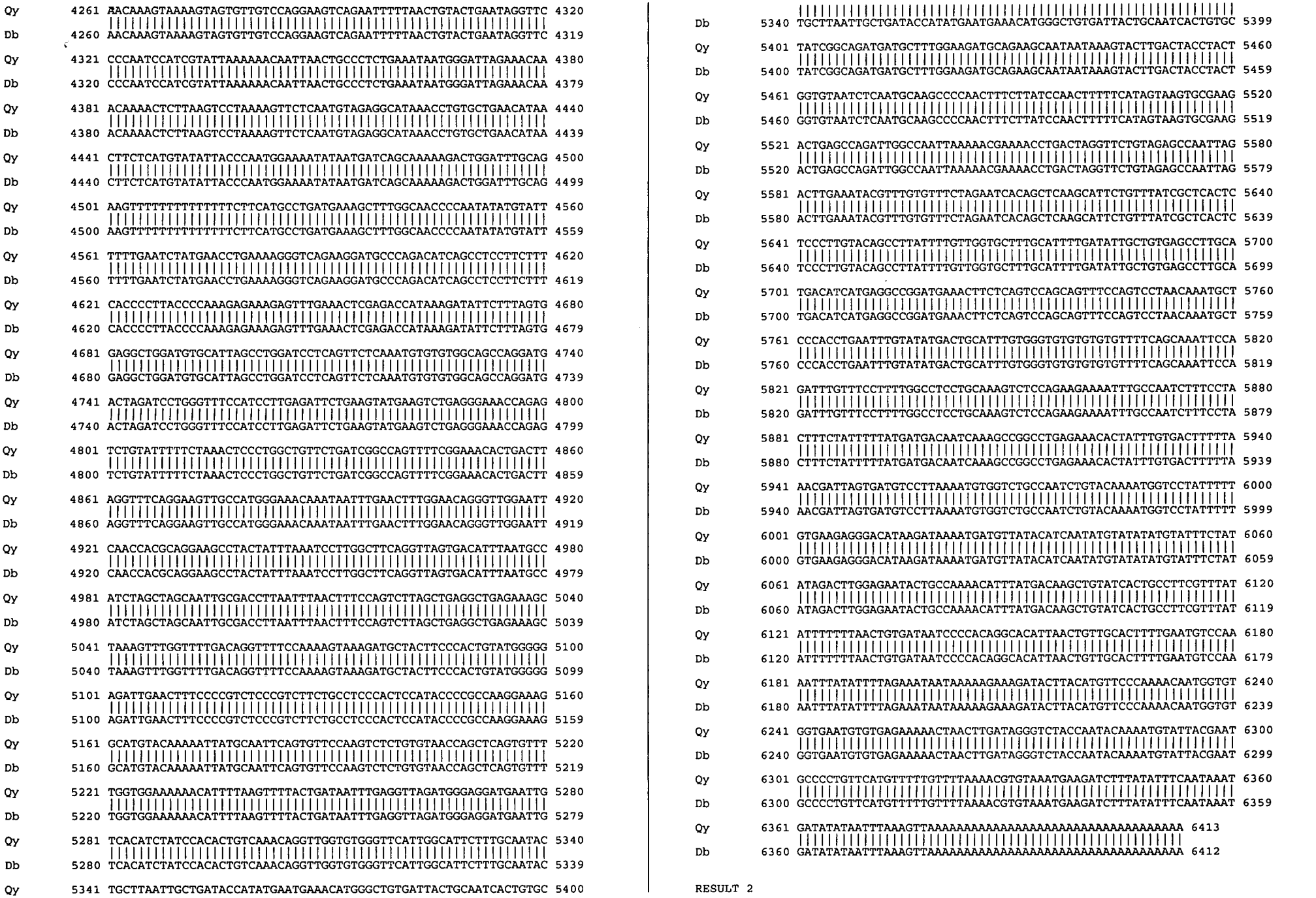
Qy       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Db       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920

Qy       1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
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Qy       1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
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Qy       2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
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RESULT 2

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US-10-700-249-1
; Sequence 1, Application US/10700249
; Publication No. US20050112582A1
; GENERAL INFORMATION:
;  APPLICANT: Matsui, Toshimitsu
;  APPLICANT:  Aaronson, Stuart A.
;  APPLICANT:  Pierce, Jacalyn H.
;  TITLE OF INVENTION: Antibodies for the Alpha Platelet-Derived Growth Factor Receptor
;  FILE REFERENCE: 14014.0266U2
;  CURRENT APPLICATION NUMBER: US/10/700,249
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: US/09/769,987
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 08/460,656
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: US 08/439,095
;  PRIOR FILING DATE: 1995-05-11
;  PRIOR APPLICATION NUMBER: US 07/915,884
;  PRIOR FILING DATE: 1992-07-20
;  PRIOR APPLICATION NUMBER: US 07/308,282
;  PRIOR FILING DATE: 1989-02-09
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 6412
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence; Note =
;   OTHER INFORMATION: synthetic construct
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;   NAME/KEY: CDS
;   LOCATION: (139)...(3406)
US-10-700-249-1

  Query Match             99.8%;  Score 6399.4;  DB 9;  Length 6412;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6411;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 60

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
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Db        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Db        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Db        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Db       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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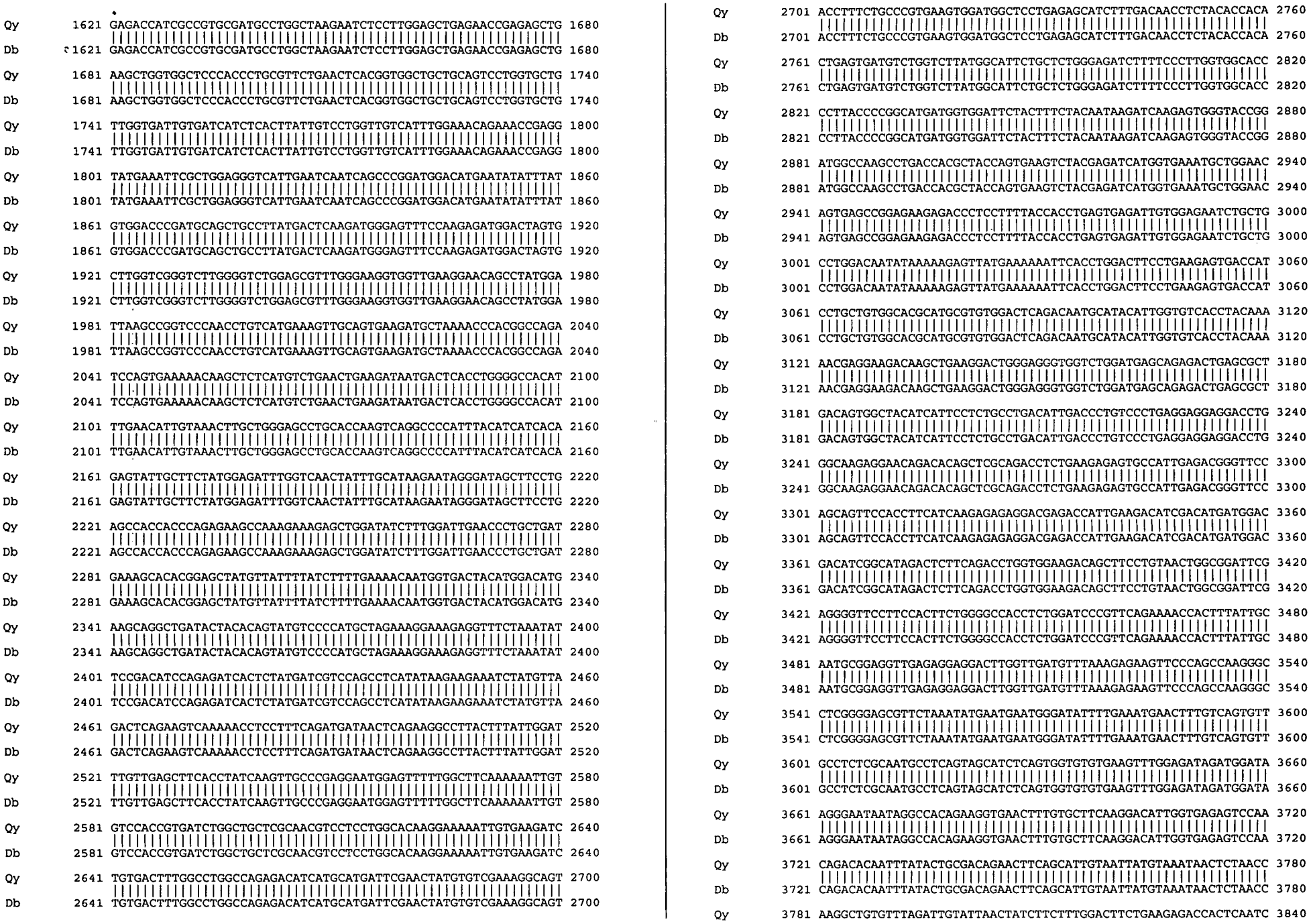
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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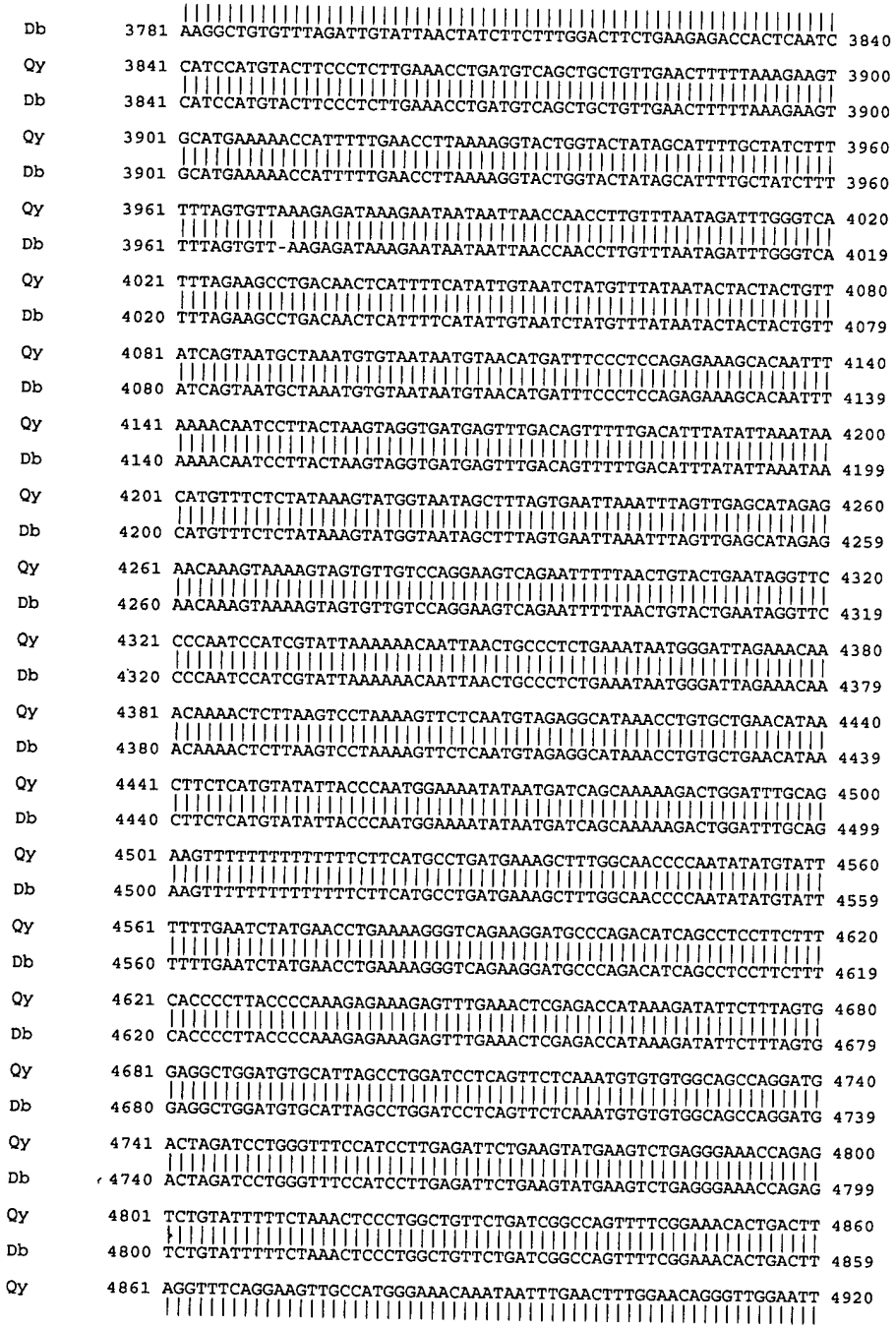
Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560

Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
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Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
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Db 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
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Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Db 5880 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5939
Qy 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db 5940 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 5999

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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6000 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6059

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6060 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6119

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6120 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6179

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6180 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6239

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6240 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6299

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6300 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6359

Qy       6361 GATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6413
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6360 GATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6412


RESULT 3
US-09-814-353-21714
; Sequence 21714, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, John
;  APPLICANT:  Thompson, Pamela
;  APPLICANT:  Lillie, James
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF OVARIAN CANCER
;  FILE REFERENCE: MRI-006B
;  CURRENT APPLICATION NUMBER: US/09/814,353
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,031
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/207,124
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: US 60/211,940
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: US 60/216,820
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/220,661
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: US 60/257,672
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 22037
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21714
;   LENGTH: 6428
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 6427, 6428
;   OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21714

  Query Match             99.4%;  Score 6373.2;  DB 3;  Length 6428;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6386;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          2 CATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGAA 61
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          9 CATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGAA 68

Qy         62 GGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGG 128

Qy        122 AGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTC 188

Qy        182 TCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAA 248

Qy        242 ATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAG 308

Qy        302 TGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAG 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAG 368

Qy        362 AAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACA 428

Qy        422 CAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCA 488

Qy        482 GGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGG 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGG 548

Qy        542 ATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATC 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 ATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATC 608

Qy        602 CCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCA 668

Qy        662 GACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAG 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAG 728

Qy        722 GAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGG 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 GAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGG 788

Qy        782 ATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCT 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCT 848

Qy        842 GTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 GTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG 908

Qy        902 GCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTT 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTT 968

Qy        962 TGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGG 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGG 1028

Qy       1022 CTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCA 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 CTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCA 1088

Qy       1082 TTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATT 1141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1089 TTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATT 1148
Qy       1142 TTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGA 1201
Db       1149 TTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGA 1208
Qy       1202 CTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGT 1261
Db       1209 CTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGT 1268
Qy       1262 ATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTG 1321
Db       1269 ATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTG 1328
Qy       1322 TAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTT 1381
Db       1329 TAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTT 1388
Qy       1382 CATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGT 1441
Db       1389 CATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGT 1448
Qy       1442 GCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGA 1501
Db       1449 GCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGA 1508
Qy       1502 AATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGG 1561
Db       1509 AATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGG 1568
Qy       1562 AGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGG 1621
Db       1569 AGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGG 1628
Qy       1622 AGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGA 1681
Db       1629 AGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGA 1688
Qy       1682 AGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGT 1741
Db       1689 AGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGT 1748
Qy       1742 TGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGT 1801
Db       1749 TGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGT 1808
Qy       1802 ATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATG 1861
Db       1809 ATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATG 1868
Qy       1862 TGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGC 1921
Db       1869 TGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGC 1928
Qy       1922 TTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGAT 1981
Db       1929 TTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGAT 1988
Qy       1982 TAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGAT 2041
Db       1989 TAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGAT 2048
Qy       2042 CCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATT 2101
Db       2049 CCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATT 2108
Qy       2102 TGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAG 2161
Db       2109 TGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAG 2168
Qy       2162 AGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGA 2221
Db       2169 AGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGA 2228

Qy       2222 GCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATG 2281
Db       2229 GCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATG 2288
Qy       2282 AAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGA 2341
Db       2289 AAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGA 2348
Qy       2342 AGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATT 2401
Db       2349 AGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATT 2408
Qy       2402 CCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAG 2461
Db       2409 CCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAG 2468
Qy       2462 ACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATT 2521
Db       2469 ACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATT 2528
Qy       2522 TGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTG 2581
Db       2529 TGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTG 2588
Qy       2582 TCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCT 2641
Db       2589 TCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCT 2648
Qy       2642 GTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTA 2701
Db       2649 GTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTA 2708
Qy       2702 CCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACAC 2761
Db       2709 CCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACAC 2768
Qy       2762 TGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCC 2821
Db       2769 TGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCC 2828
Qy       2822 CTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGA 2881
Db       2829 CTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGA 2888
Qy       2882 TGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACA 2941
Db       2889 TGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACA 2948
Qy       2942 GTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGC 3001
Db       2949 GTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGC 3008
Qy       3002 CTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATC 3061
Db       3009 CTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATC 3068
Qy       3062 CTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAA 3121
Db       3069 CTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAA 3128
Qy       3122 ACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTG 3181
Db       3129 ACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTG 3188
Qy       3182 ACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGG 3241
Db       3189 ACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGG 3248
Qy       3242 GCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCA 3301
Db       3249 GCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCA 3308
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Qy       3302 GCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACG 3361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3309 GCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACG 3368

Qy       3362 ACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGA 3421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3369 ACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGA 3428

Qy       3422 GGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCA 3481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3429 GGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCA 3488

Qy       3482 ATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCC 3541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3489 ATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCC 3548

Qy       3542 TCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3549 TCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3608

Qy       3602 CCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3661
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3609 CCTCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAA 3668

Qy       3662 GGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAC 3721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3669 GGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAC 3728

Qy       3722 AGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCA 3781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3729 AGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCA 3788

Qy       3782 AGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCC 3841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3789 AGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCC 3848

Qy       3842 ATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTG 3901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3849 ATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTG 3908

Qy       3902 CATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTT 3961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3909 CATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTT 3968

Qy       3962 TTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCAT 4021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3969 TTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCAT 4028

Qy       4022 TTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTA 4081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4029 TTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTA 4088

Qy       4082 TCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTA 4141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4089 TCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTA 4148

Qy       4142 AAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAAC 4201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4149 AAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAAC 4208

Qy       4202 ATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGA 4261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4209 ATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGA 4268

Qy       4262 ACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCC 4321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4269 ACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCC 4328

Qy       4322 CCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAA 4381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4329 CCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAA 4388

Qy       4382 CAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAAC 4441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4389 CAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAAC 4448

Qy       4442 TTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGA 4501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4449 TTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGA 4508

Qy       4502 AGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTT 4561
             || |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       4509 AG-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTT 4567

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Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
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RESULT 4
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; Sequence 40, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George L.
;  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
;  FILE REFERENCE: B0801/7225
;  CURRENT APPLICATION NUMBER: US/09/919,497
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221,735
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 6378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-919-497-40

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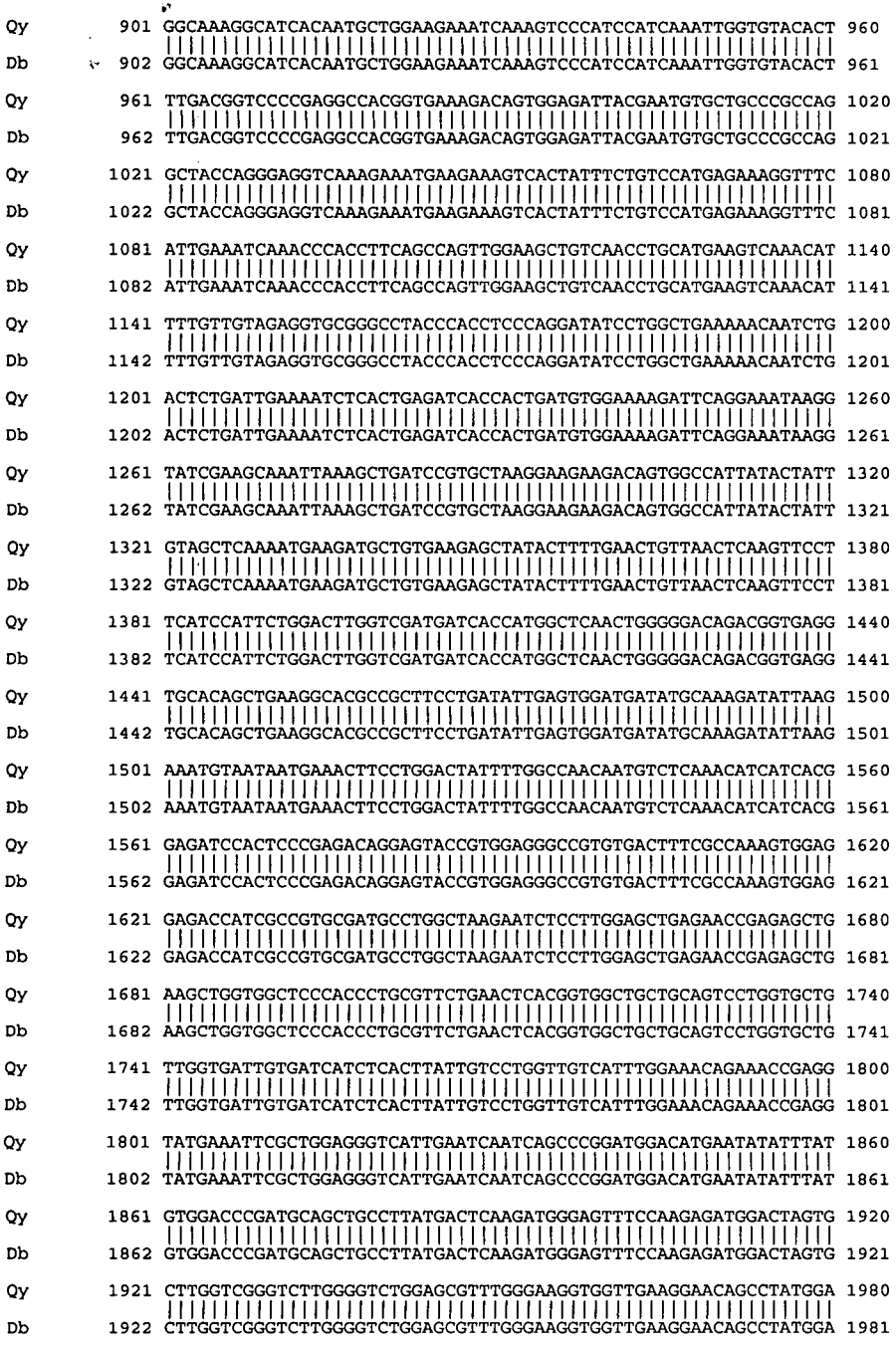
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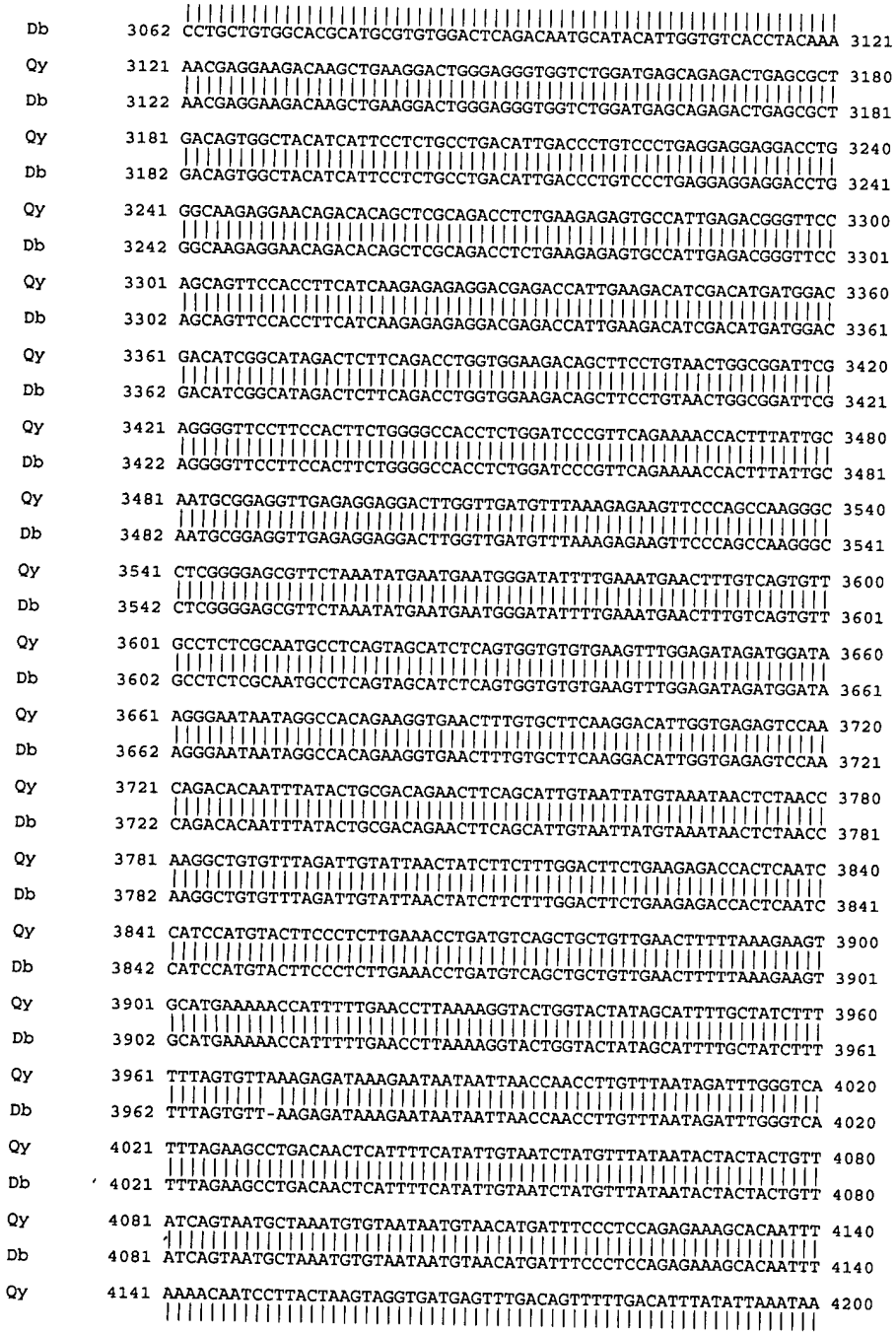
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; Publication No. US20030165839A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  APPLICANT:  Soppet, Daniel
;  APPLICANT:  Endress, Gregory
;  APPLICANT:  Augustus, Meena
;  APPLICANT:  Ebner, Reinhard
;  APPLICANT:  Carter, Kenneth
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-64
;  CURRENT APPLICATION NUMBER: US/09/873,367C
;  CURRENT FILING DATE:  2003-04-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,891
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,842
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;  PRIOR APPLICATION NUMBER: U.S. 60/244,867
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: U.S. 60/245,084
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 1067
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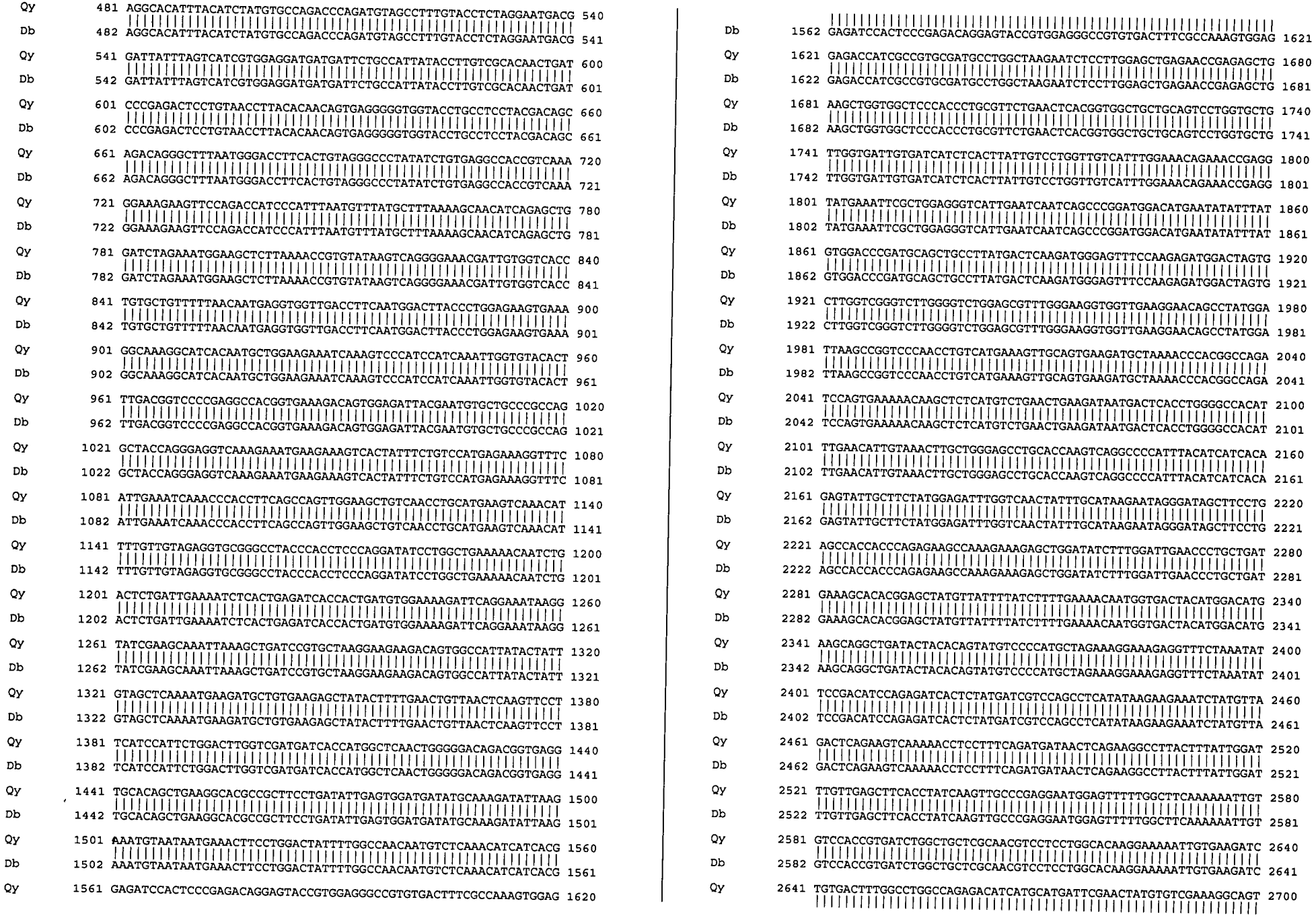
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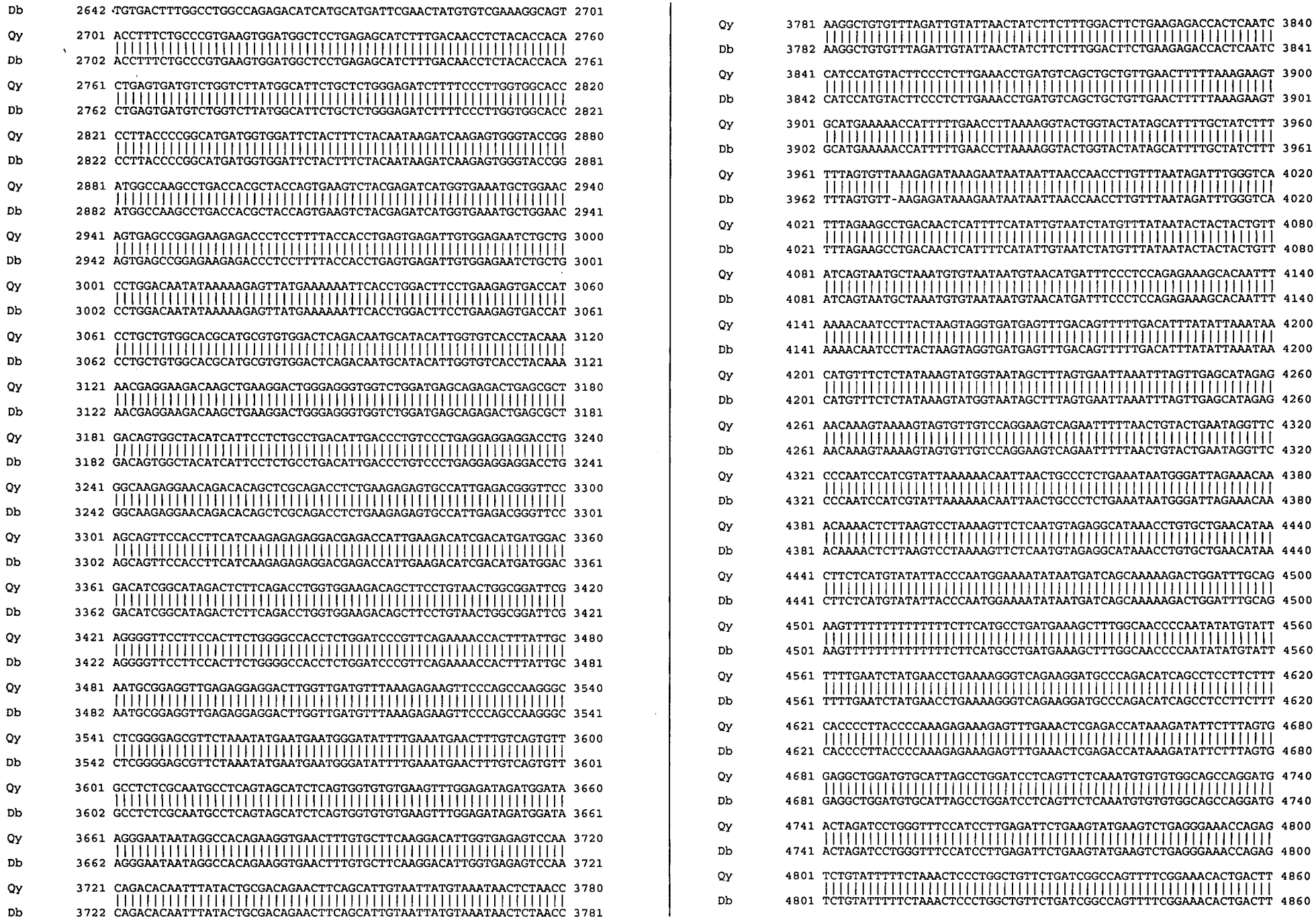
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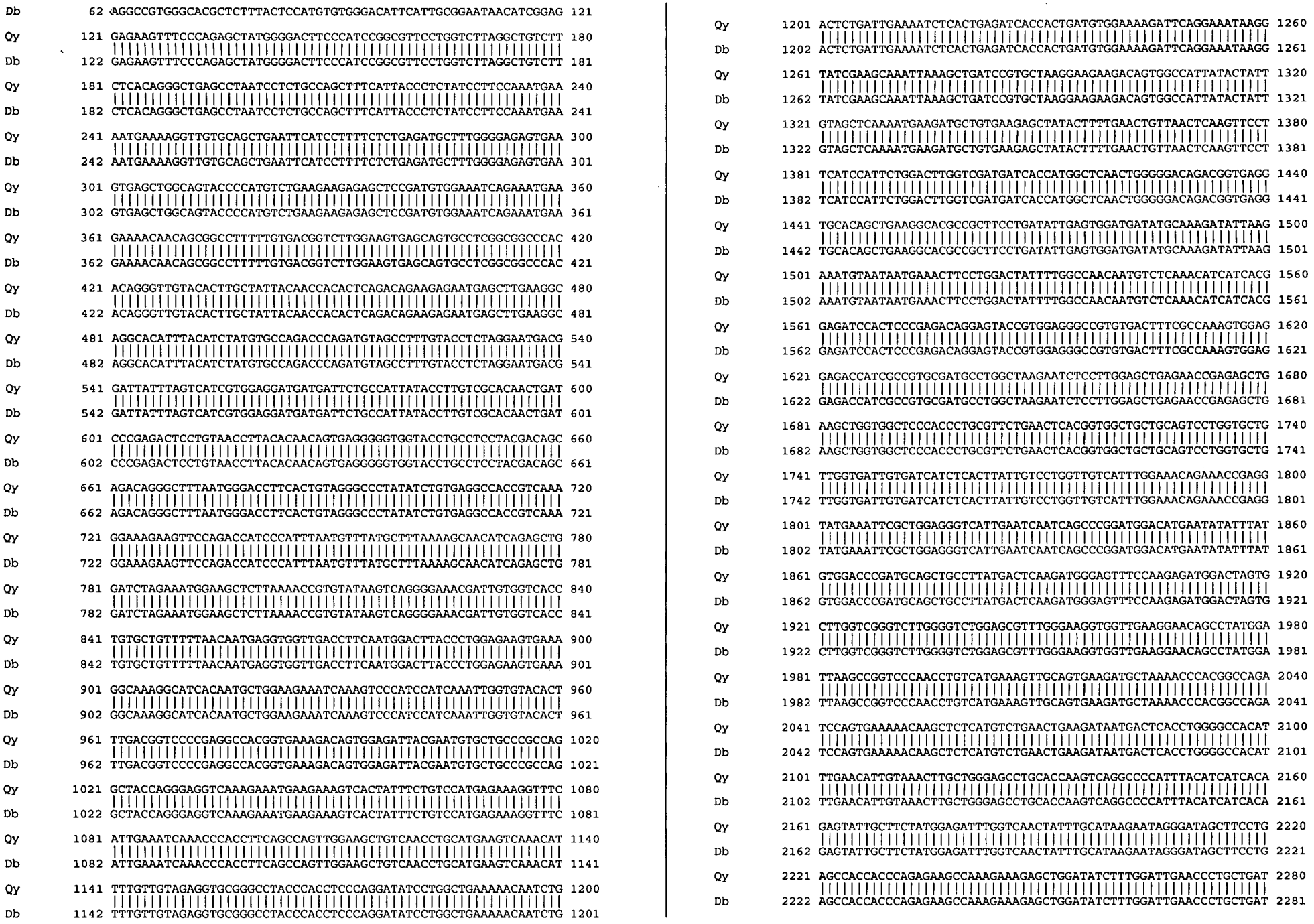
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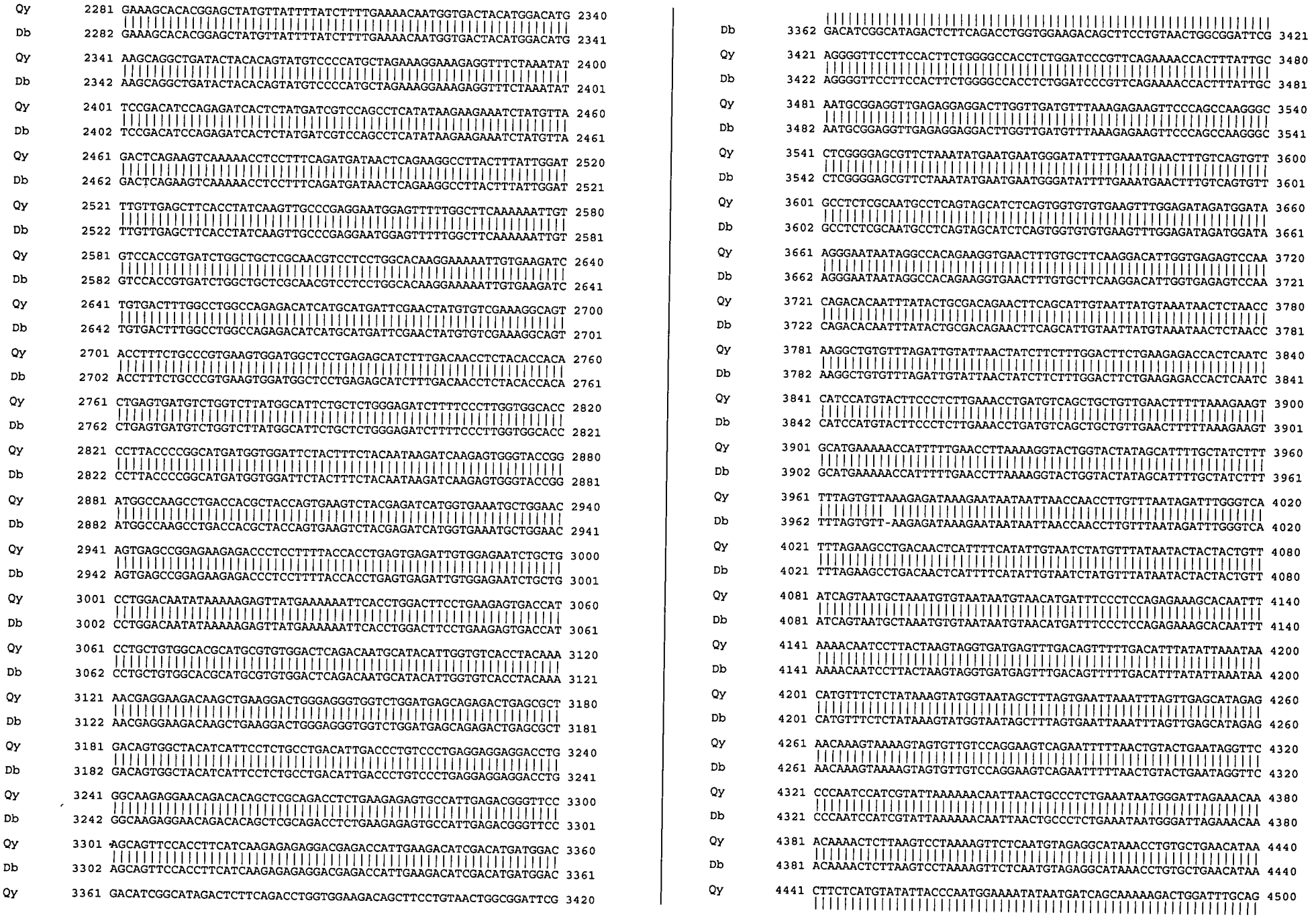
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US-09-968-007A-386
; Sequence 386, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signat
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
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; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 386
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-386

Query Match 99.2%; Score 6364.4; DB 3; Length 6378;
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Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Db       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

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RESULT 7
US-10-641-643-1194
; Sequence 1194, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g189733
; SEQUENCE DESCRIPTION: SEQ ID NO: 1194 :
US-10-641-643-1194

Query Match 99.2%; Score 6364.4; DB 7; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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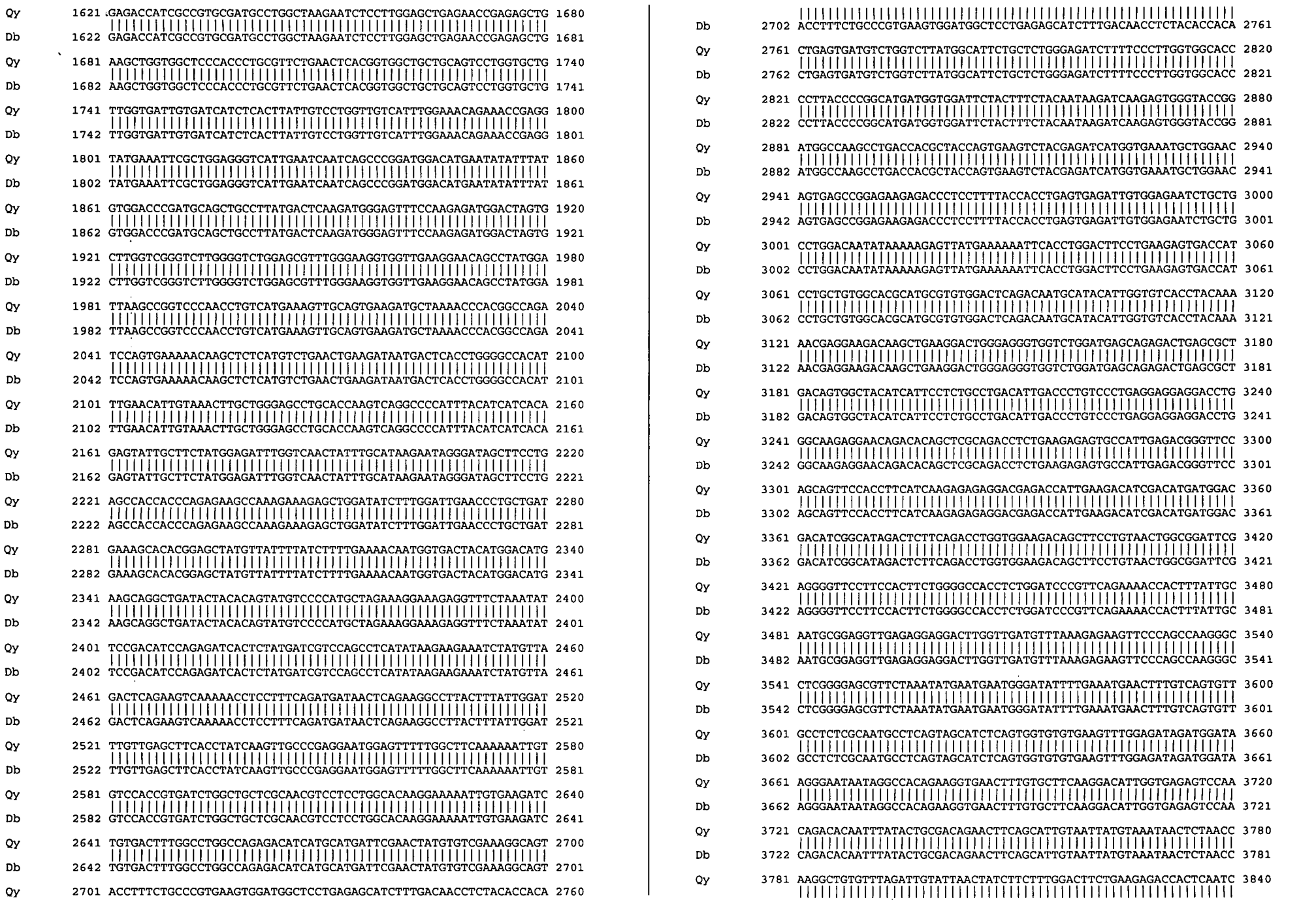
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Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Db       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Db       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Db       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Db       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Db       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Db       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
             ||||||||||||||||||
Db       6361 GATATATAATTTAAAGTT 6378


RESULT 8
US-10-723-860-649
; Sequence 649, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 649
;   LENGTH: 6378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-860-649

  Query Match             99.2%;  Score 6364.4;  DB 8;  Length 6378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db       1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441
Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db       1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501
Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db       1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561
Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db       1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621
Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db       1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681
Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741
Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db       1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db       1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861
Qy       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db       1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921
Qy       1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db       1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy       1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db       1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041
Qy       2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db       2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101
Qy       2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db       2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161
Qy       2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db       2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy       2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db       2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281
Qy       2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db       2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy       2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db       2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401
Qy       2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db       2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461

Qy       2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db       2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy       2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db       2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy       2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db       2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy       2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db       2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy       2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db       2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy       2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db       2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821
Qy       2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db       2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
Qy       2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db       2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941
Qy       2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db       2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001
Qy       3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db       3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061
Qy       3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db       3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
Qy       3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db       3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db       3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
Qy       3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db       3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301
Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db       3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361
Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db       3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421
Qy       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db       3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481
Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db       3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
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Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Db       3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601

Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
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Db       3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661

Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721

Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
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Db       3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781

Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Qy       3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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RESULT 9
US-10-843-641A-709
; Sequence 709, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
;  APPLICANT: Avalon Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-189
;  CURRENT APPLICATION NUMBER: US/10/843,641A
;  CURRENT FILING DATE:  2004-05-12
;  PRIOR APPLICATION NUMBER: US/09/873,367
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US/09/954,531
;  PRIOR FILING DATE: 2001-09-18
;  PRIOR APPLICATION NUMBER: US/09/954,456
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,436
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/962,832
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/964,824
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US/09/967,768
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/09/968,007
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,347
;  PRIOR FILING DATE: 2001-10-02
;  PRIOR APPLICATION NUMBER: US/09/969,708
;  PRIOR FILING DATE: 2001-10-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 8447
;  SOFTWARE: PatentIn version 3.0
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;   LENGTH: 6378
;   TYPE: DNA
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US-10-843-641A-709

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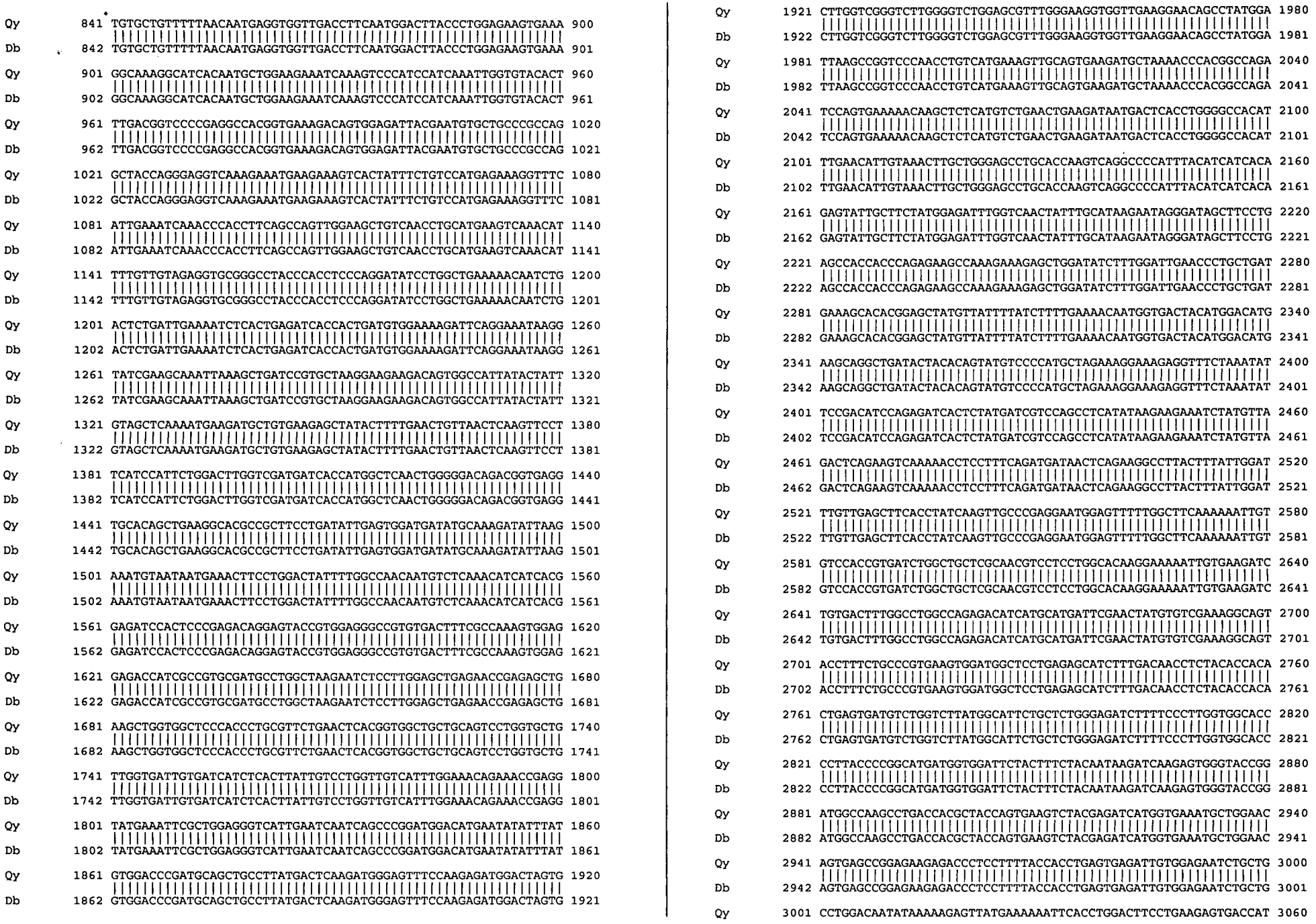
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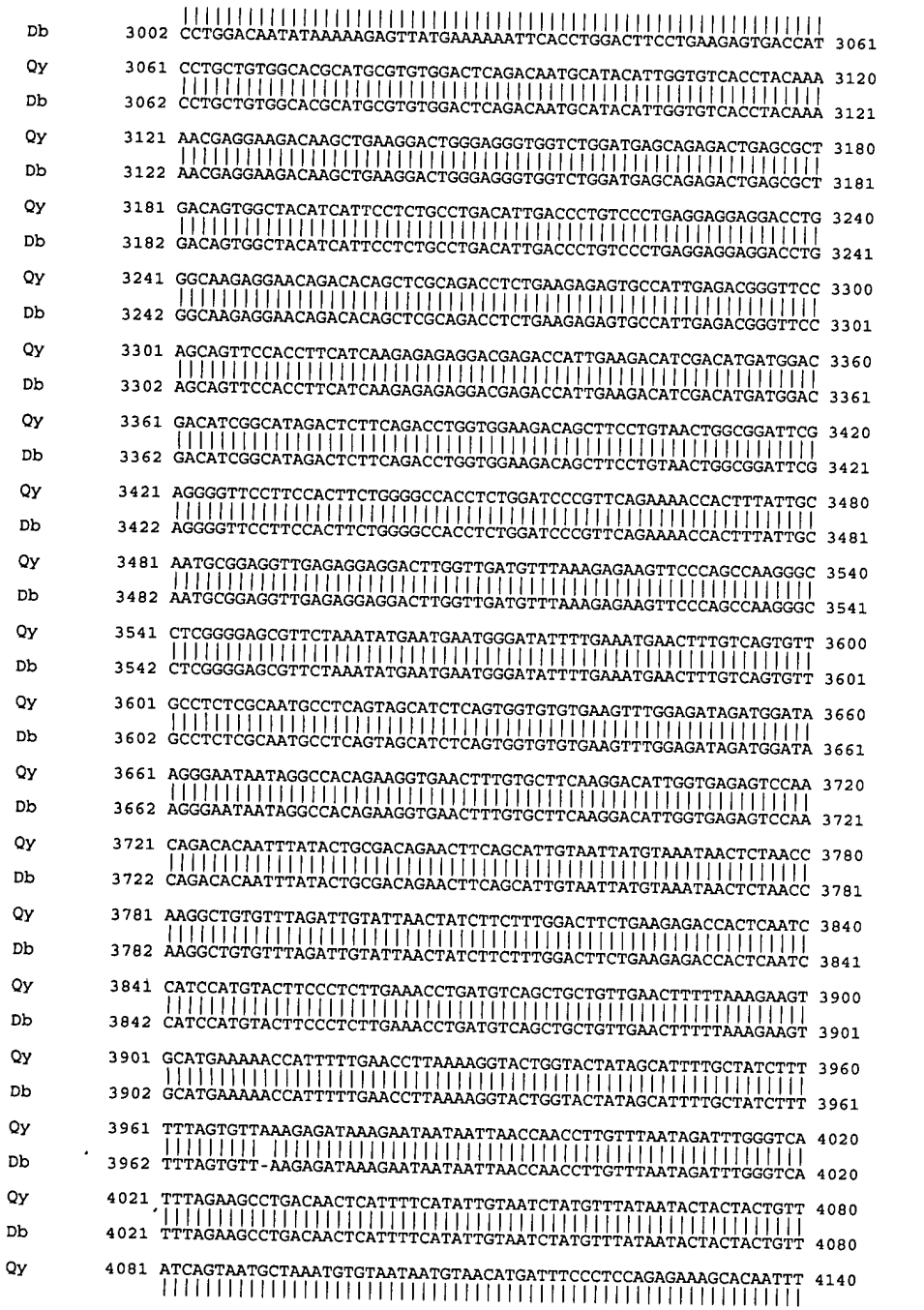
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Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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RESULT 10
US-10-843-641A-6856
; Sequence 6856, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
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US-10-843-641A-6856

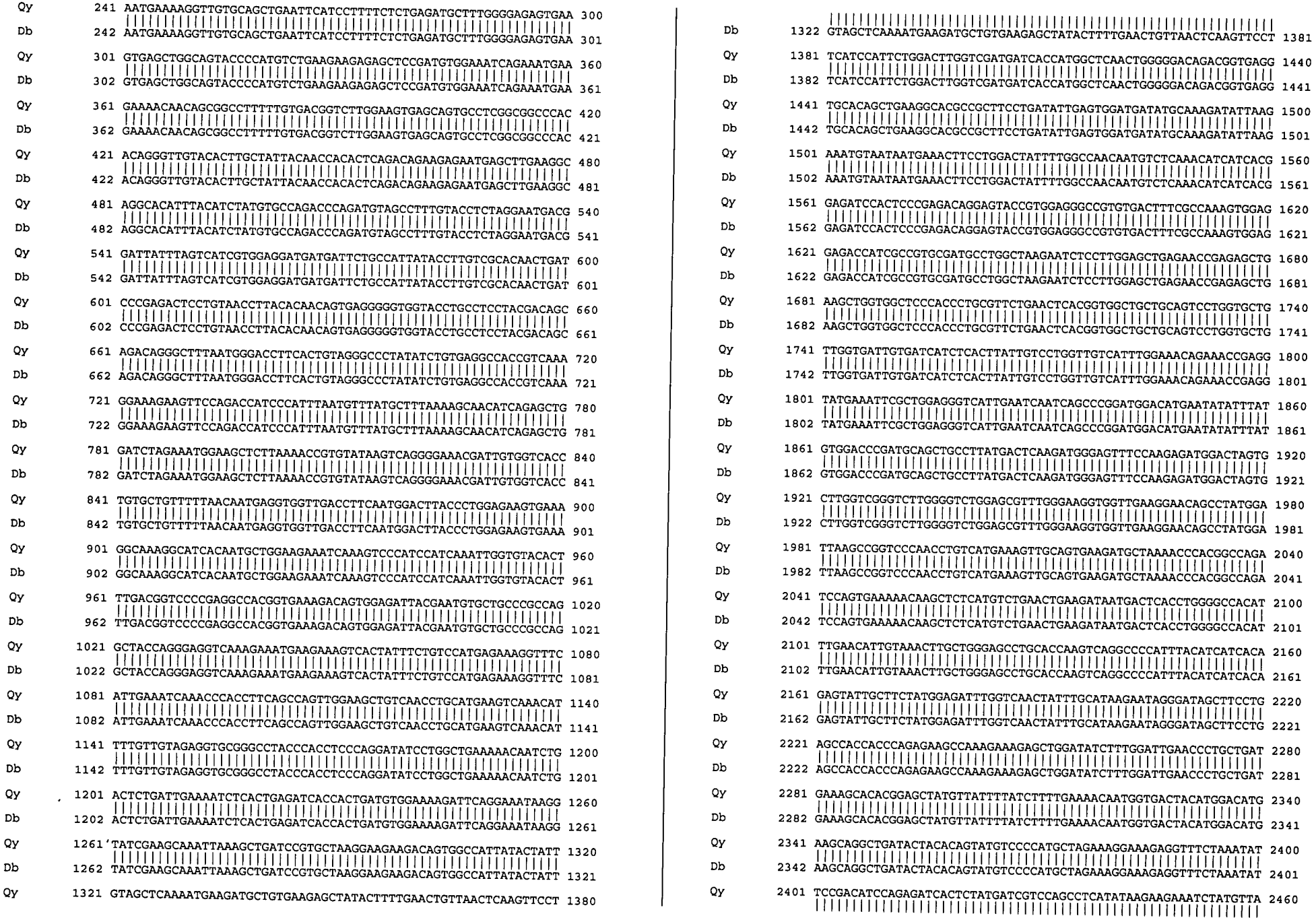
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
Db 1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141
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Db 1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
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Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
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Db      2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
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Db      3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
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Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
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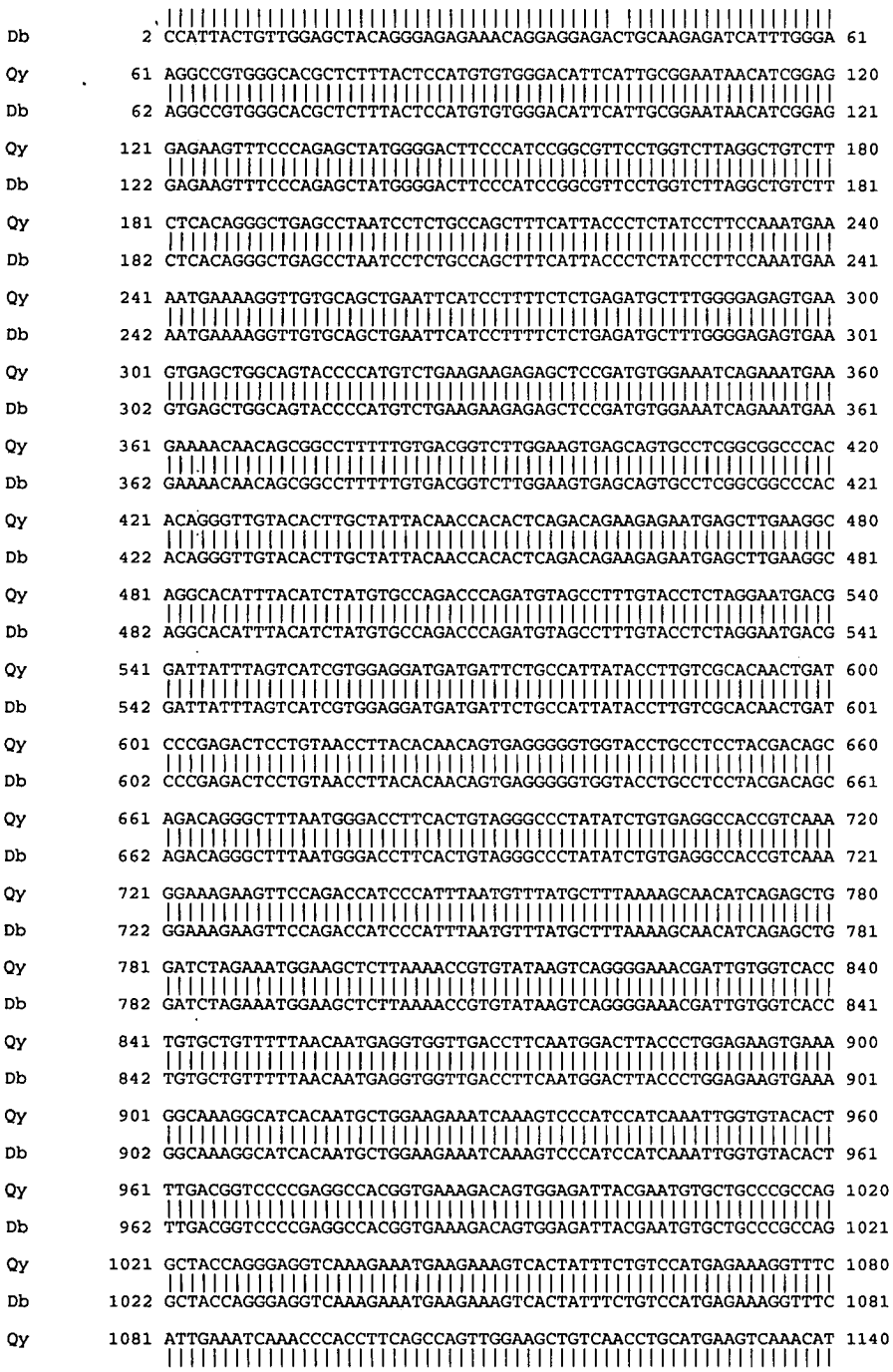
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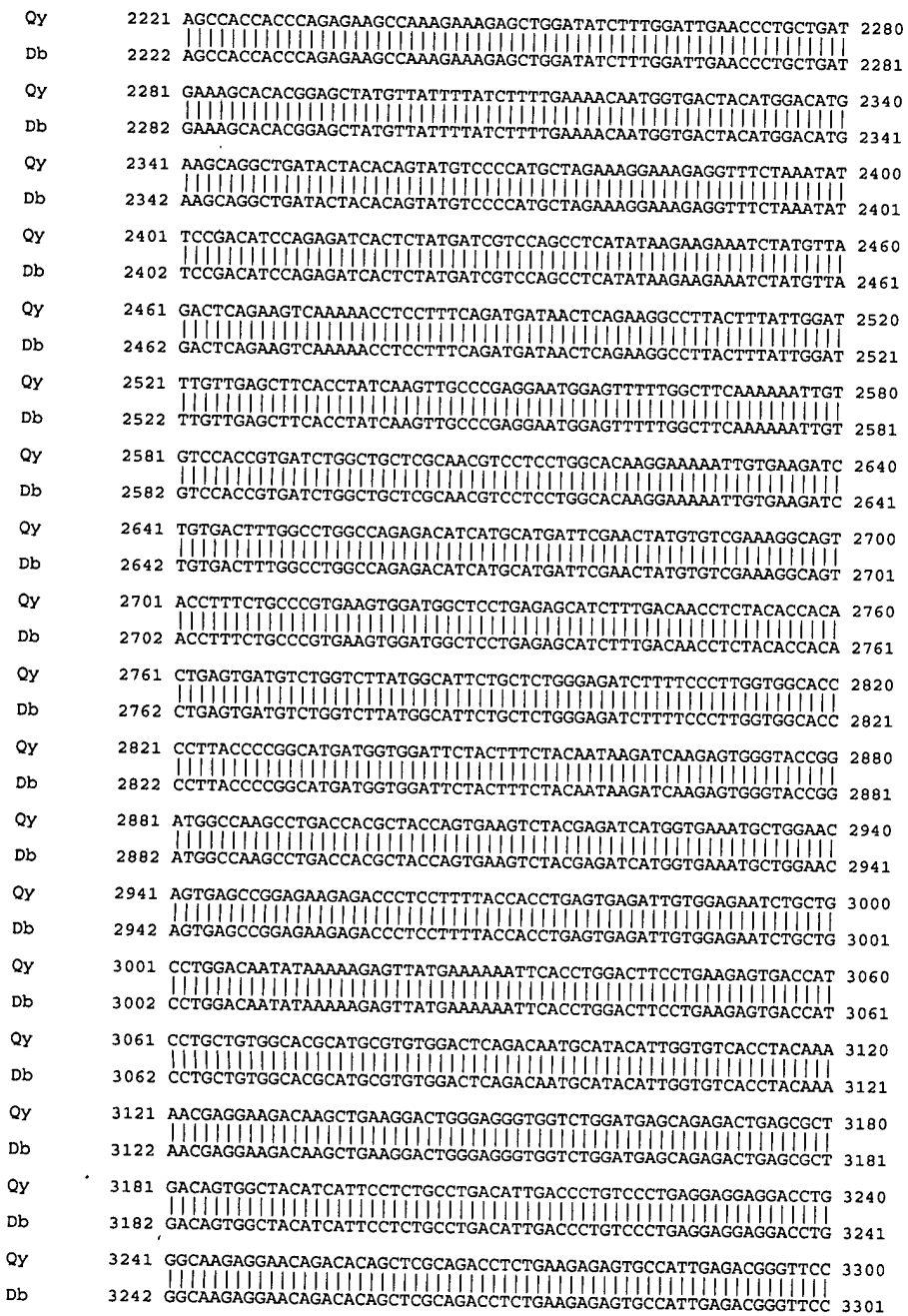
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RESULT 11
US-10-756-149-672
; Sequence 672, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 672
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-672

Query Match 99.2%; Score 6364.4; DB 9; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121
Qy 121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
Db 122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181
Qy 181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
Db 182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241
Qy 241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
Db 242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301
Qy 301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
Db 302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361
Qy 361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
Db 362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421
Qy 421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
Db 422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481
Qy 481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
Db 482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541
Qy 541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Qy 601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
Db 602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661
Qy 661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
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Qy 841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
Db 842 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901
Qy 901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
Db 902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961
Qy 961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy 1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Db 1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201
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Db 1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381
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Db 1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621
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Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
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Db 2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221


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Db 2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
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Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
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Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
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Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
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Db 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440

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Db       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440

Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Qy       4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
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Db       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 12
US-10-388-360-337
; Sequence 337, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve

; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 337
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-337

Query Match 99.2%; Score 6364.4; DB 6; Length 6633;
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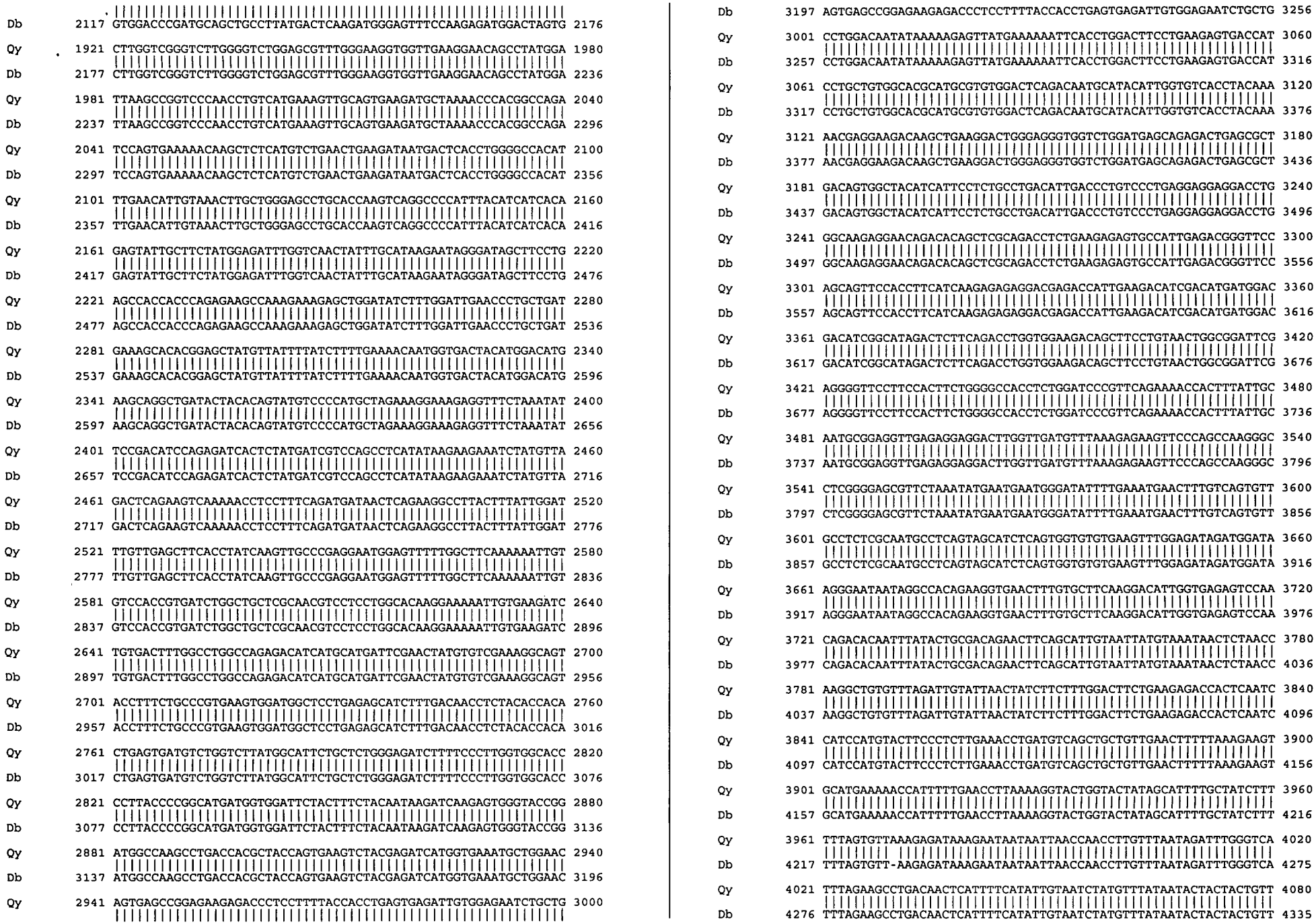
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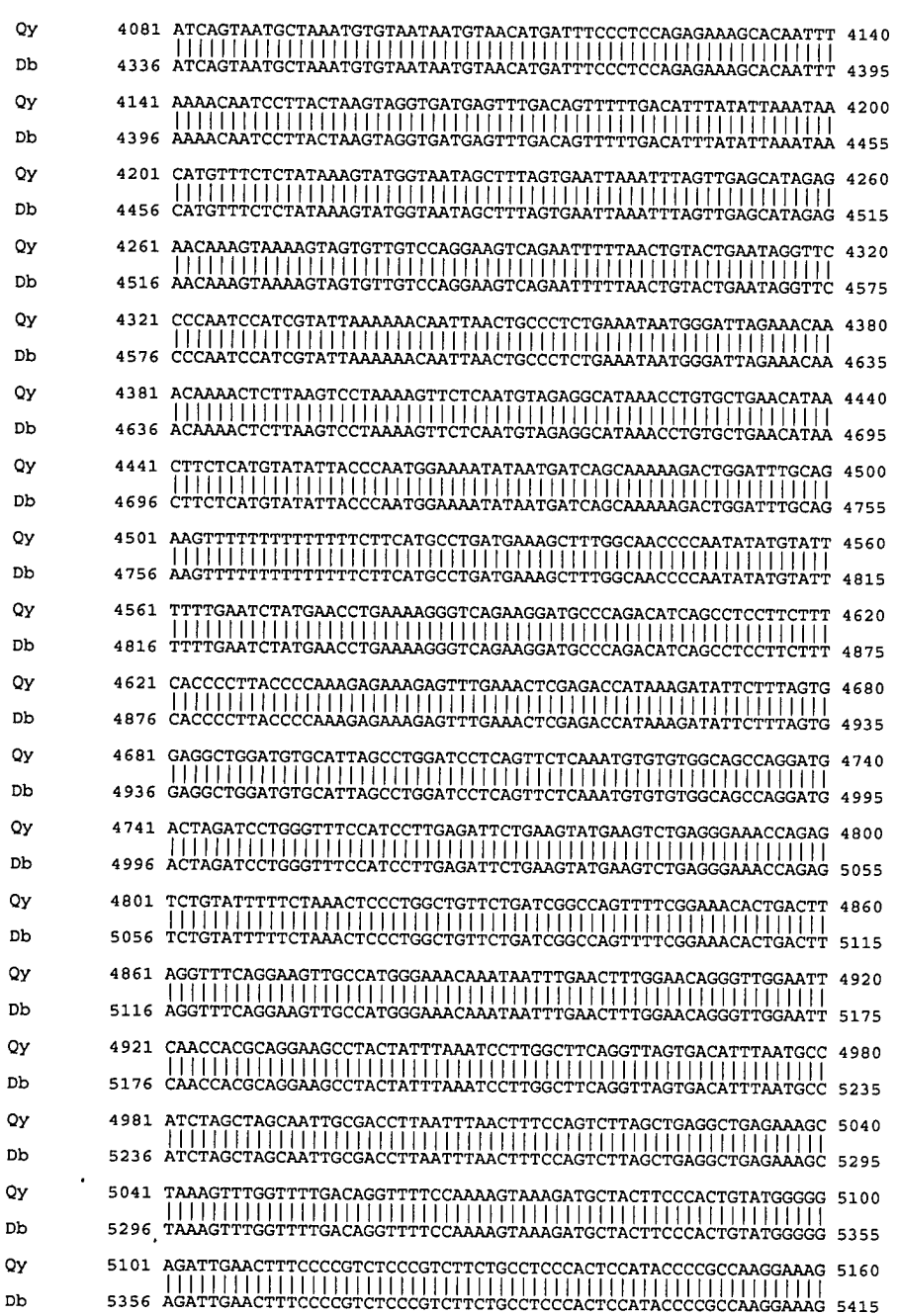
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Db       1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Db       2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116

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Qy 5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db 5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535
Qy 5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Db 5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595
Qy 5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db 5596 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5655
Qy 5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db 5656 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5715
Qy 5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Db 5716 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5775
Qy 5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Db 5776 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5835
Qy 5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
Db 5836 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5895
Qy 5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Db 5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955
Qy 5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
Db 5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015
Qy 5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Db 6016 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6075
Qy 5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Db 6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135
Qy 5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Db 6136 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6195
Qy 5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db 6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255
Qy 6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
Db 6256 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6315
Qy 6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
Db 6316 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6375
Qy 6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
Db 6376 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6435
Qy 6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
Db 6436 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6495
Qy 6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

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Db       6496 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6556 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6615

Qy       6361 GATATATAATTTAAAGTT 6378
              ||||||||||||||||||
Db       6616 GATATATAATTTAAAGTT 6633


RESULT 13
US-10-159-563-124
; Sequence 124, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
;  APPLICANT: Khan, Javed
;  APPLICANT:  Ringner, Markus
;  APPLICANT:  Peterson, Carsten
;  APPLICANT:  Meltzer, Paul
;  TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;  TITLE OF INVENTION:  DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;  FILE REFERENCE: 11613.56USI1
;  CURRENT APPLICATION NUMBER: US/10/159,563
;  CURRENT FILING DATE:  2002-12-09
;  PRIOR APPLICATION NUMBER: US 10/133,937
;  PRIOR FILING DATE: 2002-04-25
;  NUMBER OF SEQ ID NOS: 444
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 6633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-159-563-124

  Query Match            99.2%;  Score 6364.4;  DB 6;  Length 6633;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1516

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816

Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876
Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db       1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936
Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db       1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996
Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db       1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056
Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db       2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116
Qy       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db       2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176
Qy       1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db       2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
Qy       1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db       2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
Qy       2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db       2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356
Qy       2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db       2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416
Qy       2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db       2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476
Qy       2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db       2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536
Qy       2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db       2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596
Qy       2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db       2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656
Qy       2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db       2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716
Qy       2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db       2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776
Qy       2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db       2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy       2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db       2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896
Qy       2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db       2897 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2956

Qy       2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db       2957 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3016
Qy       2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db       3017 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3076
Qy       2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db       3077 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3136
Qy       2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db       3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196
Qy       2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db       3197 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3256
Qy       3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db       3257 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3316
Qy       3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db       3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy       3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db       3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy       3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db       3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496
Qy       3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db       3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556
Qy       3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db       3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616
Qy       3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db       3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy       3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db       3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy       3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db       3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796
Qy       3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db       3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy       3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db       3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
Qy       3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db       3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976
Qy       3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db       3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
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Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Db       4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096

Qy       3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156

Qy       3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216

Qy       3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275

Qy       4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335

Qy       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395

Qy       4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455

Qy       4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4456 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4515

Qy       4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4516 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4575

Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635

Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Db       4636 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4695

Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Db       4696 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4755

Qy       4501 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4756 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4815

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Db       5116 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5175

Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5176 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 5235

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5236 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5295

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5296 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5355

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
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Db       5356 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5415

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Db       5416 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5475

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
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Db       5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
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Db       5596 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5655

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Db       5656 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5715

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Db       5716 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5775

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5776 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5835

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
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Db       5836 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5895

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
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Db       5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Db       5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Db       6016 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6075

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6195

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6315

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Db       6316 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6375

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Db       6376 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6435

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6436 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6495

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6496 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6555

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6556 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6615

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 14
US-10-926-806-13
; Sequence 13, Application US/10926806
; Publication No. US20050096257A1
; GENERAL INFORMATION:
; APPLICANT: SHIMA, DAVID
; APPLICANT: CALIAS, PERRY
; APPLICANT: ADAMIS, ANTHONY P.
; TITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCULAR
; TITLE OF INVENTION: NEOVASCULAR DISORDERS
; FILE REFERENCE: 112089.184 EYE-013
; CURRENT APPLICATION NUMBER: US/10/926,806
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/556,837
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 60/498,407
; PRIOR FILING DATE: 2003-08-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-926-806-13

Query Match 99.2%; Score 6364.4; DB 9; Length 6633;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy     .    61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Db        437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
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Db        677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
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Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
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Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1516

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576

Qy      1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Db      1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636

Qy      1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696

Qy      1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Db      1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756

Qy      1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816

Qy      1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876

Qy      1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
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Db      1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936

Qy      1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996

Qy      1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Db      1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056

Qy      1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116

Qy      1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176

Qy      1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236

Qy      1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296

Qy      2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
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Db      2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356

Qy      2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
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Db      2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416

Qy      2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476

Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536

Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
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Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
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Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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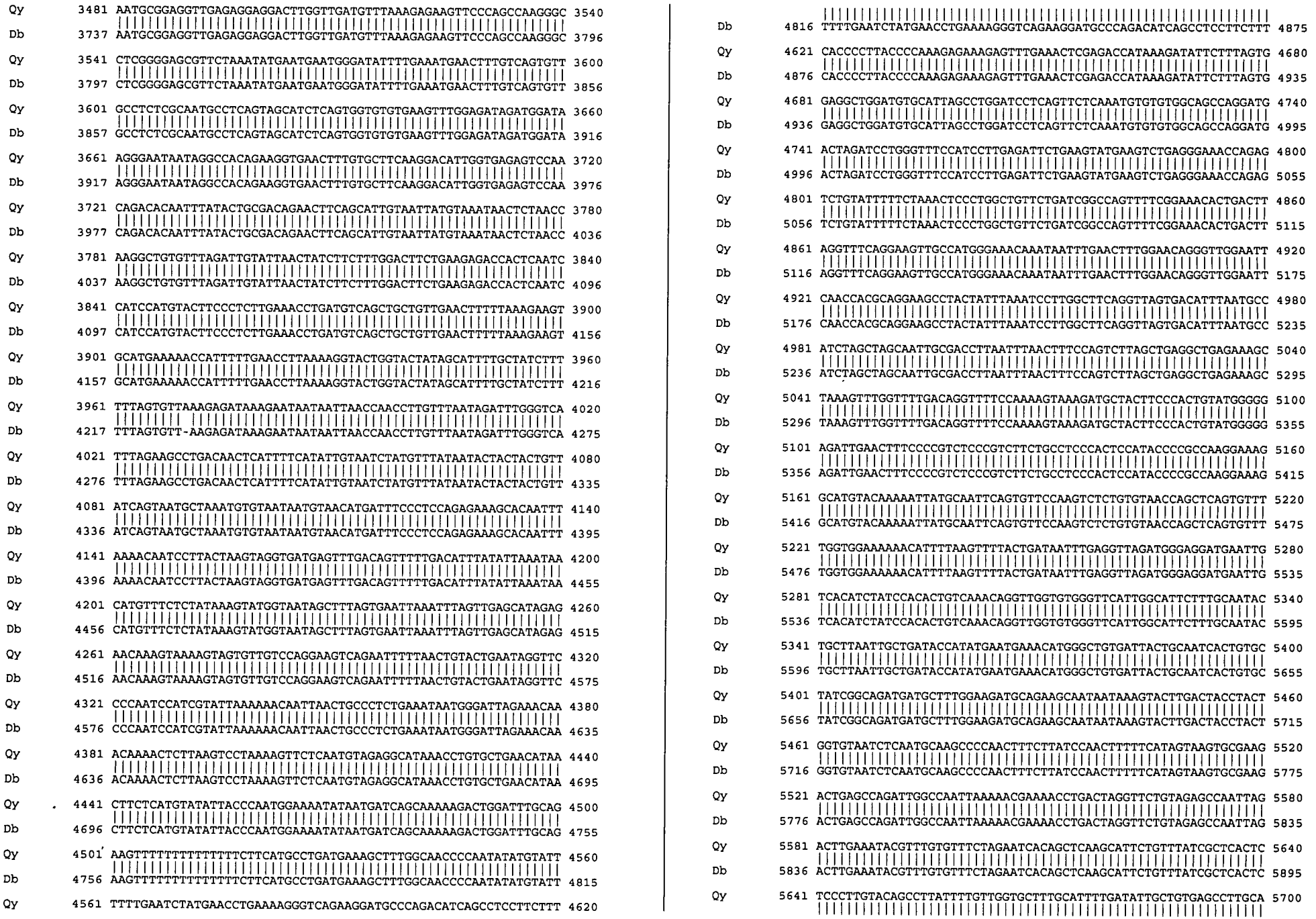
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RESULT 15
US-10-723-860-5285
; Sequence 5285, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Ginsburg, Wendy M.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
;  TITLE OF INVENTION:  Methods for Screening for Soft Tissue Sarcoma Modulators
;  FILE REFERENCE: 05882.0193.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/723,860
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: 60/429,739
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 8393
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US-10-723-860-5285

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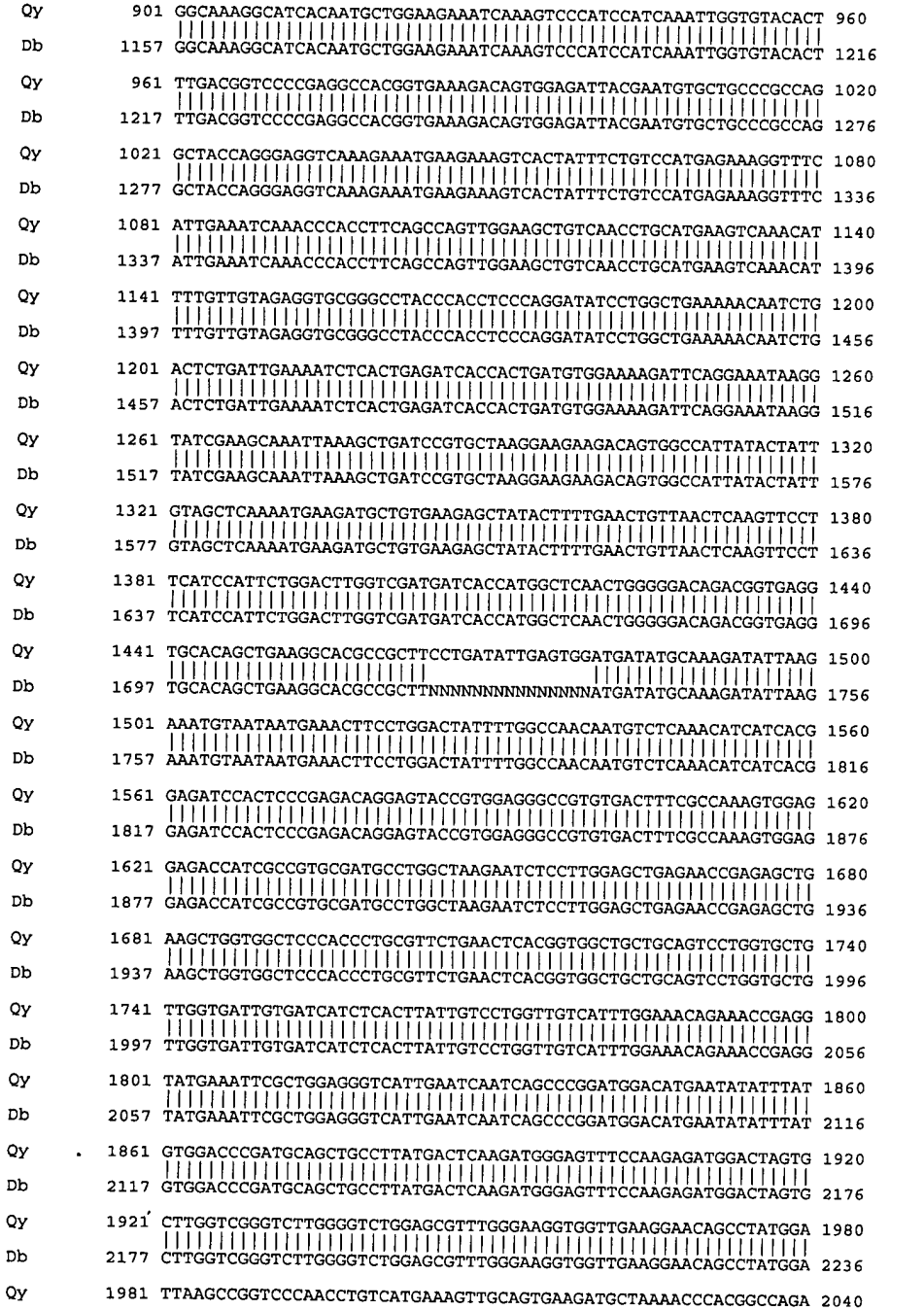
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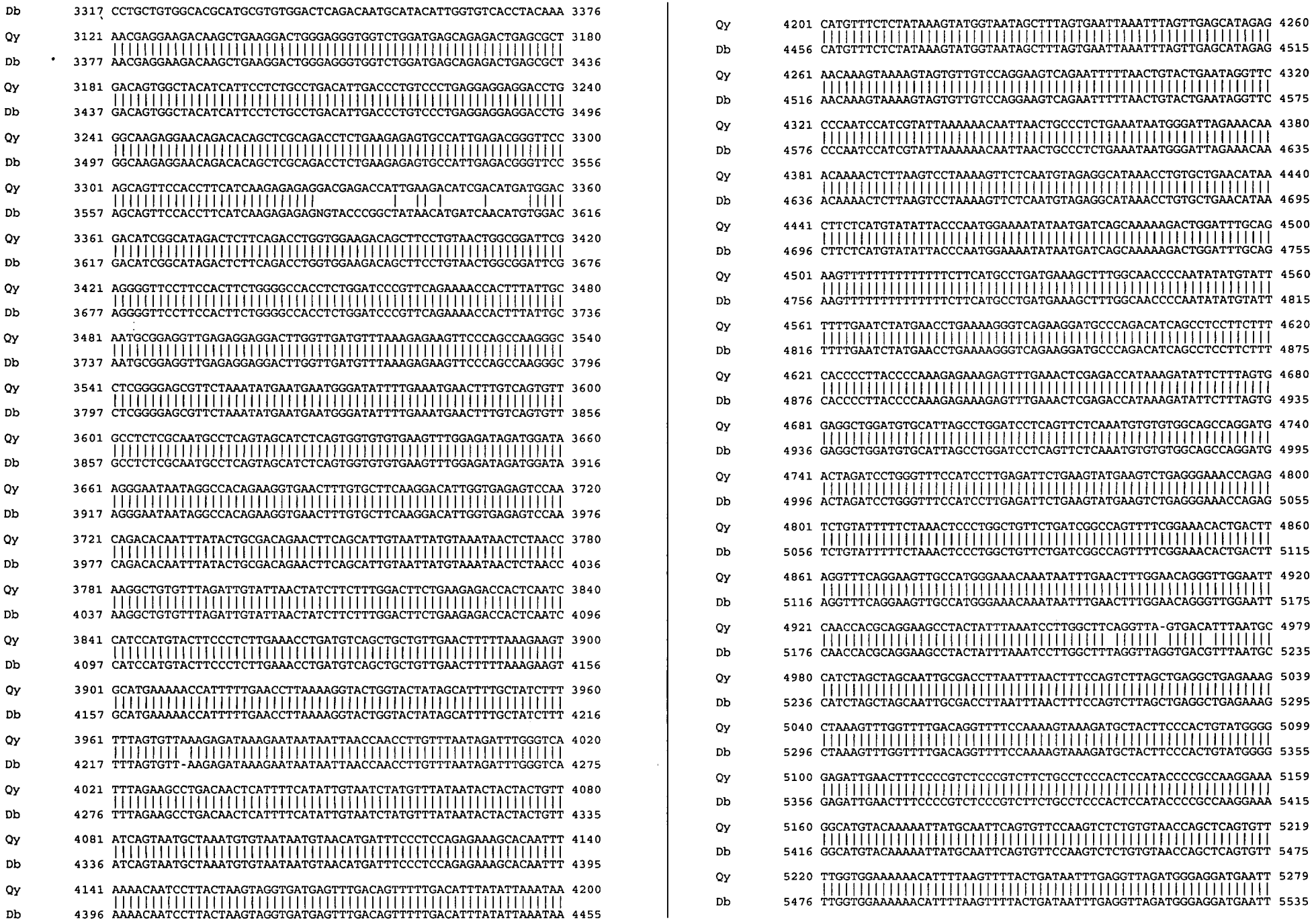
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Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
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Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3257 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3316
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120


Db 3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556
Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3557 AGCAGTTCCACCTTCATCAAGAGAGAGNGTACCCGGCTATAACATGATCAACATGTGGAC 3616
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
Db 4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
Db 4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455
Qy 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
Db 4456 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4515
Qy 4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
Db 4516 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4575
Qy 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
Db 4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635
Qy 4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db 4636 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4695
Qy 4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db 4696 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4755
Qy 4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db 4756 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4815
Qy 4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db 4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875
Qy 4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db 4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935
Qy 4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db 4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995
Qy 4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db 4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055
Qy 4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db 5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115
Qy 4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db 5116 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5175
Qy 4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTA-GTGACATTTAATGC 4979
Db 5176 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTTAGGTTAGGTGACGTTTAATGC 5235
Qy 4980 CATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAG 5039
Db 5236 CATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAG 5295
Qy 5040 CTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGG 5099
Db 5296 CTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGG 5355
Qy 5100 GAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAA 5159
Db 5356 GAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAA 5415
Qy 5160 GGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTT 5219
Db 5416 GGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTT 5475
Qy 5220 TTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATT 5279
Db 5476 TTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATT 5535

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Qy       5280 GTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATA 5339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5536 GTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATA 5595

Qy       5340 CTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTG 5399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5596 CTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTG 5655

Qy       5400 CTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTAC 5459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5656 CTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTAC 5715

Qy       5460 TGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAA 5519
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5716 TGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAA 5775

Qy       5520 GACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTA 5579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5776 GACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTA 5835

Qy       5580 GACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACT 5639
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5836 GACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACT 5895

Qy       5640 CTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGC 5699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5896 CTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGC 5955

Qy       5700 ATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGC 5759
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5956 ATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGC 6015

Qy       5760 TCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCC 5819
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6016 TCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTTTTCAGCAAATTCC 6075

Qy       5820 AGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCT 5879
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6076 AGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCT 6135

Qy       5880 ACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTT 5939
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6136 ACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTT 6195

Qy       5940 AAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTT 5999
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6196 AAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTT 6255

Qy       6000 TGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTA 6059
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6256 TGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTA 6315

Qy       6060 TATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTA 6119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6316 TATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTA 6375

Qy       6120 TATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCA 6179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6376 TATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCA 6435

Qy       6180 AAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTG 6239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6436 AAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTG 6495

Qy       6240 TGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAA 6299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6496 TGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAA 6555

Qy       6300 TGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAA 6359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6556 TGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAA 6615

Qy       6360 TGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6413
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Db       6616 TGATATATAATTTAAAGTTAAAAAAAAAAAAAAAAAAAAACAAAACAAACAAACA 6669


RESULT 16
US-10-741-601-155
; Sequence 155, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 155
;   LENGTH: 6633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-155

  Query Match             98.7%;  Score 6327;  DB 7;  Length 6633;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 6357;  Conservative   14;  Mismatches    4;  Indels    6;  Gaps    3;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCRGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 778

Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGCAACATCAGAGC 1033

Qy        779 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 838

Db       1034 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 1093

Qy        839 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 898

Db       1094 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 1153

Qy        899 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 958

Db       1154 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 1213

Qy        959 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1018

Db       1214 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1273

Qy       1019 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTT 1078

Db       1274 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGKT 1333

Qy       1079 TCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAAC 1138

Db       1334 TCATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAAC 1393

Qy       1139 ATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATC 1198

Db       1394 ATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATC 1453

Qy       1199 TGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAA 1258

Db       1454 TGACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAA 1513

Qy       1259 GGTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTA 1318

Db       1514 GSTATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTA 1573

Qy       1319 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1378

Db       1574 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1633

Qy       1379 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1438

Db       1634 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTYAACTGGGGGACAGACGGTGA 1693

Qy       1439 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1498

Db       1694 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1753

Qy       1499 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1558

Db       1754 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1813

Qy       1559 CGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1618

Db       1814 CGGAGATCCACYCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1873

Qy       1619 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1678

Db       1874 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1933

Qy       1679 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1738

Db       1934 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1993

Qy       1739 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 1798

Db       1994 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 2053

Qy       1799 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTT 1858

Db       2054 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCRGATGGACATGAATATATTT 2113

Qy       1859 ATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAG 1918

Db       2114 ATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAG 2173

Qy       1919 TGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATG 1978

Db       2174 TGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATG 2233

Qy       1979 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2038

Db       2234 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2293

Qy       2039 GATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCAC 2098

Db       2294 GATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCAC 2353

Qy       2099 ATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCA 2158

Db       2354 ATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCA 2413

Qy       2159 CAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCC 2218

Db       2414 CAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCC 2473

Qy       2219 TGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTG 2278

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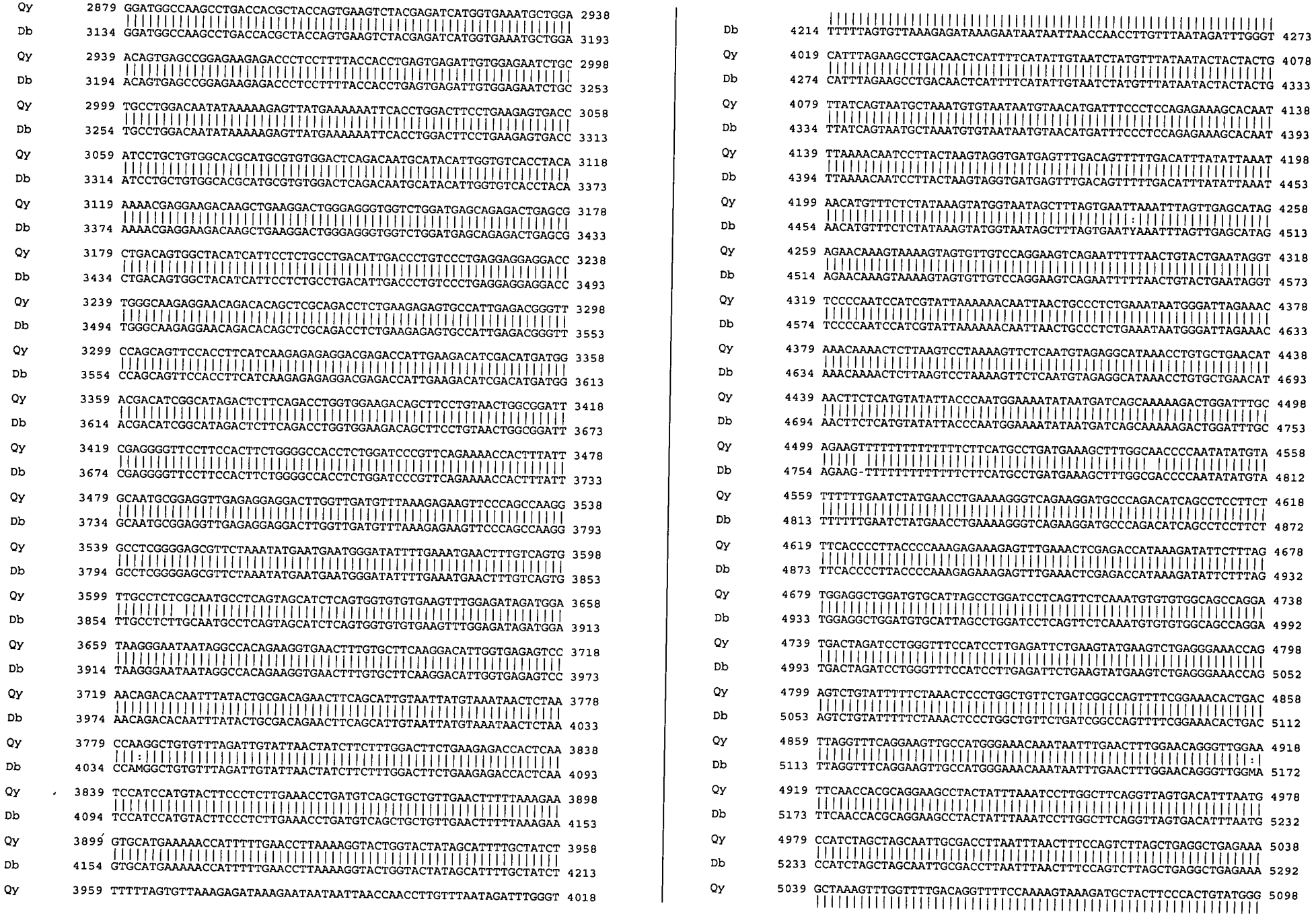
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RESULT 17
US-10-741-600-476
; Sequence 476, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 476
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-476

Query Match 98.7%; Score 6327; DB 8; Length 6633;
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Matches 6357; Conservative 14; Mismatches 4; Indels 6; Gaps 3;

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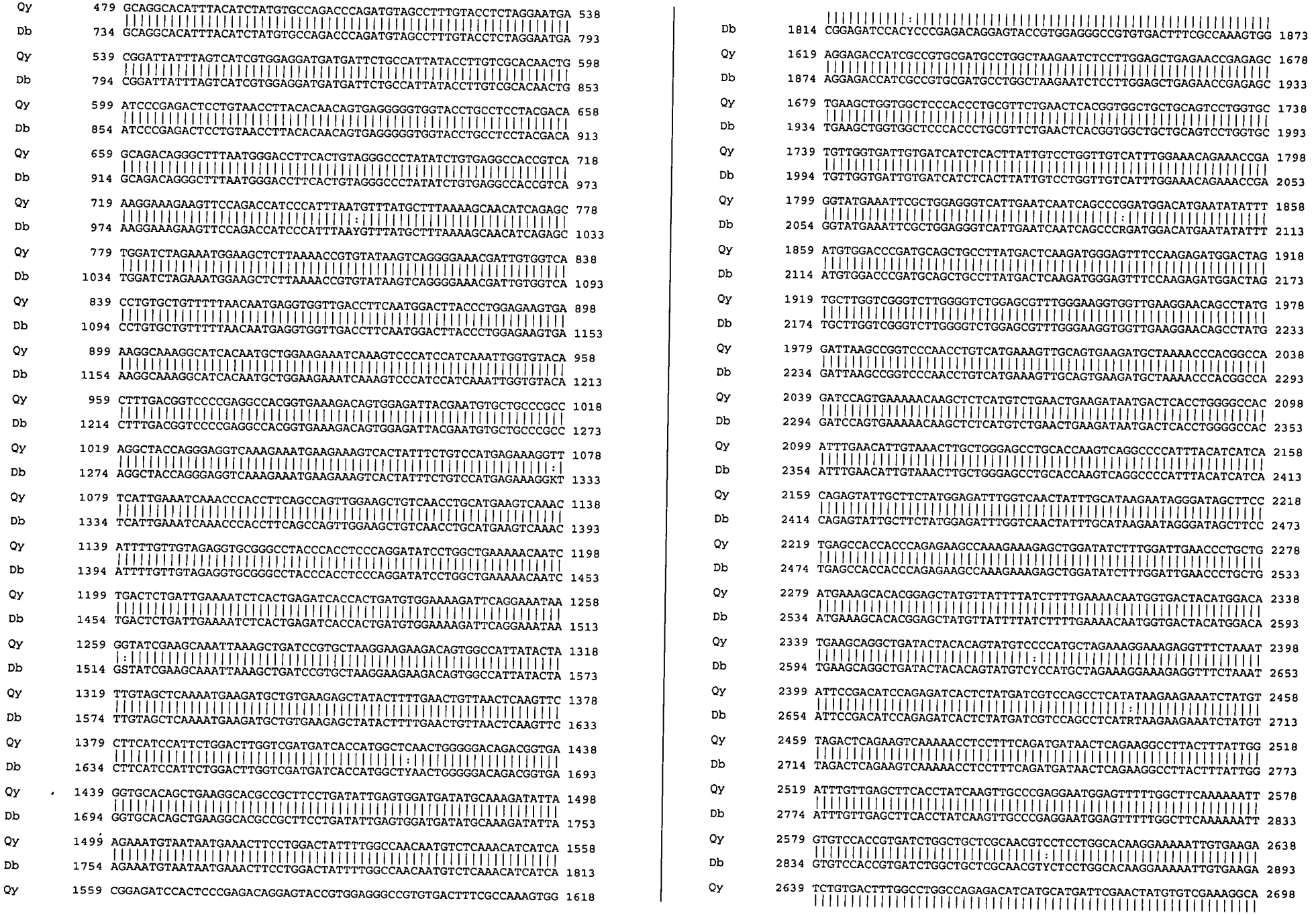
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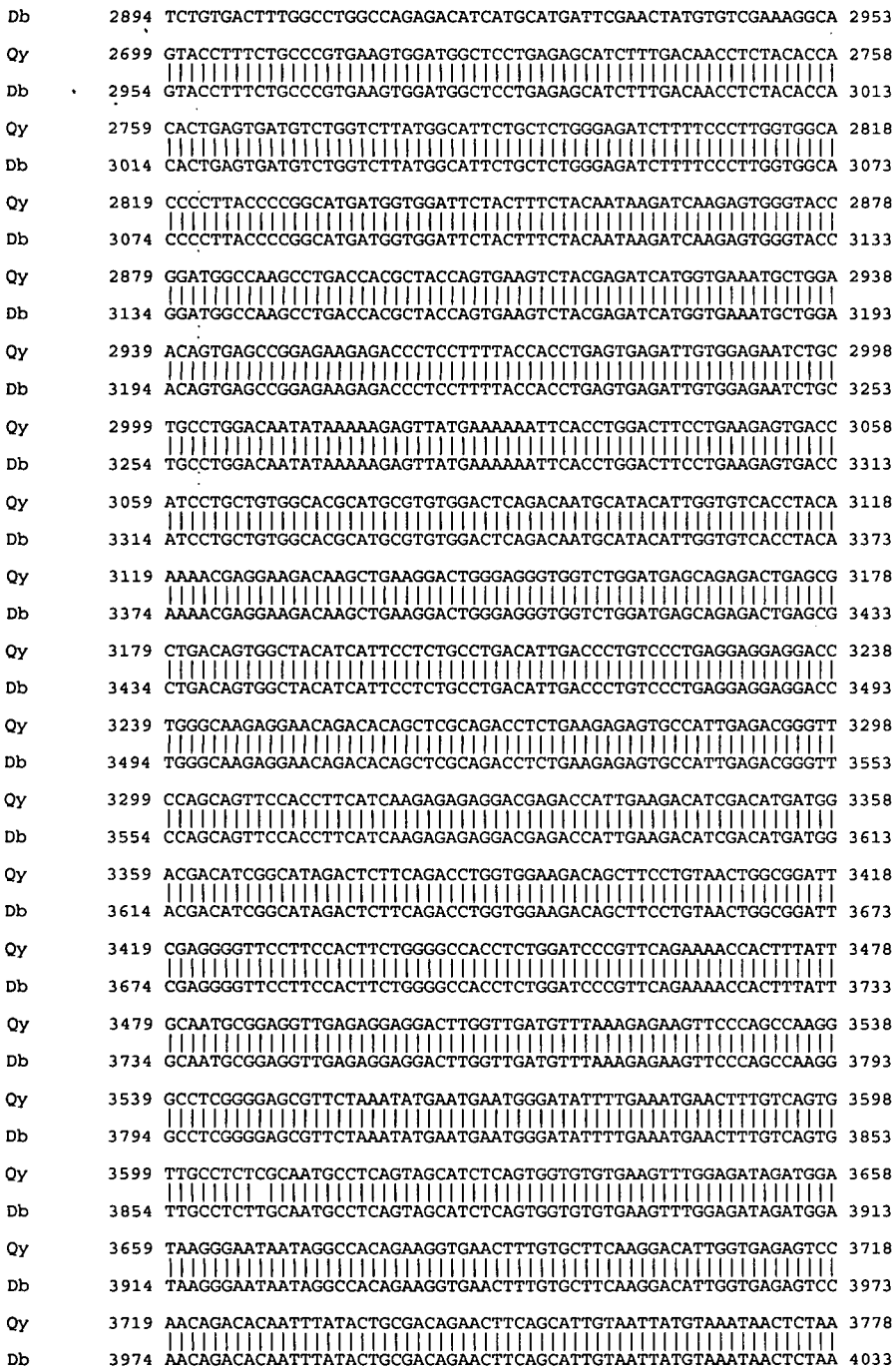
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Qy 1379 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1438
Db 1634 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTYAACTGGGGGACAGACGGTGA 1693
Qy 1439 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1498
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Qy 1499 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1558
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Qy 1559 CGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1618
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Qy 1799 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTT 1858
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Db 4993 TGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAG 5052
Qy 4799 AGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGAC 4858
Db 5053 AGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGAC 5112

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Qy       4859 TTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAA 4918
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Db       5113 TTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGMA 5172

Qy       4919 TTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATG 4978
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Db       5173 TTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATG 5232

Qy       4979 CCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAA 5038
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Qy       5399 GCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 5458
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Db       5653 GCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTA 5712

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Qy       5519 AGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATT 5578
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Qy       5879 TACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTT 5938
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Qy       6059 ATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTT 6118
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RESULT 18
US-10-322-696-167
; Sequence 167, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 6240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-696-167

Query Match 97.1%; Score 6224.2; DB 7; Length 6240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6237; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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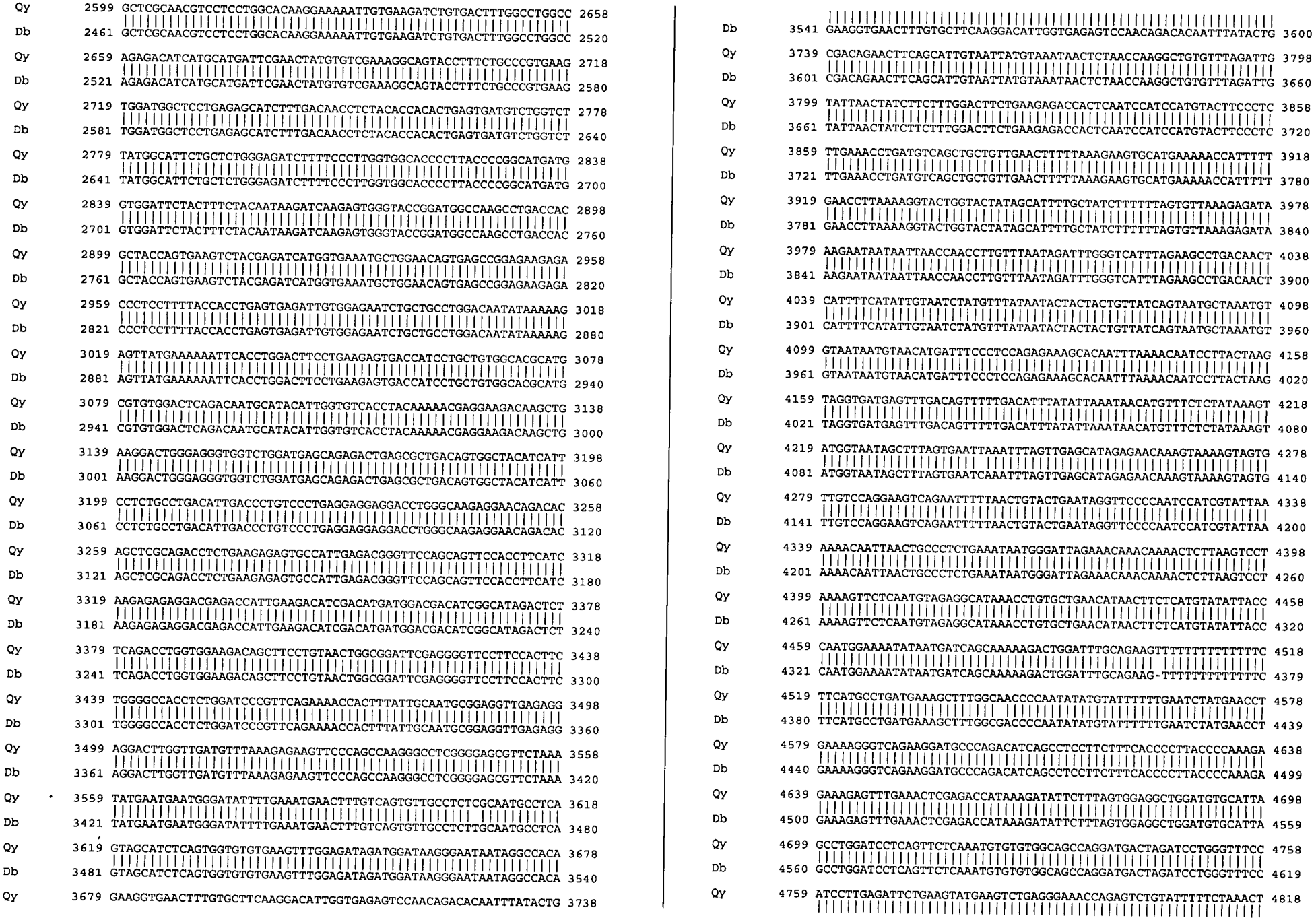
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Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
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Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

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Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600
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Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660
Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720
Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db        721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780
Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840
Qy        979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db        841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900
Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960
Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020
Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140
Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200
Qy       1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260
Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320
Qy       1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440
Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560
Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680
Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740
Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db       1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800
Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860
Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920
Qy       2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980
Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040
Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
Db       2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100
Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220
Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280
Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340
Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400
Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db       2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460
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Qy 2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
Db 2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520
Qy 2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db 2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580
Qy 2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db 2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
Qy 2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db 2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy 2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
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Db 2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820
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Qy 3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Qy 3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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Qy 3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
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Qy 3439 TGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGG 3498
Db 3301 TGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGG 3360
Qy 3499 AGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAA 3558
Db 3361 AGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAA 3420
Qy 3559 TATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTCA 3618
Db 3421 TATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTCA 3480
Qy 3619 GTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACA 3678
Db 3481 GTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACA 3540
Qy 3679 GAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTG 3738
Db 3541 GAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTG 3600
Qy 3739 CGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTG 3798
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Db 3661 TATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTC 3720
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Db 3721 TTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTT 3780
Qy 3919 GAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATA 3978
Db 3781 GAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATA 3840
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Db 3961 GTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAG 4020
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Db 4201 AAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCT 4260
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Db 4261 AAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACC 4320
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Db 4321 CAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTTC 4379
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Qy 4579 GAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGA 4638
Db 4440 GAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGA 4499
Qy 4639 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 4698
Db 4500 GAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTA 4559
Qy 4699 GCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCC 4758
Db 4560 GCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCC 4619
Qy 4759 ATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACT 4818

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Db       4620 ATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACT 4679

Qy       4819 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 4878
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Db       4680 CCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCC 4739

Qy       4879 ATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCT 4938
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Db       4740 ATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCT 4799

Qy       4939 ACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCG 4998
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Db       4800 ACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCG 4859

Qy       4999 ACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACA 5058
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Db       4860 ACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACA 4919

Qy       5059 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 5118
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Db       4920 GGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGT 4979

Qy       5119 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 5178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4980 CTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATG 5039

Qy       5179 CAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTT 5238
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Db       5040 CAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTT 5099

Qy       5239 AAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTG 5298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 AAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTG 5159

Qy       5299 TCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACC 5358
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Db       5160 TCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACC 5219

Qy       5359 ATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTT 5418
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Qy       5419 TGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAA 5478
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Db       5280 TGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAA 5339

Qy       5479 GCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCA 5538
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Db       5340 GCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCA 5399

Qy       5539 ATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTG 5598
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Qy       5599 TTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTAT 5658
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Qy       5659 TTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGA 5718
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Qy       5719 TGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATA 5778
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Qy       5779 TGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGC 5838
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Qy       5839 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5898
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Db       5700 CTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATG 5759

Qy       5899 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 5958
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Db       5760 ACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCT 5819

Qy       5959 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 6018
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Db       5820 TAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGA 5879

Qy       6019 TAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACT 6078
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Qy       6079 GCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATA 6138
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Db       5940 GCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATA 5999

Qy       6139 ATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAAT 6198
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Db       6000 ATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAAT 6059

Qy       6199 AATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAA 6258
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Db       6060 AATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAA 6119

Qy       6259 ACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTT 6318
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Qy       6319 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 6378
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Db       6180 GTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTT 6239

Qy       6379 A 6379
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Db       6240 A 6240
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RESULT 19
US-10-027-400-1
; Sequence 1, Application US/10027400
; Publication No. US20030017535A1
;  GENERAL INFORMATION:
;       APPLICANT: WILLIAMS, Lewis T.
;                  ESCOBEDO, Jaime A.
;       TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;       NUMBER OF SEQUENCES: 14
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew
;            STREET: One Market, Steuart Street Tower, 20th Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94105
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/027,400
;            FILING DATE: 19-Dec-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/461,917
;            FILING DATE: 05-JUN-1995
;            APPLICATION NUMBER: US 07/151,414
;            FILING DATE: 02-FEB-1988
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dow, Karen B.
;            REGISTRATION NUMBER: 29,684
;            REFERENCE/DOCKET NUMBER: 2307K-267-2-4
;       TELECOMMUNICATION INFORMATION:
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;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6373 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  129..3398
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-027-400-1

  Query Match             74.5%;  Score 4777;  DB 5;  Length 6373;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   11;  Gaps    8;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

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Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
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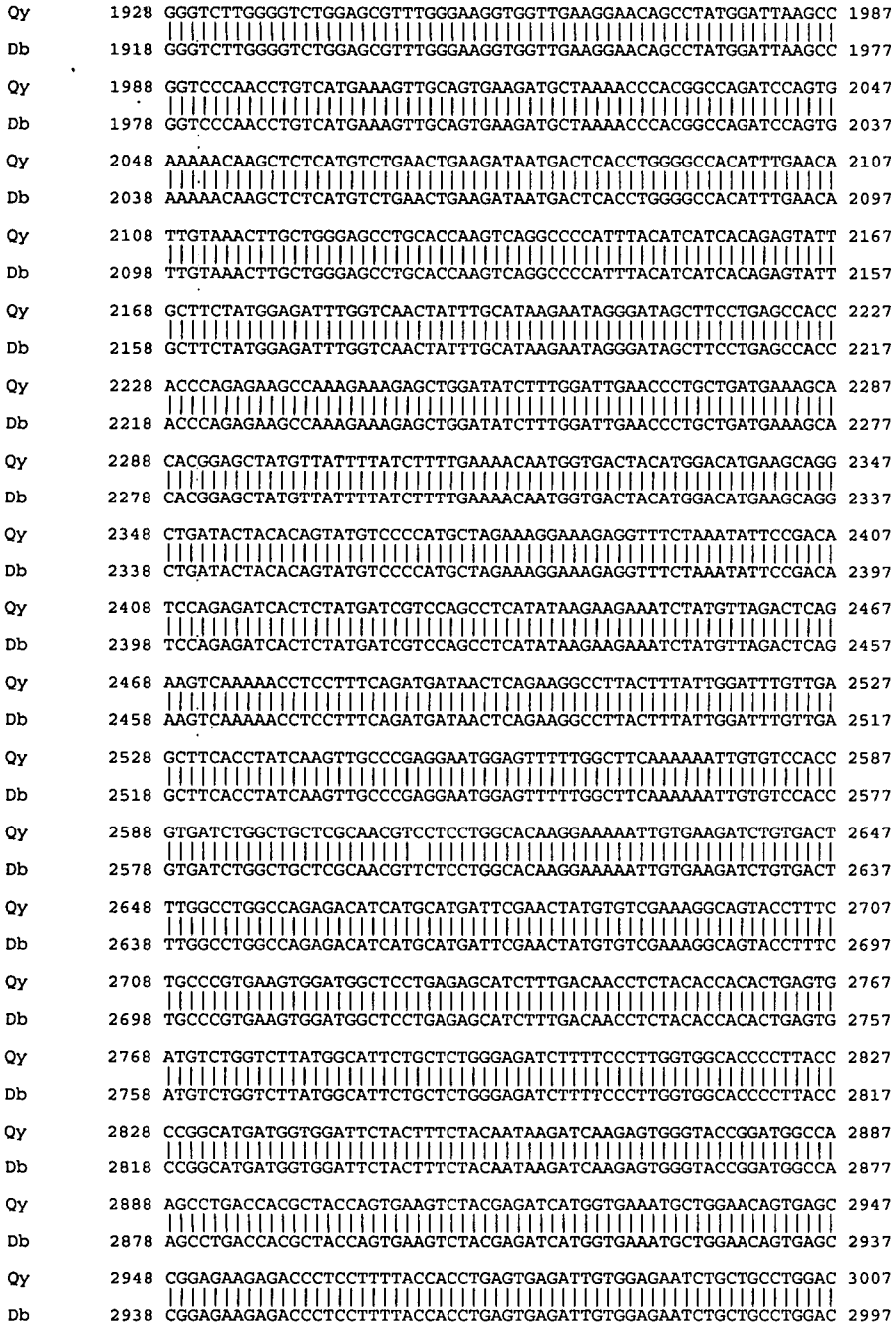
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Qy       1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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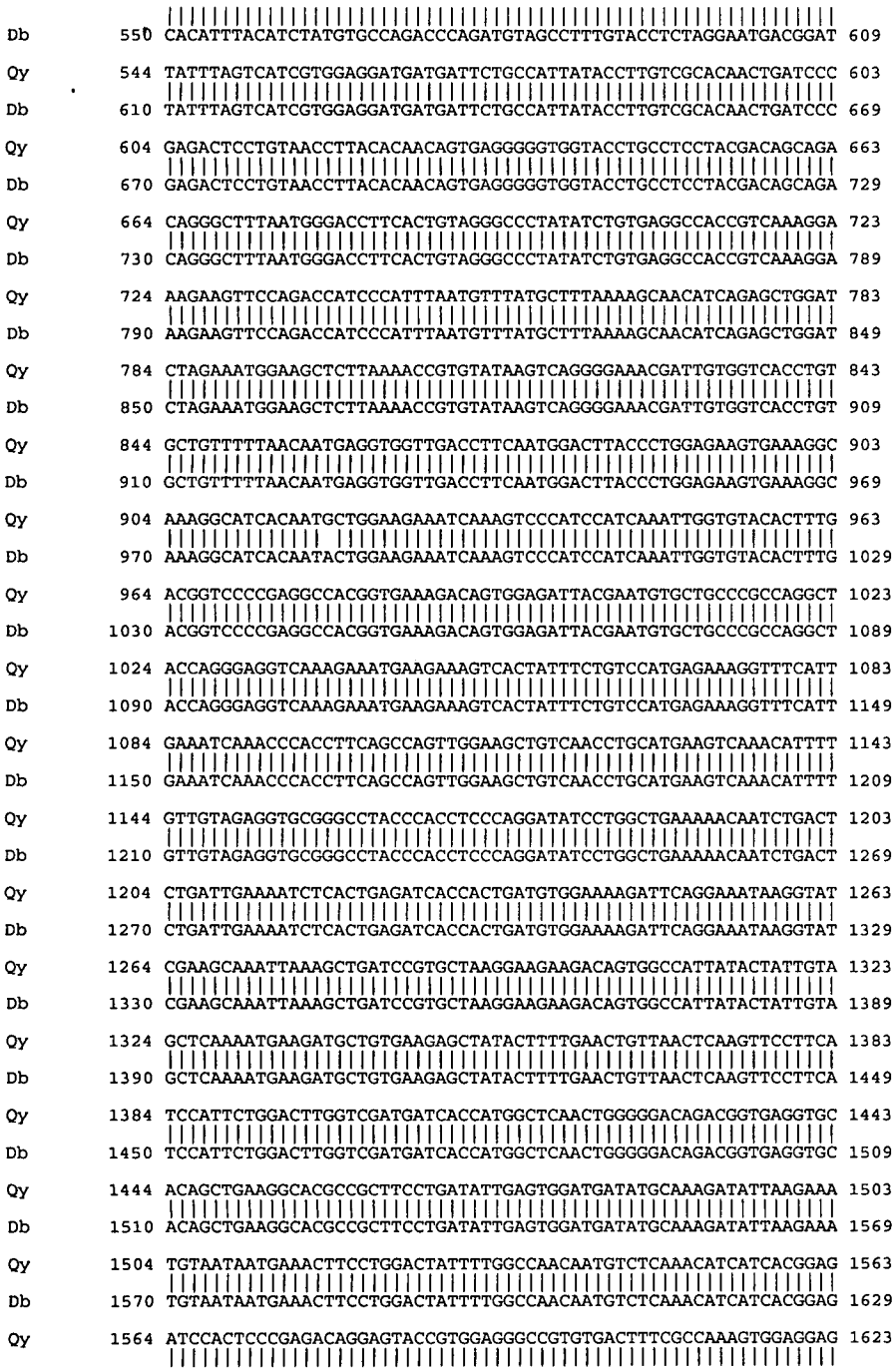
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
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Db 2290 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2349
Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
Db 2350 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2409
Qy 2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
Db 2410 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2469
Qy 2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463
Db 2470 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2529
Qy 2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
Db 2530 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2589
Qy 2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
Db 2590 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2649
Qy 2584 CACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGT 2643
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Qy      2704 TTTCTGCCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
Db      2770 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2829

Qy      2764 AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCT 2823
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Qy      2824 TACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATG 2883
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Qy      3004 GGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCT 3063
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Qy      3064 GCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAAC 3123
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Qy      3124 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3183
Db      3190 GAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGAC 3249

Qy      3184 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3243
Db      3250 AGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGC 3309

Qy      3244 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3303
Db      3310 AAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGC 3369

Qy      3304 AGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGAC 3363
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Qy      3364 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3423
Db      3430 ATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGG 3489

Qy      3424 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
Db      3490 GGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3549

Qy      3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Qy      3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
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Qy      3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
Db      3670 TCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3729

Qy      3664 GAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG 3723
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Qy      3784 GCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCAT 3843
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Qy      3844 CCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3903
Db      3910 CC-TGTACTTCCCTCTTGAAACCTGATGT-AGCTGCTGTTGAACTTTTTAAAGAAGTGCA 3967

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RESULT 21
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; Sequence 914, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 914
; LENGTH: 6576
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-914

Query Match 55.9%; Score 3585; DB 9; Length 6576;
Best Local Similarity 76.2%; Pred. No. 0;
Matches 5013; Conservative 0; Mismatches 1305; Indels 265; Gaps 38;

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Qy        64 CCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAG 123
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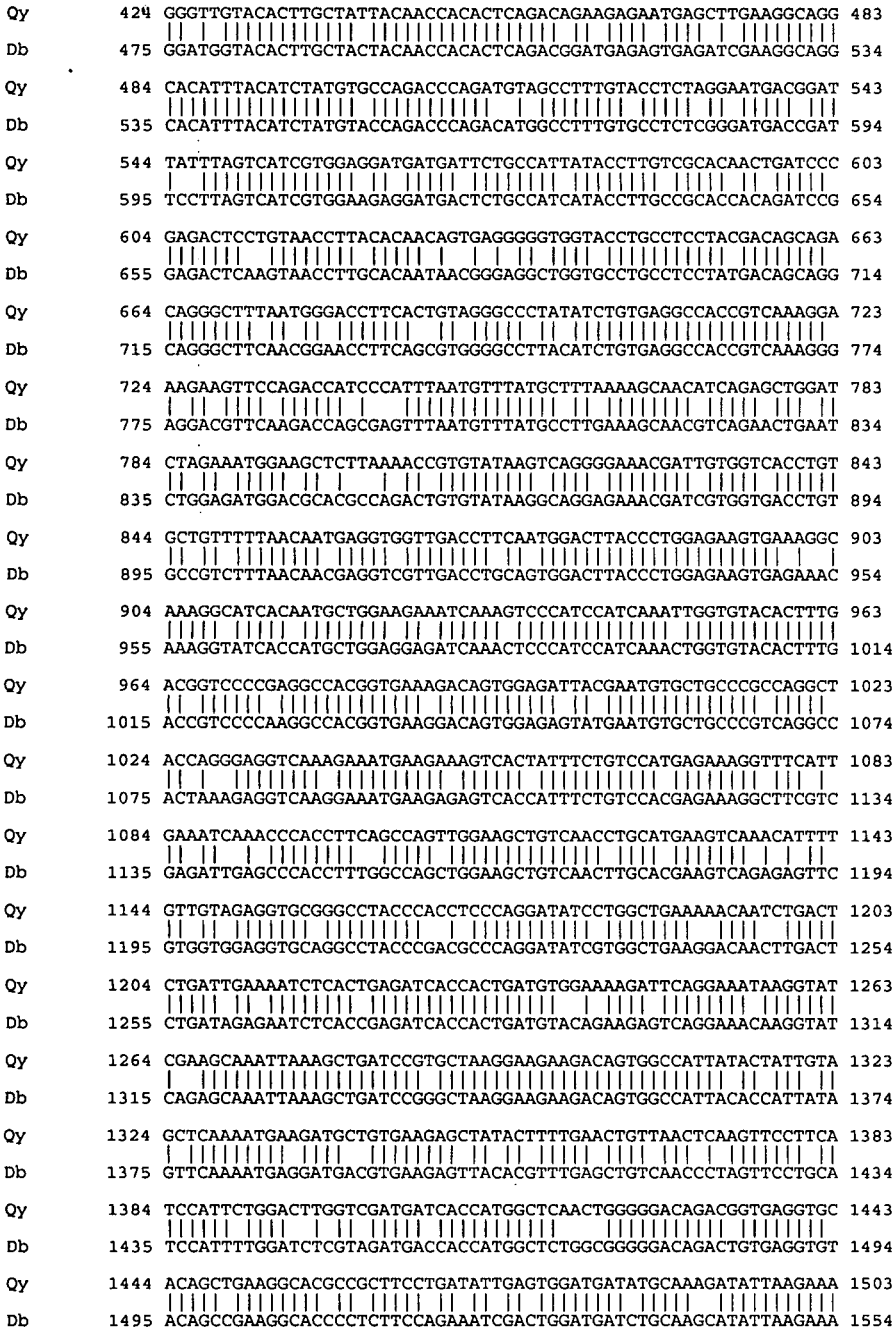
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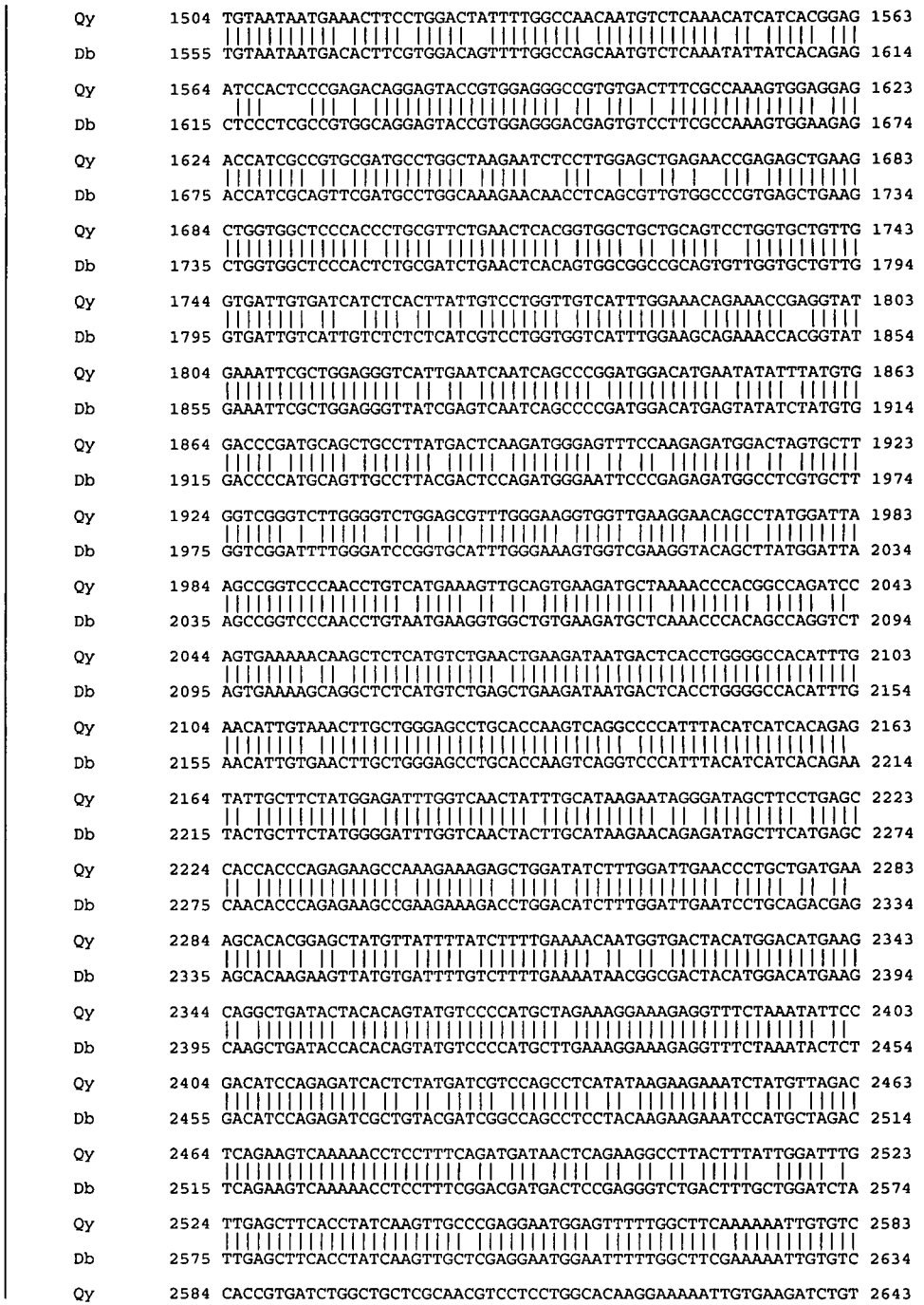
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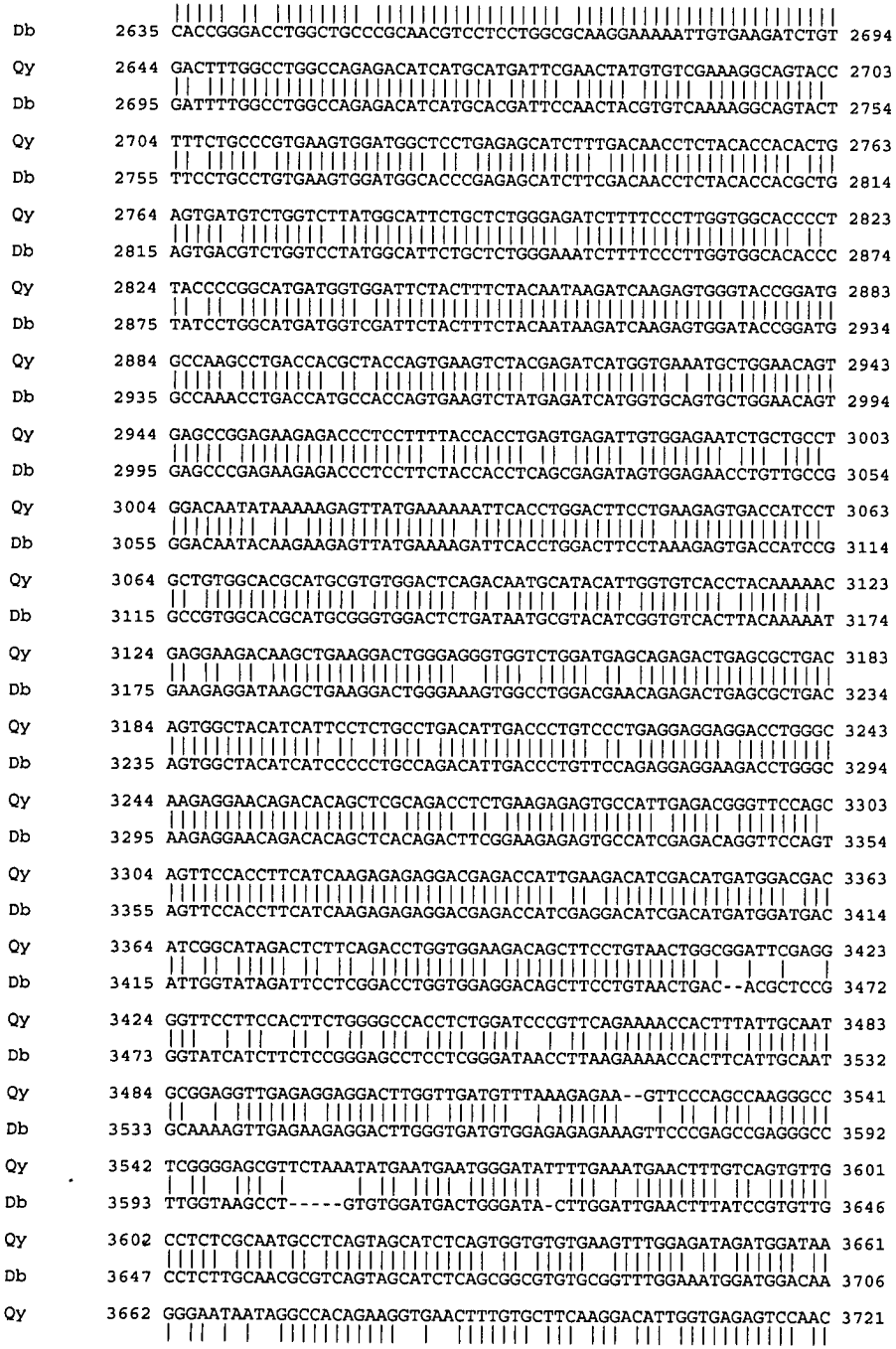
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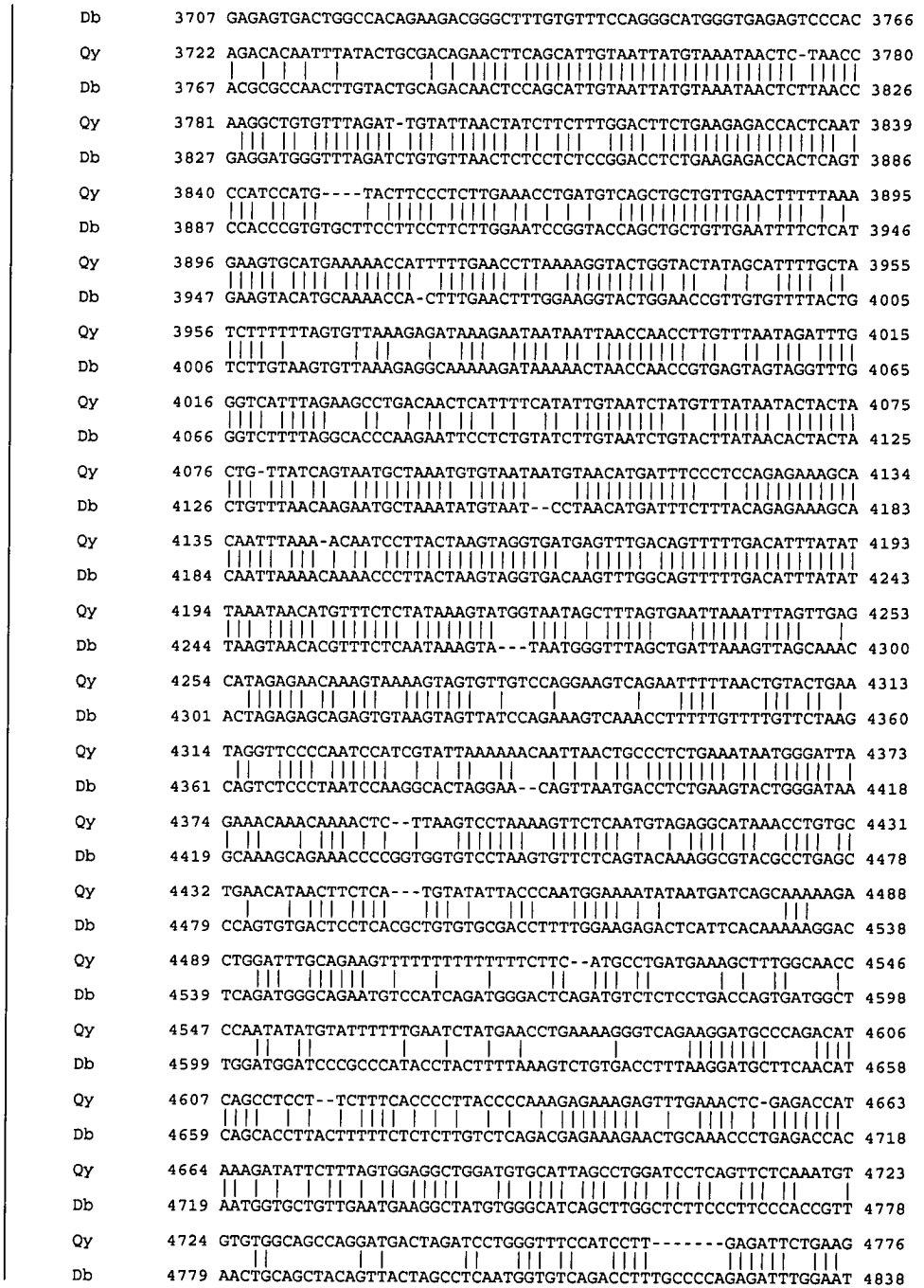
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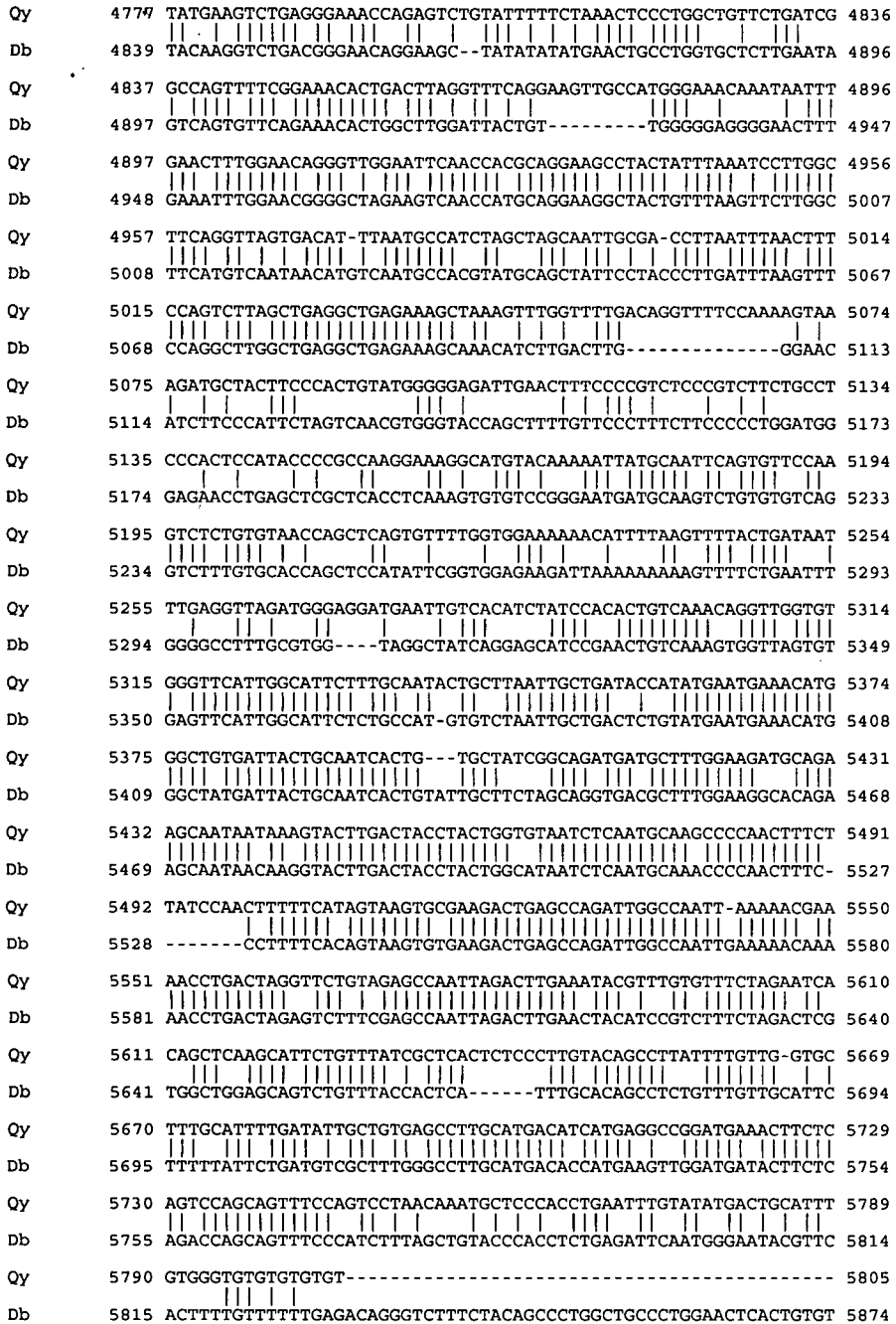
Qy       364 AACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACA 423
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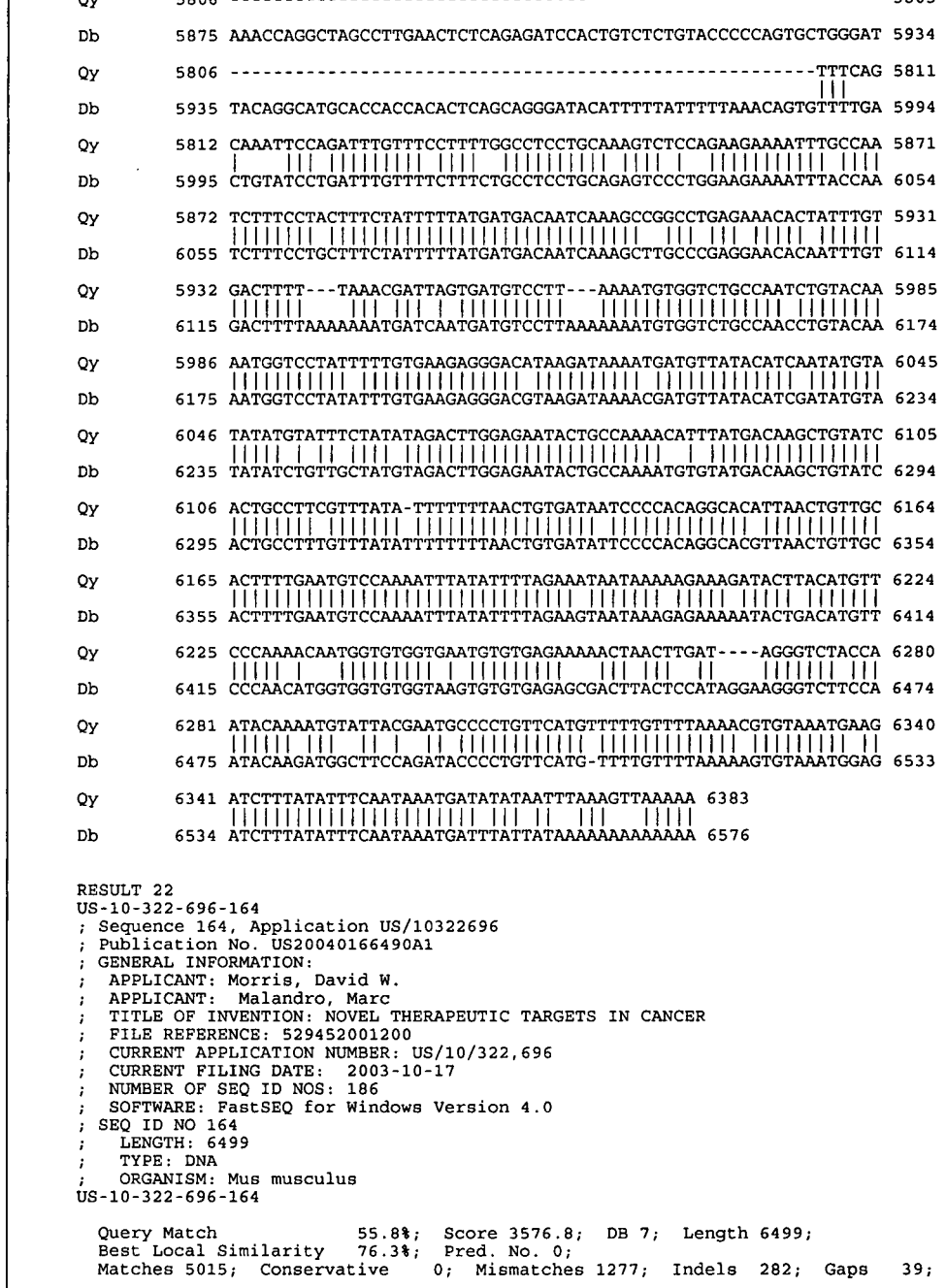








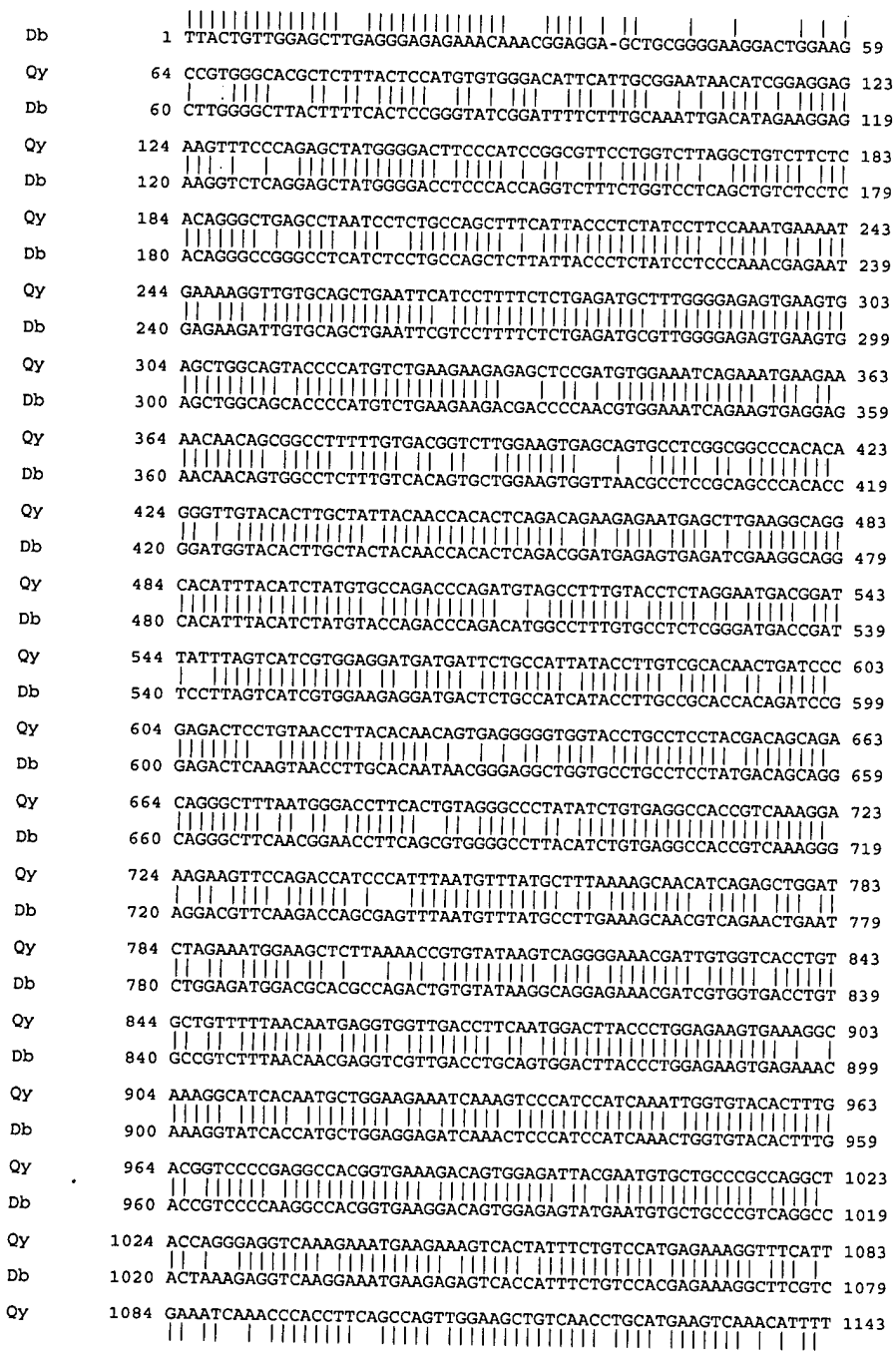


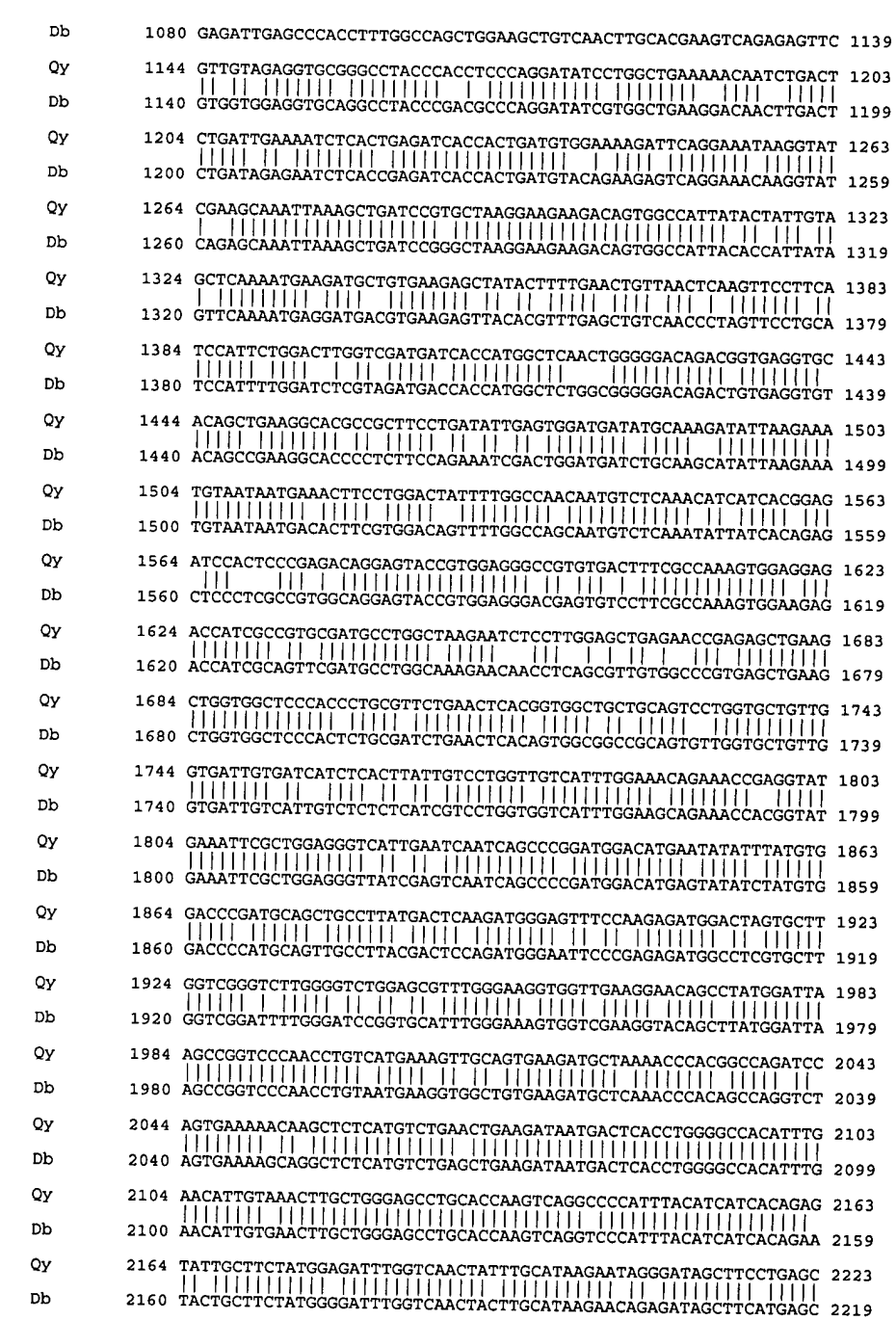


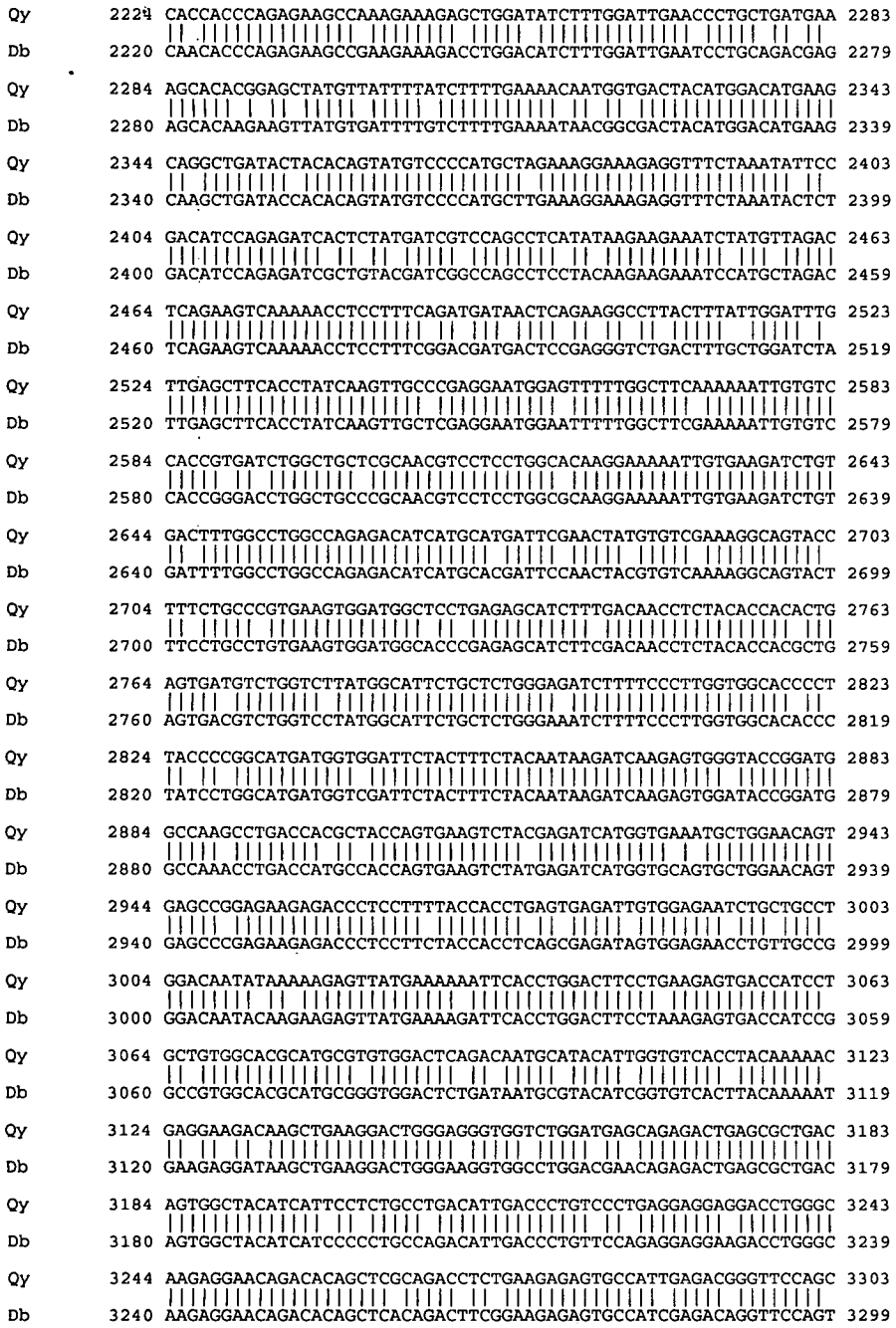
RESULT 22
US-10-322-696-164
; Sequence 164, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 6499
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-696-164

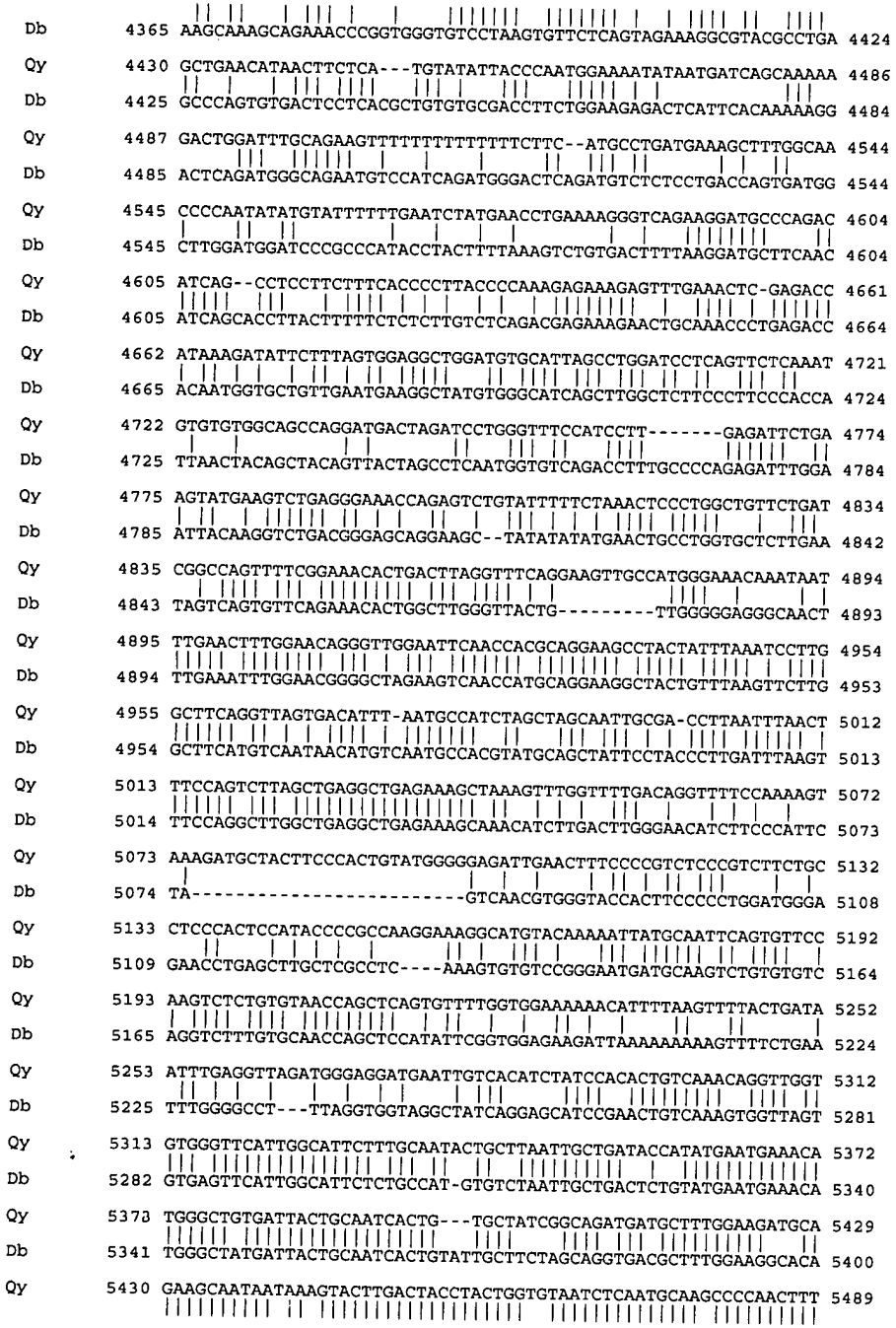
Query Match 55.8%; Score 3576.8; DB 7; Length 6499;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 5015; Conservative 0; Mismatches 1277; Indels 282; Gaps 39;

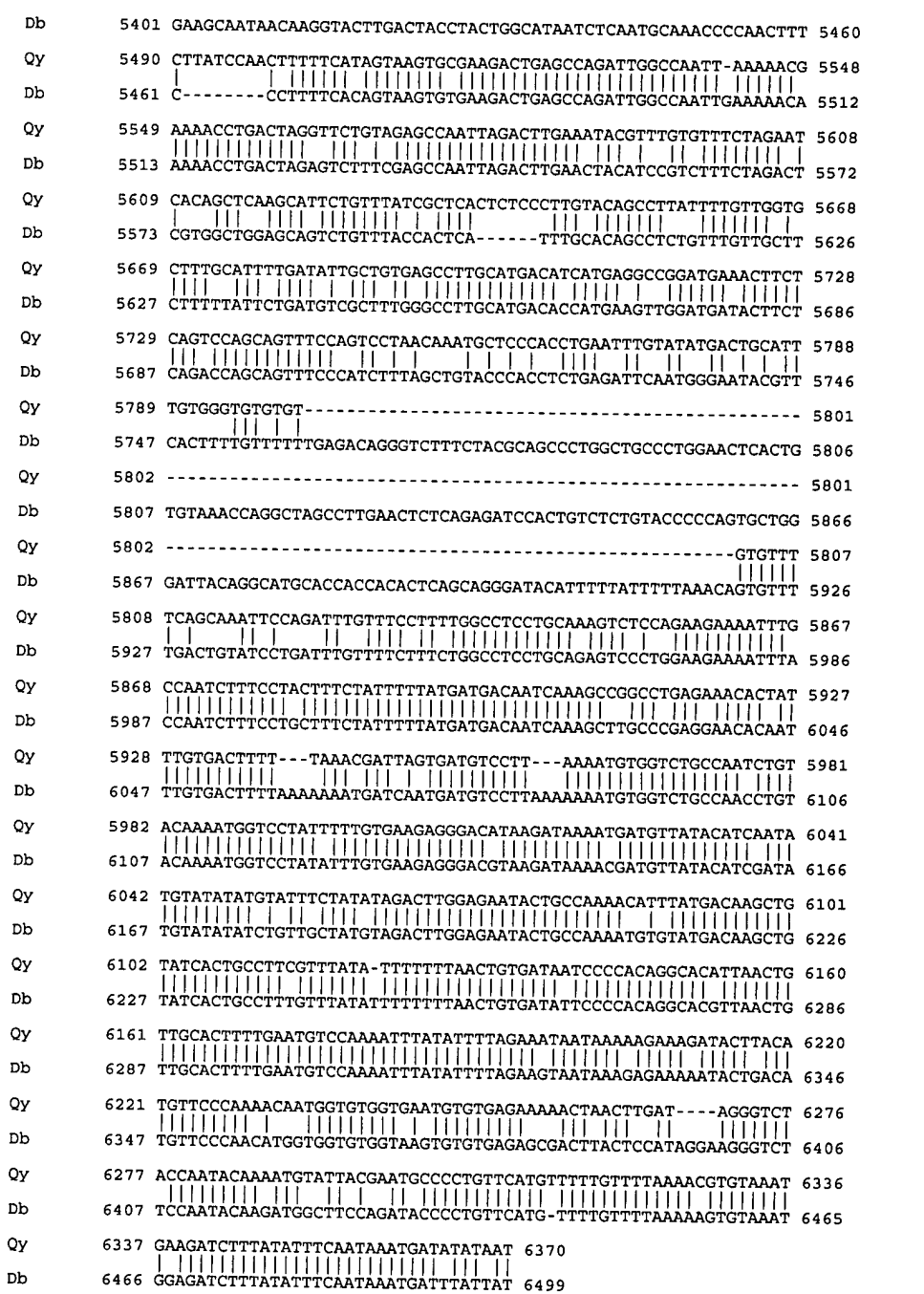
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Db 2220 CAACACCCAGAGAAGCCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGCAGACGAG 2279
Qy 2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343
Db 2280 AGCACAAGAAGTTATGTGATTTTGTCTTTTGAAAATAACGGCGACTACATGGACATGAAG 2339
Qy 2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403
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Qy 2464 TCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTG 2523
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Qy 2524 TTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTC 2583
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Qy 2704 TTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTG 2763
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; Sequence 1, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-1

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Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
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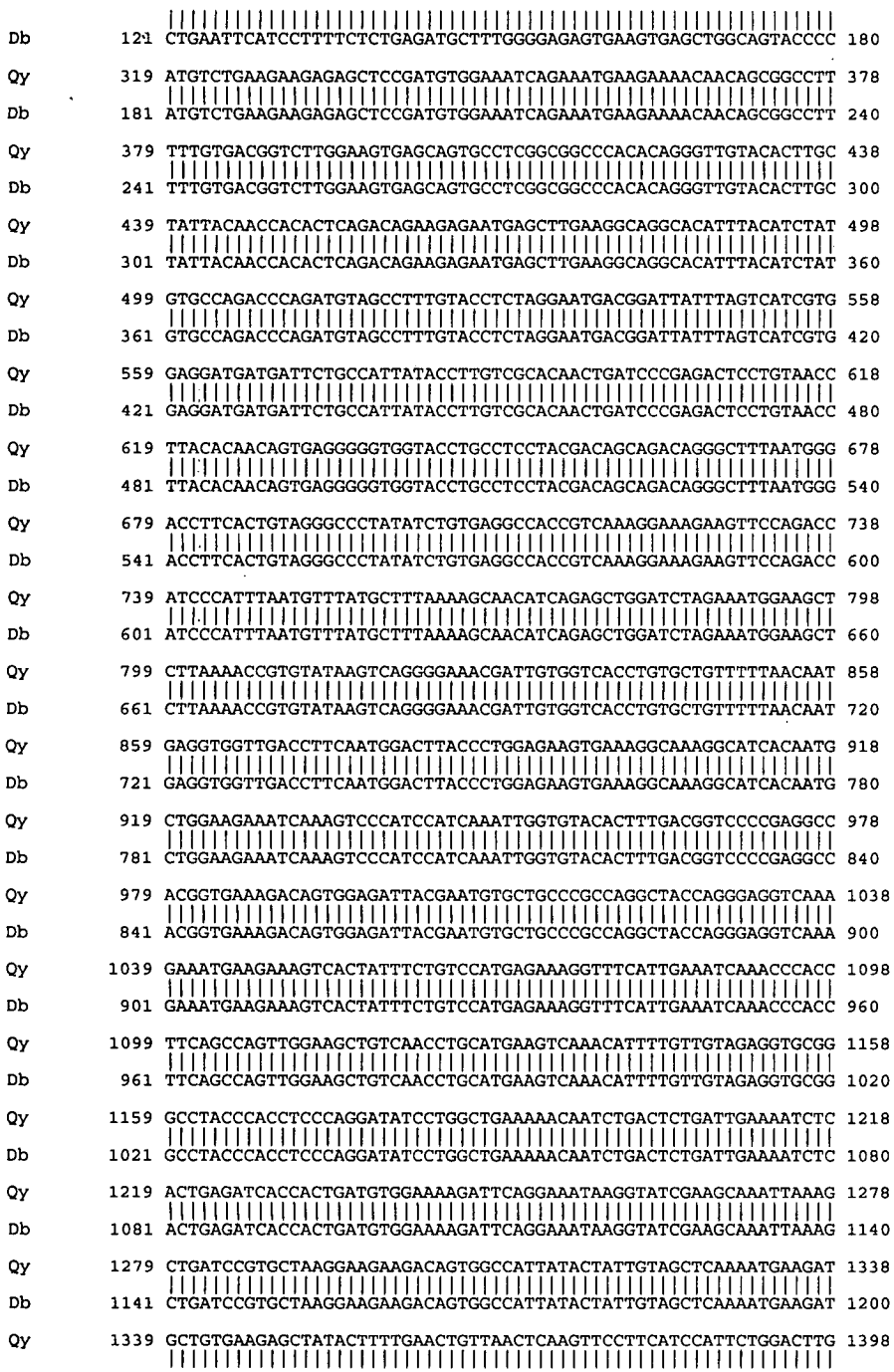
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Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
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Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760
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RESULT 24
US-09-866-510-3
; Sequence 3, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-3

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  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3269;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
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Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
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RESULT 25
US-09-866-510-7
; Sequence 7, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3267)
US-09-866-510-7

Query Match 51.0%; Score 3268.4; DB 3; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3269; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258
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Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318
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Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
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Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
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Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy        499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
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Db        361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy        559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

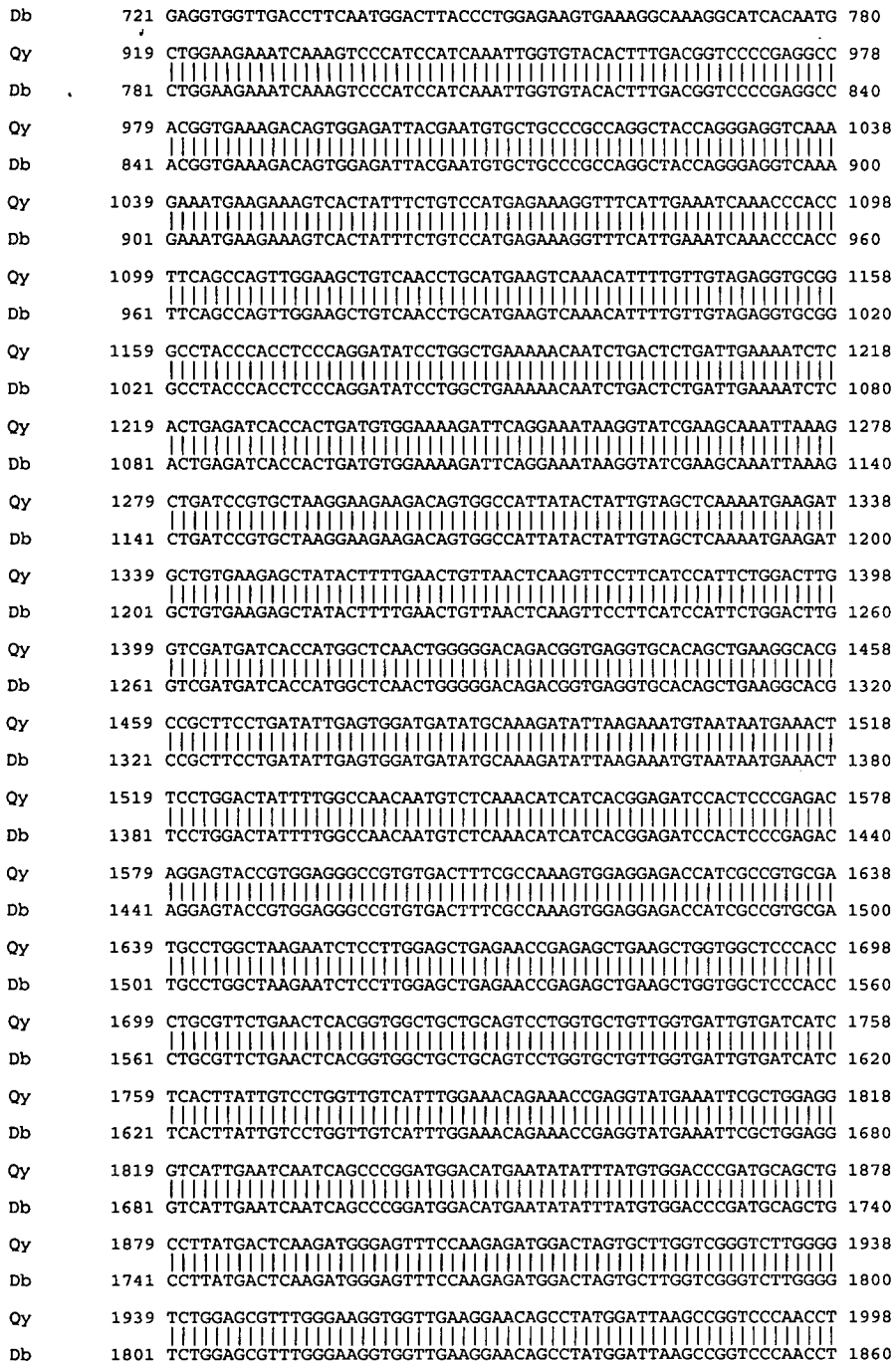
Qy        619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
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Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy        679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Db 721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780
Qy 919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db 781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840
Qy 979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db 841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900
Qy 1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db 901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960
Qy 1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db 961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020
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Db 1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080
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Db 1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140
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Qy 1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
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Qy 1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db 1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320
Qy 1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db 1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380
Qy 1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db 1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440
Qy 1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db 1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500
Qy 1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db 1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560
Qy 1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db 1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620
Qy 1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db 1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680
Qy 1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db 1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740
Qy 1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
Db 1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800
Qy 1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
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Qy 1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
Db 1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920
Qy 2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
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Qy 2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db 1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040
Qy 2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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Db 2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160
Qy 2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
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Qy 2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
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Qy 2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Qy 2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Db 2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640
Qy 2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db 2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700
Qy 2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
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Qy 2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
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Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
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Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

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Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270
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RESULT 26
US-09-866-510-9
; Sequence 9, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3267)
US-09-866-510-9

Query Match 51.0%; Score 3268.4; DB 3; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3269; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
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Db        481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

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Qy        739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
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Db        601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy        799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
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Db        661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy        859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Qy        919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
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Db        781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

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Qy       1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy       1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy       1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy       1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy       1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy       1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy       1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy       1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
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Db       1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380
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Qy       1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy       1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy       1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy       1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy       1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
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Db       1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy       1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
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Db       1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy       1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy       1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy       1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 1920

Qy       2059 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTG 1980

Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
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Db       1981 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
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Db       2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100

Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
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Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
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Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
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Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
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Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
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Db       2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCATGAAG 2580

Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
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Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
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Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
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Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3060

Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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Db       3061 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3120

Qy       3259 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3318
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Db       3121 AGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATC 3180

Qy       3319 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3378
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Db       3181 AAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCT 3240

Qy       3379 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3408
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Db       3241 TCAGACCTGGTGGAAGACAGCTTCCTGTAA 3270
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RESULT 27
US-09-866-510-5
; Sequence 5, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33

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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 3270
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3267)
US-09-866-510-5

  Query Match           50.9%;  Score 3266.8;  DB 3;  Length 3270;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3268;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198
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Db        61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

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Db       121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy       319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378
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Db       181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy       379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438
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Db       241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy       439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360

Qy       499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy       559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy       619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
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Db       481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy       679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
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Db       541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy       739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
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Db       601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy       799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
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Qy       859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
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Qy       919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
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Qy       979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
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Qy      1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
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Db       901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy      1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
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Db       961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy      1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
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Db      1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
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Db      1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
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Db      1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
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Db      1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy      1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
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Db      1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
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Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
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Db      1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
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Db      1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy      1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
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Db      1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
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Db      1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1938
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Db      1741 CCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGG 1800

Qy      1939 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1998
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Db      1801 TCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCT 1860

Qy      1999 GTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCT 2058
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Qy       2119 CTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2178
Db       1981 CTGGGAGCCTGCATGAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGA 2040

Qy       2179 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2238
Db       2041 GATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG 2100

Qy       2239 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2298
Db       2101 CCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTAT 2160

Qy       2299 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2358
Db       2161 GTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACA 2220

Qy       2359 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2418
Db       2221 CAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCA 2280

Qy       2419 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2478
Db       2281 CTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAAC 2340

Qy       2479 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2538
Db       2341 CTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTAT 2400

Qy       2539 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2598
Db       2401 CAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCT 2460

Qy       2599 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2658
Db       2461 GCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCC 2520

Qy       2659 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2718
Db       2521 AGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAG 2580

Qy       2719 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2778
Db       2581 TGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCT 2640

Qy       2779 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2838
Db       2641 TATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATG 2700

Qy       2839 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2898
Db       2701 GTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCAC 2760

Qy       2899 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2958
Db       2761 GCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGA 2820

Qy       2959 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 3018
Db       2821 CCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAG 2880

Qy       3019 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 3078
Db       2881 AGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATG 2940

Qy       3079 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3138
Db       2941 CGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTG 3000

Qy       3139 AAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATT 3198
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Qy       3199 CCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACAC 3258
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RESULT 28
US-10-764-420-481
; Sequence 481, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 6264
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-764-420-481

Query Match 50.8%; Score 3260.6; DB 9; Length 6264;
Best Local Similarity 74.9%; Pred. No. 0;
Matches 4766; Conservative 0; Mismatches 1269; Indels 324; Gaps 42;

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Db          6 ACTGTTGGAGCTTGAGGGAGTGAAACAAACAGAGGAACTGTGGGCGAGGACTGGAGGCTT 65

Qy         66 GTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAA 125
Db         66 GGGGCTCACTTTTTCCTCCGGGCTATCGGATTTTCTTAGCAAACTGACGTAGGAGGAGAA 125

Qy        126 GTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCAC 185
Db        126 GTTCTCAGGAGCGATGGGGACCTCCCA---GGCCTTTCTGGTCCTCAGCTGTCTCCTCAC 182

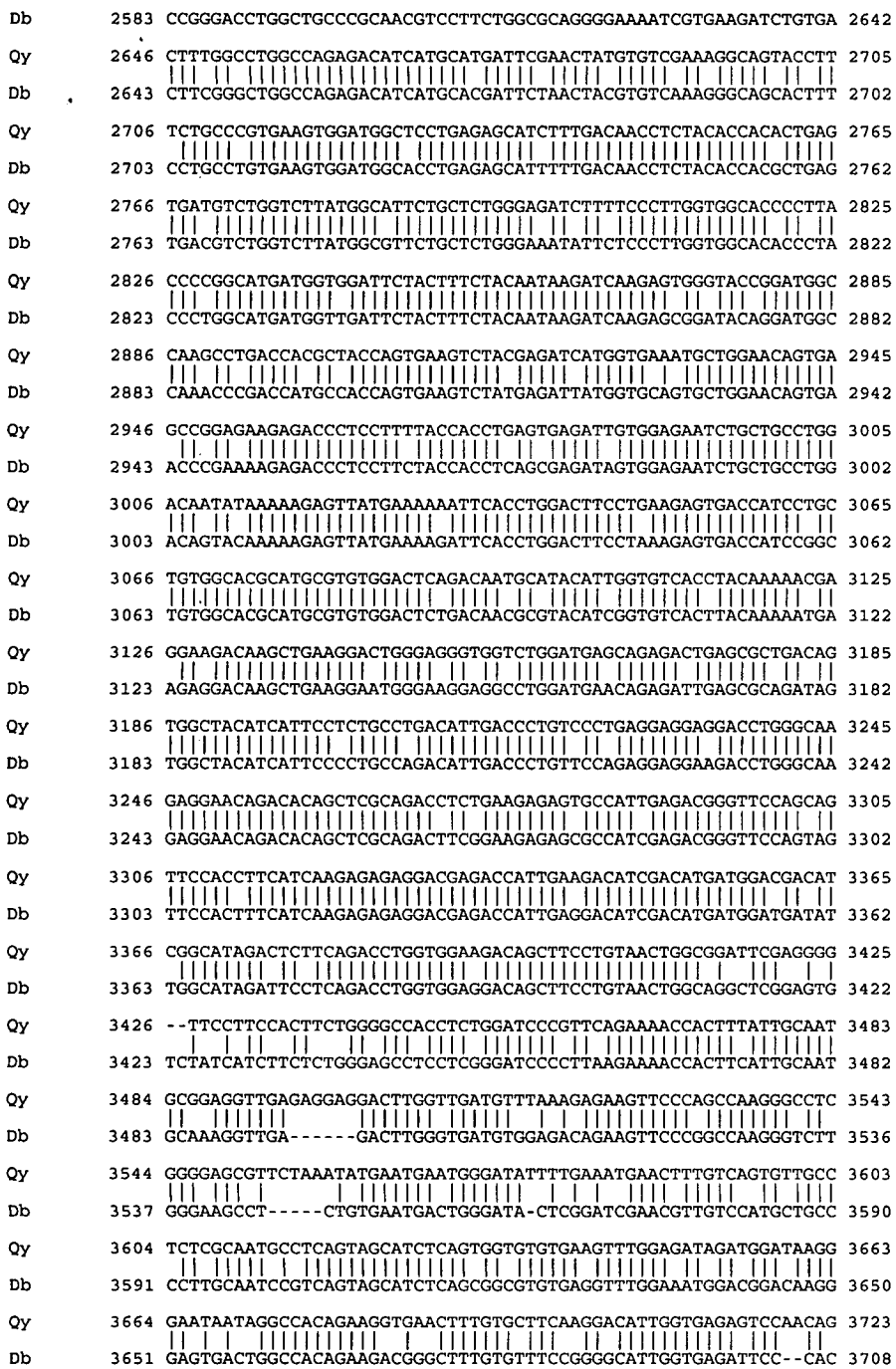
Qy        186 AGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGA 245
Db        183 AGGGCCGAGCCTCATCGTCTGCCAGCTCTTATTACCCTCCATCCTTCCAAATGAGAATGA 242

Qy        246 AAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAG 305
Db        243 GAAGATTGTGCCGCTGAGTTCGTCCTTCTCTCTGAGATGCTTCGGGGAGAGCGAAGTGAG 302

Qy        306 CTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAA 365
Db        303 CTGGCAGCACCCCATGTCTGAAGAAGAGGACCCCAACGTGGAAATCAGAACCGAGGAGAA 362

Qy        366 CAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGG 425
Db        363 CAACAGTAGCCTCTTTGTCACGGTGCTGGAAGTGGTCAACGCCTCAGCGGCCCACACCGG 422
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Qy 426 GTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCA 485
Db 423 ATGGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAGTGAGATCGAAGGCAGGCA 482
Qy 486 CATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTA 545
Db 483 CATTTATATCTATGTACCAGACCCAGACATGGCCTTCGTGCCTCTCGGCATGACGGATTC 542
Qy 546 TTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGA 605
Db 543 TTTAGTCATTGTGGAAGAGGACGATTCTGCCATCATACCCTGCCTCACCACGGATCCAGA 602
Qy 606 GACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACA 665
Db 603 CACTGAAGTAACCTTGCACAATAACGGGAGGCTGGTGCCTGCCTCCTACGACAGCAGGCA 662
Qy 666 GGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAA 725
Db 663 GGGCTTCAACGGAACCTTCAGTGTGGGGCCTTACATCTGTGAGGCCACCGTCAGAGGGAG 722
Qy 726 GAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCT 785
Db 723 GACGTTCAAGACCAGCGAGTTTAACGTTTATGCCTTGAAAGCCACGTCAGAACTGAATCT 782
Qy 786 AGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGC 845
Db 783 GGAGATGGACACACGCCAGACTGTGTATAAGGCAGGAGAAACGATCGTGGTGACCTGCGC 842
Qy 846 TGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAA 905
Db 843 CGTCTTTAACAATGAGGTGGTTGACCTGCAGTGGACTTACCCTGGAGAGGTGAGAAACAA 902
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Qy 966 GGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTAC 1025
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Qy 1026 CAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGA 1085
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Qy 1086 AATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGT 1145
Db 1083 GATCAGGCCCACCTTTGGCCATCTGGAAACTGTGAACCTGCATCAGGTCAGAGAGTTCGT 1142
Qy 1146 TGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCT 1205
Db 1143 GGTGGAGGTGCAGGCCTACCCGACCCCCAGGATATCCTGGCTGAAGGACAACTTGACCCT 1202
Qy 1206 GATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCG 1265
Db 1203 GATTGAGAATCTCACTGAGATCACCACCGATGTGCAGAGGAGCCAGGAGACGAGGTATCA 1262
Qy 1266 AAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGC 1325
Db 1263 AAGCAAATTAAAGCTGATCCGGGCTAAGGAAGAAGACAGCGGCCATTATACCATTATAGT 1322
Qy 1326 TCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATC 1385
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Qy 1386 CATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCAC 1445
Db 1383 CATTCTGGAGCTTGTGGATGACCACCATGGCTCTGGCGGGGGACAGACTGTGAGGTGCAC 1442
Qy 1446 AGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATG 1505
Db 1443 GGCTGAAGGCACCCCTCTTCCGAACATCGAGTGGATGATCTGCAAGGATATTAAGAAATG 1502
Qy 1506 TAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGAT 1565
Db 1503 TAATAATGACACTTCATGGACAGTTTTGGCCAGCAACGTCTCGAATATTATCACGGAGTT 1562
Qy 1566 CCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGAC 1625
Db 1563 CCACCAGCGAGGCAGGAGTACAGTGGAGGGACGAGTGTCCTTCGCCAAGGTGGAAGAGAC 1622
Qy 1626 CATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCT 1685
Db 1623 CATCGCAGTTCGGTGCTTGGCAAAGAACGACCTTGGCATTGGGAACAGAGAGCTGAAGCT 1682
Qy 1686 GGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGT 1745
Db 1683 GGTGGCTCCCTCCCTGCGATCTGAGCTCACGGTGGCGGCCGCGGTGCTGGTGCTGTTGGT 1742
Qy 1746 GATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGA 1805
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Qy 1806 AATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGA 1865
Db 1803 AATTCGATGGAGGGTCATTGAGTCAATCAGCCCTGATGGACATGAGTATATTTATGTGGA 1862
Qy 1866 CCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGG 1925
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Qy 1926 TCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAG 1985
Db 1923 TCGGATCTTGGGATCCGGTGCATTTGGGAAAGTGGTTGAAGGCACAGCTTATGGATTAAG 1982
Qy 1986 CCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAG 2045
Db 1983 CCGGTCCCAGCCTGTAATGAAGGTGGCTGTGAAGATGCTCAAACCCACAGCCAGGTCTAG 2042
Qy 2046 TGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAA 2105
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Qy 2106 CATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTA 2165
Db 2103 CATTGTGAATTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAATA 2162
Qy 2166 TTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCA 2225
Db 2163 CTGCTTCTATGGGGATTTGGTCAATTACCTGCATAAGAACAGAGATAGCTTCATGAGCCG 2222
Qy 2226 CCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAG 2285
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Qy 2286 CACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCA 2345
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Db 3063 TGTGGCACGCATGCGTGTGGACTCTGACAACGCGTACATCGGTGTCACTTACAAAAATGA 3122
Qy 3126 GGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAG 3185
Db 3123 AGAGGACAAGCTGAAGGAATGGGAAGGAGGCCTGGATGAACAGAGATTGAGCGCAGATAG 3182
Qy 3186 TGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAA 3245
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Qy 3246 GAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAG 3305
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Qy 3426 --TTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAAT 3483
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Qy 3484 GCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTC 3543
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Qy 3544 GGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCC 3603
Db 3537 GGGAAGCCT-----CTGTGAATGACTGGGATA-CTCGGATCGAACGTTGTCCATGCTGCC 3590
Qy 3604 TCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGG 3663
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Qy 4472 AATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTCTTCATGCCTGATG 4531
Db 4482 CCGTCCACAAAAAGGACTCCGGTGGGCAGAAGTATCTTTTGTGGCCAGTGATGACTTGGA 4541
Qy 4532 AAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGA 4591
Db 4542 T--------GGATCCCACCCATACTTACCTTTTAAATCTATGACC----------TCTTA 4583
Qy 4592 AGGATGCCCAGACATCAGCCTCCTTCTTTCACCC-CTTACCCCAAAGAGAAAGAGTTTGA 4650
Db 4584 AGGATGCGTCAACATCAGCGCCTCACTTTTCCTCTCTTGTCTCAAAGAGAAAGAGCTGGG 4643
Qy 4651 AACTC-GAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCT 4709
Db 4644 AACCCTGAAACCACGGTGGAGCTGAAGATTCGAAGGCTATGTGGGCGTGAACTGGCTCCT 4703
Qy 4710 CAGTTCTCAAATGTGTGTGGCAG----CCAGGATGACTAGATCCTGGGTTTCCATCCTTG 4765
Db 4704 TCATTCCCACCGTTTGCAACTAGGGTCACAAGCCTCAGTGGTTTCAGACCTCCGCCCCAG 4763

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Qy       4766 AGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTA-----TTTTTCTAAACTCC 4820
Db       4764 AGATCTGGAATTACGAGGTCTGACGGGAGCAAGAAGCTATATTATGTTTTAATTAACTCC 4823

Qy       4821 CTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC--- 4877
Db       4824 TTGGCGCTCTTGAGGAGTCAGTGTTCAGAAACGCTGGCTTGGGTTACAGGGGTTTGCTGC 4883

Qy       4878 -CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGC 4936
Db       4884 GGGTGGGGCAGGGCAGCCTTGAAAATTGGAACTGAGCTAGAAGTCGACCACGCAGGAAGG 4943

Qy       4937 CTACTA--TTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAAT 4994
Db       4944 CTACTATTTTTAAGTCCTTGGCTTCATG----------TCAATGCCACGTATCCAGCAAT 4993

Qy       4995 TGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTT 5054
Db       4994 TCCTGCCCTTGATTAACTT--CCAGCTTAGCCGAGGCTGAGAAAACAAGATCTTGGCTTG 5051

Qy       5055 GACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCC 5114
Db       5052 GGCACATCTTCCAGTTCTAGTCAGCGTGGGTACCACTTCCCACCGGATGGAGGACCTGAG 5111

Qy       5115 CCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAAT 5174
Db       5112 CTCGCTCACCTC----------AAAGAGGGCCCACAAAT 5140

Qy       5175 TATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACA 5234
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Db       5253 ACTGCCAAACTGGTTAGTGTGGGTTCATTGGCATTCTCTGCAAT-GTGTCTAATTGCTGA 5311

Qy       5355 TACCATATGAATGAAACATGGGCTGTGATT-ACTGCAATCACTGTG----CTATCGGCAG 5409
Db       5312 CTCTGTATGAATGAAACATGGGGTATGATTAACTGCAATCACTGTATGCACTTCCAGCAG 5371

Qy       5410 ATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATC 5469
Db       5372 GTGATGCTTTGGAAGGCGCAGAAGCAATAACAAGGTACTTGACTACCTACTGGCATAATC 5431

Qy       5470 TCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCA 5529
Db       5432 TCAATGCAAACCCCAACTTTC-------CCCCTCTCACAGTCAGTGTGAGGACTGAGCCA 5484

Qy       5530 GATTGGCCAATT-AAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAA 5588
Db       5485 GATTGGCCAATTGAGAAGCAAAAACCTGACTAGATTCTTTTGAGCCAATTAGACTTGAAA 5544

Qy       5589 TACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGT 5648
Db       5545 TACGCCCATGTTTCTAGACTCGCAGCTCAAGTGGTCTGTTTACCACGC-GTTTGCACAGC 5603

Qy       5649 ACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCA 5708
Db       5604 CTTGGTTTTGTTGCTTCCTTTTACTCTAATGTCTGTCACTTGGGACCTTGCATGACAATT 5663

Qy       5709 TGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTT-CCAGTCCTAACAAATGCTCCCACCT 5767
Db       5664 TGAGGTTGGAGGAAGCTTCTCAGACCGACAGTTTGGCCATCCCTACCAGTACTTGCCTCT 5723

Qy       5768 GAATTTGTATATGACTGCATTTGT---------------------------------- 5791
Db       5724 GAGATTAAATGGGATTGCATTCGTTTTGTTTCTGAGACAGGGCCTCTCTATGTAGCCCTG 5783

Qy       5792 ---------------------------------------------------------- 5791
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Db       5784 GCTGCCCTGGAACTCACTGTGTAAACCAGGCTGGCCTTGAACTCCCAGAGATCCATTGTC 5843

Qy       5792 ----------------------------------------------------GGGTGTGTGT 5801
Db       5844 TCTGTCCCCCCAGGGCTGGGATTGCTGGTGTGTACCACCACACTCAGCAGGGATACATTT 5903

Qy       5802 GTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCT-----CCTGCAAAGTCTCCAG 5856
Db       5904 TTATTTTCAAACAGTGTTTTGACTGTATCCTGGTTTCTTTTTGGCCTCTGCAGAGTCCTG 5963

Qy       5857 AAGAAAATTTGCCAATCTTTCCTACTTTC------TATTTTTATGATGACAATCAAAGCC 5910
Db       5964 GAAGAAATTTACCAATTTTCTCTGCTTTCTATTCTTATTTTTATGATGACAATCAAAGCT 6023

Qy       5911 GGCCTGAGAAACACTATTTGTGACTTTT-------TAAACGATTAGTGATGTCCTTAAAA 5963
Db       6024 GGCCCGAAGAACACAATTTGTGACTTTTTTTTTTTTAAATAATCAGTGATGTCCTTAAAA 6083

Qy       5964 TGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAA 6023
Db       6084 TGTGGTCTGCCAACCTGTACAAAATGGTCCTATATTTTTGAAGAGGGACGTGAGATAAAA 6143

Qy       6024 TGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAA 6083
Db       6144 TGATGTTATACATCGATATGTATATATCTGTTGCTATGTAGACTTGGAGAATACTGCCAA 6203

Qy       6084 AACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCC 6142
Db       6204 AACGTGTATGACAAGCTGTATCACTGCCTTTGTTTATATTTTTTTAACTGTGATATTCC 6262
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RESULT 29
US-10-741-601-5664
; Sequence 5664, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5664
; LENGTH: 81210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-5664

Query Match 48.4%; Score 3106.8; DB 7; Length 81210;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3119; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

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Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
Db      72089 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 72148

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
Db      72149 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 72208

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
Db      72209 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 72268

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
Db      72269 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 72328

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
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Db      72329 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 72388

Qy       3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      72389 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 72448

Qy       3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72449 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 72508

Qy       3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72509 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 72568

Qy       3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
             ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db      72569 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAMGGCTGTGTTTAGATT 72628

Qy       3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72629 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 72688

Qy       3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72689 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 72748

Qy       3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72749 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 72808

Qy       3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72809 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 72868

Qy       4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72869 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 72928

Qy       4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72929 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 72988

Qy       4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72989 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 73048

Qy       4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
             ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db      73049 TATGGTAATAGCTTTAGTGAATYAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 73108

Qy       4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73109 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 73168

Qy       4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73169 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 73228

Qy       4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73229 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 73288

Qy       4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      73289 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 73347

Qy       4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      73348 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 73407

Qy       4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73408 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 73467
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Qy       4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73468 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 73527

Qy       4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73528 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 73587

Qy       4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73588 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 73647

Qy       4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73648 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 73707

Qy       4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937
             ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db      73708 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCC 73767

Qy       4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73768 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 73827

Qy       4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73828 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 73887

Qy       5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73888 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 73947

Qy       5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73948 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 74007

Qy       5178 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74008 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 74067

Qy       5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74068 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 74127

Qy       5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74128 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 74187

Qy       5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 5417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74188 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 74247

Qy       5418 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 5477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74248 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 74307

Qy       5478 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 5537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74308 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 74367

Qy       5538 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 5597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74368 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 74427

Qy       5598 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 5657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74428 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 74487

Qy       5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74488 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 74547
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Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74548 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 74607

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74608 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 74667

Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74668 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 74727

Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74728 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 74787

Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74788 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 74847

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74848 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 74907

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74908 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 74967

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74968 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 75027

Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75028 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 75087

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75088 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 75147

Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75148 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 75207

Qy       6378 TAAAAAAA 6385
              || |  ||
Db      75208 TATACTAA 75215


RESULT 30
US-10-741-600-17691
; Sequence 17691, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17691
;   LENGTH: 81210
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-17691

  Query Match             48.4%;  Score 3106.8;  DB 8;  Length 81210;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3119;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72089 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 72148

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72149 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 72208

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72209 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 72268

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72269 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 72328

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72329 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 72388

Qy       3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72389 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 72448

Qy       3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72449 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 72508

Qy       3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72509 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 72568

Qy       3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db      72569 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAMGGCTGTGTTTAGATT 72628

Qy       3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72629 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 72688

Qy       3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72689 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 72748

Qy       3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72749 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 72808

Qy       3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72809 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 72868

Qy       4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72869 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 72928

Qy       4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72929 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 72988

Qy       4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72989 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 73048

Qy       4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
             ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db      73049 TATGGTAATAGCTTTAGTGAATYAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 73108

Qy       4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73109 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 73168

Qy       4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      73169 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 73228

Qy       4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457

Db      73229 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 73288

Qy       4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517

Db      73289 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 73347

Qy       4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577

Db      73348 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 73407

Qy       4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637

Db      73408 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 73467

Qy       4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697

Db      73468 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 73527

Qy       4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757

Db      73528 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 73587

Qy       4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817

Db      73588 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 73647

Qy       4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877

Db      73648 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 73707

Qy       4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937

Db      73708 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCC 73767

Qy       4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997

Db      73768 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 73827

Qy       4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057

Db      73828 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 73887

Qy       5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117

Db      73888 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 73947

Qy       5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177

Db      73948 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 74007

Qy       5178 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237

Db      74008 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 74067

Qy       5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297

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Qy       5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357

Db      74128 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 74187

Qy       5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 5417

Db      74188 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 74247

Qy       5418 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 5477

Db      74248 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 74307

Qy       5478 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 5537

Db      74308 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 74367

Qy       5538 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 5597

Db      74368 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 74427

Qy       5598 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 5657

Db      74428 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 74487

Qy       5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717

Db      74488 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 74547

Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777

Db      74548 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 74607

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837

Db      74608 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 74667

Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897

Db      74668 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 74727

Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957

Db      74728 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 74787

Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017

Db      74788 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 74847

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077

Db      74848 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 74907

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137

Db      74908 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 74967

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197

Db      74968 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 75027

Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257

Db      75028 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 75087

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317

Db      75088 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 75147

Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377

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Qy       6378 TAAAAAAA 6385

Db      75208 TATACTAA 75215
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RESULT 31
US-10-322-696-166
; Sequence 166, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc

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;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 529452001200
;  CURRENT APPLICATION NUMBER: US/10/322,696
;  CURRENT FILING DATE:  2003-10-17
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166
;   LENGTH: 59475
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(59475)
;   OTHER INFORMATION: n = A,T,C or G
US-10-322-696-166

  Query Match            48.4%;  Score 3106.4;  DB 7;  Length 59475;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3121;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
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Db      46355 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 46414

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
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Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46475 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 46534

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46535 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 46594

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46595 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 46654

Qy       3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Qy       3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
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Db      46715 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 46774

Qy       3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46775 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 46834

Qy       3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46835 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 46894

Qy       3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
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Db      46895 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 46954

Qy       3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      46955 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 47014

Qy       3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
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Db      47015 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 47074

Qy       3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47075 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 47134

Qy       4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
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Db      47135 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 47194

Qy       4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
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Db      47195 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 47254

Qy       4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47255 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 47314

Qy       4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      47315 TATGGTAATAGCTTTAGTGAATCAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 47374

Qy       4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47375 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 47434

Qy       4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47435 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 47494

Qy       4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47495 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 47554

Qy       4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      47555 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 47613

Qy       4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      47614 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 47673

Qy       4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47674 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 47733

Qy       4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697
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Db      47734 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 47793

Qy       4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47794 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 47853

Qy       4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47854 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 47913

Qy       4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47914 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 47973

Qy       4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47974 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 48033

Qy       4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997
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Db      48034 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 48093

Qy       4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057
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Qy       5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
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Db      48154 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 48213

Qy       5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177
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Db      48214 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 48273

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Qy       5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297
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Qy       5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357
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Qy       5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 5417
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Db      48454 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 48513

Qy       5418 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 5477
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Qy       5478 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 5537
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Db      48574 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 48633

Qy       5538 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 5597
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Db      48634 AATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 48693

Qy       5598 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 5657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48694 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 48753

Qy       5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48754 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 48813

Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48814 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 48873

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48874 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 48933

Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48934 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 48993

Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      48994 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 49053

Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49054 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 49113

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49114 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 49173

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49174 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 49233

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49234 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 49293

Qy       6198 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49294 TAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 49353

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49354 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 49413

Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      49414 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 49473

Qy       6378 TAAAAAAA 6385
              || |  ||
Db      49474 TATACTAA 49481
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RESULT 32
US-09-925-301-349
; Sequence 349, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 349
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-349

Query Match 28.6%; Score 1836.4; DB 3; Length 1842;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1837; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy       4549 AATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCA 4608
             |||||:|||||||||||  ||:||||||||||||||||||||||||||||||||||||||
Db          1 AATATWTGTATTTTTTGATCCTWTGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCA 60

Qy       4609 GCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGA 4668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGA 120

Qy       4669 TATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTG 4728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTG 180

Qy       4729 GCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGA 4788
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGA 240

Qy       4789 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 4848
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 300

Qy       4849 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 4908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 360

Qy       4909 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 4968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 420

Qy       4969 ACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGA 5028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGA 480

Qy       5029 GGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCC 5088
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Db        481 GGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCC 540

Qy       5089 ACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCC 5148

Db        541 ACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCC 600

Qy       5149 CGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACC 5208

Db        601 CGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACC 660

Qy       5209 AGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGG 5268

Db        661 AGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGG 720

Qy       5269 GAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCAT 5328

Db        721 GAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCAT 780

Qy       5329 TCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTG 5388

Db        781 TCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTG 840

Qy       5389 CAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACT 5448

Db        841 CAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACT 900

Qy       5449 TGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATA 5508

Db        901 TGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATA 960

Qy       5509 GTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGT 5568

Db        961 GTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGT 1020

Qy       5569 AGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTT 5628

Db       1021 AGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTT 1080

Qy       5629 TATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCT 5688

Db       1081 TATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCT 1140

Qy       5689 GTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTC 5748

Db       1141 GTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTC 1200

Qy       5749 CTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 5808

Db       1201 CTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTT 1260

Qy       5809 CAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGC 5868

Db       1261 CAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGC 1320

Qy       5869 CAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATT 5928

Db       1321 CAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATT 1380

Qy       5929 TGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAAT 5988

Db       1381 TGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAAT 1440

Qy       5989 GGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATAT 6048

Db       1441 GGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATAT 1500

Qy       6049 ATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACT 6108

Db       1501 ATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACT 1560

Qy       6109 GCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTT 6168

Db       1561 GCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTT 1620

Qy       6169 TTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCA 6228

Db       1621 TTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCA 1680

Qy       6229 AAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAA 6288

Db       1681 AAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAA 1740

Qy       6289 TGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTAT 6348

Db       1741 TGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTAT 1800

Qy       6349 ATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAA 6390

Db       1801 ATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAGA 1842
```

RESULT 33
US-09-866-510-11
; Sequence 11, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
US-09-866-510-11

Query Match 27.6%; Score 1767; DB 3; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        139 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 198

Db          1 ATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGGCTGAGCCTA 60

Qy        199 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 258

Db         61 ATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAG 120

Qy        259 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 318

Db        121 CTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCC 180

Qy        319 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 378

Db        181 ATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAACAGCGGCCTT 240

Qy        379 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 438

Db        241 TTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTACACTTGC 300

Qy        439 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 498

Db        301 TATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTAT 360
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Qy       499 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 558
Db       361 GTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATCGTG 420

Qy       559 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 618
Db       421 GAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACC 480

Qy       619 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 678
Db       481 TTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGGGCTTTAATGGG 540

Qy       679 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 738
Db       541 ACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGAAGTTCCAGACC 600

Qy       739 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 798
Db       601 ATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAGAAATGGAAGCT 660

Qy       799 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 858
Db       661 CTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTGTTTTTAACAAT 720

Qy       859 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 918
Db       721 GAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAGGCATCACAATG 780

Qy       919 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 978
Db       781 CTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGGTCCCCGAGGCC 840

Qy       979 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 1038
Db       841 ACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCAGGGAGGTCAAA 900

Qy      1039 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 1098
Db       901 GAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAATCAAACCCACC 960

Qy      1099 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1158
Db       961 TTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTGTAGAGGTGCGG 1020

Qy      1159 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1218
Db      1021 GCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTC 1080

Qy      1219 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1278
Db      1081 ACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGCAAATTAAAG 1140

Qy      1279 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1338
Db      1141 CTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTCAAAATGAAGAT 1200

Qy      1339 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1398
Db      1201 GCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTG 1260

Qy      1399 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1458
Db      1261 GTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCTGAAGGCACG 1320

Qy      1459 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1518
Db      1321 CCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTAATAATGAAACT 1380

Qy      1519 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1578
Db      1381 TCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCCACTCCCGAGAC 1440

Qy      1579 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1638
Db      1441 AGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGA 1500

Qy      1639 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1698
Db      1501 TGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACC 1560

Qy      1699 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1758
Db      1561 CTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATC 1620

Qy      1759 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1818
Db      1621 TCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGG 1680

Qy      1819 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1878
Db      1681 GTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTG 1740

Qy      1879 CCTTATGACTCAAGATGGGAGTTTCCA 1905
Db      1741 CCTTATGACTCAAGATGGGAGTTTCCA 1767
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RESULT 34
US-10-637-356-8
; Sequence 8, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
; APPLICANT: Briesewitz, Roger
; APPLICANT: Griffin, John
; TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
; TITLE OF INVENTION: ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P-153-US1
; CURRENT APPLICATION NUMBER: US/10/637,356
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,330
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/440,491
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2427
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-637-356-8

Query Match 23.7%; Score 1522.8; DB 7; Length 2427;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
Db       902 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 961

Qy      1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
Db       962 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1021

Qy      2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
Db      1022 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1081

Qy      2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
Db      1082 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1141

Qy      2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
Db      1142 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1201
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Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1261

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1321

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1381

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1441

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1501

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1561

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1621

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1681

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1741

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1801

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1861

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1921

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 1981

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2041

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2101

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2161

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2221

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2222 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2281

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2282 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2341

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2342 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2401

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||
Db       2402 ACCTGGTGGAAGACAGCTTCCTGTAA 2427
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RESULT 35
US-10-637-356-7
; Sequence 7, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
; APPLICANT: Briesewitz, Roger
; APPLICANT: Griffin, John
; TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
; TITLE OF INVENTION: ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P-153-US1
; CURRENT APPLICATION NUMBER: US/10/637,356
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,330
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/440,491
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2472
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-637-356-7

Query Match 23.7%; Score 1522.8; DB 7; Length 2472;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        947 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1006

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1007 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1066

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1126

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1186

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1246

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1247 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1306

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1366

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1426
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Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1486

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1546

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1547 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1606

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1607 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1666

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1726

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1786

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1846

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1906

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1966

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1967 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2026

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2027 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2086

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2146

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2206

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2266

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2267 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2326

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2327 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2386

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2446

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||
Db       2447 ACCTGGTGGAAGACAGCTTCCTGTAA 2472
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RESULT 36
US-10-637-356-6
; Sequence 6, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
;  APPLICANT: Briesewitz, Roger
;  APPLICANT:  Griffin, John
;  TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
;  TITLE OF INVENTION:  ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
;  TITLE OF INVENTION:  NUCLEIC ACIDS ENCODING THE SAME
;  FILE REFERENCE: P-153-US1
;  CURRENT APPLICATION NUMBER: US/10/637,356
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: 60/402,330
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/440,491
;  PRIOR FILING DATE: 2003-01-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 2496
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-637-356-6

  Query Match             23.7%;  Score 1522.8;  DB 7;  Length 2496;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1524;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1030

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1090

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1150

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1151 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1210

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1270

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1330

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1331 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1390

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1391 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1450

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1451 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1510

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1511 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1570

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1571 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1630
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Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1631 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1690

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1691 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1750

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1751 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1810

Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1811 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1870

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1871 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1930

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1931 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 1990

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1991 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2050

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2051 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2110

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2111 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2170

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2171 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2230

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2231 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2290

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2291 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2350

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2351 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2410

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2411 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2470

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||
Db       2471 ACCTGGTGGAAGACAGCTTCCTGTAA 2496


RESULT 37
US-10-637-356-5
; Sequence 5, Application US/10637356
; Publication No. US20040045044A1
; GENERAL INFORMATION:
;  APPLICANT: Briesewitz, Roger
;  APPLICANT:  Griffin, John
;  TITLE OF INVENTION: ONCOKINASE FUSION POLYPEPTIDES
;  TITLE OF INVENTION:  ASSOCIATED WITH HYPERPROLIFERATIVE AND RELATED DISORDERS AND
;  TITLE OF INVENTION:  NUCLEIC ACIDS ENCODING THE SAME
;  FILE REFERENCE: P-153-US1
;  CURRENT APPLICATION NUMBER: US/10/637,356
;  CURRENT FILING DATE:  2003-08-08
;  PRIOR APPLICATION NUMBER: 60/402,330
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/440,491
;  PRIOR FILING DATE: 2003-01-16
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2541
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-637-356-5

  Query Match            23.7%;  Score 1522.8;  DB 7;  Length 2541;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1524;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1883 ATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1942
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AGGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTG 1075

Qy       1943 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 2002
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 GAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCA 1135

Qy       2003 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 2062
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 TGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCA 1195

Qy       2063 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 2122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGG 1255

Qy       2123 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 2182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATT 1315

Qy       2183 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 2242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 TGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAA 1375

Qy       2243 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 2302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTA 1435

Qy       2303 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 2362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGT 1495

Qy       2363 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 2422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 ATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCT 1555

Qy       2423 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 2482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 ATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCC 1615

Qy       2483 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 2542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 TTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAG 1675

Qy       2543 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 2602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 TTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTC 1735

Qy       2603 GCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 2662
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAG 1795

Qy       2663 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 2722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 ACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGA 1855
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Qy       2723 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 2782
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 TGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATG 1915

Qy       2783 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 2842
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 GCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGG 1975

Qy       2843 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2902
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 ATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTA 2035

Qy       2903 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2962
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCT 2095

Qy       2963 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 3022
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 CCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTT 2155

Qy       3023 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 3082
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 ATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTG 2215

Qy       3083 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 3142
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGGAAGACAAGCTGAAGG 2275

Qy       3143 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 3202
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 ACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTGGCTACATCATTCCTC 2335

Qy       3203 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 3262
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 TGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCT 2395

Qy       3263 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 3322
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGA 2455

Qy       3323 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 3382
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAG 2515

Qy       3383 ACCTGGTGGAAGACAGCTTCCTGTAA 3408
             |||||||||||||||||||||||||
Db       2516 ACCTGGTGGAAGACAGCTTCCTGTAA 2541


RESULT 38
US-11-060-756-713
; Sequence 713, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William Martin
;  TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
;  TITLE OF INVENTION:  Target Genes
;  FILE REFERENCE: AM101083 (031896-042000)
;  CURRENT APPLICATION NUMBER: US/11/060,756
;  CURRENT FILING DATE:  2005-02-18
;  NUMBER OF SEQ ID NOS: 303284
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 713
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-060-756-713

  Query Match            21.8%;  Score 1397.8;  DB 10;  Length 1400;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-308;
  Matches 1396;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5015 CCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAA 5074
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAA 60

Qy       5075 AGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCT 5134
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCT 120

Qy       5135 CCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAA 5194
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAA 180

Qy       5195 GTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAAT 5254
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAAT 240

Qy       5255 TTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGT 5314
             |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         241 TTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTSTCAAACAGGTTGGTGT 300

Qy       5315 GGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATG 5374
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATG 360

Qy       5375 GGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGC 5434
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGC 420

Qy       5435 AATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTAT 5494
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTAT 480

Qy       5495 CCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACC 5554
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACC 540

Qy       5555 TGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGC 5614
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGC 600

Qy       5615 TCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGC 5674
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGC 660

Qy       5675 ATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCC 5734
             |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db         661 ATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGSATGAAACTTCTCAGTCC 720

Qy       5735 AGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGG 5794
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db         721 AGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGKG 780

Qy       5795 TGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCC 5854
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCC 840

Qy       5855 AGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCC 5914
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCC 900

Qy       5915 TGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCC 5974
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 TGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCC 960

Qy       5975 AATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATAC 6034
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATAC 1020

Qy       6035 ATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGA 6094
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGA 1080

Qy       6095 CAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACAT 6154
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Db       1081 CAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACAT 1140

Qy       6155 TAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATA 6214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATA 1200

Qy       6215 CTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGT 6274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGT 1260

Qy       6275 CTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAA 6334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAA 1320

Qy       6335 ATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAA 6394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAA 1380

Qy       6395 AAAAAAAAAAAAAAAAAA 6413
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Db       1381 AAAAAAAAAAAAAAAAAA 1399
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RESULT 39
US-11-060-756-4985
; Sequence 4985, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4985
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-4985

Query Match 21.8%; Score 1397.8; DB 10; Length 1400;
Best Local Similarity 99.8%; Pred. No. 1.2e-308;
Matches 1396; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy       5015 CCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAA 5074
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAA 60

Qy       5075 AGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCT 5134
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCT 120

Qy       5135 CCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAA 5194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAA 180

Qy       5195 GTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAAT 5254
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAAT 240

Qy       5255 TTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGT 5314
             ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        241 TTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTSTCAAACAGGTTGGTGT 300

Qy       5315 GGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATG 5374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATG 360

Qy       5375 GGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGC 5434
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGC 420

Qy       5435 AATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTAT 5494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTAT 480

Qy       5495 CCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACC 5554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACC 540

Qy       5555 TGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGC 5614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGC 600

Qy       5615 TCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGC 5674
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGC 660

Qy       5675 ATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCC 5734
             ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        661 ATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGSATGAAACTTCTCAGTCC 720

Qy       5735 AGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGG 5794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        721 AGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGKG 780

Qy       5795 TGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCC 5854
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCC 840

Qy       5855 AGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCC 5914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCC 900

Qy       5915 TGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCC 5974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCC 960

Qy       5975 AATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATAC 6034
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATAC 1020

Qy       6035 ATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGA 6094
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGA 1080

Qy       6095 CAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACAT 6154
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACAT 1140

Qy       6155 TAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATA 6214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATA 1200

Qy       6215 CTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGT 6274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGT 1260

Qy       6275 CTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAA 6334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAA 1320

Qy       6335 ATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAA 6394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAAAAAAAAAAA 1380

Qy       6395 AAAAAAAAAAAAAAAAAA 6413
              ||||||||||||||||||
Db       1381 AAAAAAAAAAAAAAAAAA 1399
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RESULT 40

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US-10-322-696-163
; Sequence 163, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Malandro, Marc
;  TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
;  FILE REFERENCE: 529452001200
;  CURRENT APPLICATION NUMBER: US/10/322,696
;  CURRENT FILING DATE:  2003-10-17
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 163
;   LENGTH: 65952
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(65952)
;   OTHER INFORMATION: n = A,T,C or G
US-10-322-696-163

  Query Match             17.1%;  Score 1094.6;  DB 7;  Length 65952;
  Best Local Similarity   67.3%;  Pred. No. 2.5e-238;
  Matches 2241;  Conservative    0;  Mismatches  809;  Indels  281;  Gaps   38;

Qy       3258 CAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCAT 3317
Db      52707 CAGCTCACAGACTTCGGAAGAGAGTGCCATCGAGACAGGTTCCAGTAGTTCCACCTTCAT 52766

Qy       3318 CAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCGGCATAGACTC 3377
Db      52767 CAAGAGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATTC 52826

Qy       3378 TTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTT 3437
Db      52827 CTCGGACCTGGTGGAGGACAGCTTCCTGTAACTGAC--ACGCTCCGGGTATCATCTTCTC 52884

Qy       3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
Db      52885 CGGGAGCCTCCTCGGGATAACCTTAAGAAAACCACTTCATTGCAATGCAAAAGTTGAGAA 52944

Qy       3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCC---AGCCAAGGGCCTCGGGGAGCGTTC 3554
Db      52945 GAGGACTTGGGTGATGTGGAGAGAGAAAGTTCCCGAGGCCGAGGGCCTTGGTAAGCCT-- 53002

Qy       3555 TAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGC 3614
Db      53003 ---GTGTGGATGACTGGGATA-CTTGGATTGAACTTTATCCGTGTTGCCTCTTGCAACGC 53058

Qy       3615 CTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGC 3674
Db      53059 GTCAGTAGCATCTCAGCGGCGTGTGCGGTTTGGAAATGGATGGACAAGAGAGTGACTGGC 53118

Qy       3675 CACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTAT 3734
Db      53119 CACAGAAGACGGGCTTTGTGTTTCCAGGGCATGGGTGAGAGTCCCACACGCGCCAACTTG 53178

Qy       3735 ACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTC-TAACCAAGGCTGTGTTTA 3793
Db      53179 TACTGCAGACAACTCCAGCATTGTAATTATGTAAATAACTCTTAACCGAGGATGGGTTTA 53238

Qy       3794 GAT-TGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATG---- 3848
Db      53239 GATCTGTGTTAACTCTCCTCTCCGGACCTCTGAAGAGACCACTCAGTCCACCCGTGTGCT 53298

Qy       3849 TACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAA 3908
Db      53299 TCCTTCCTTCTTGGAATCCGGTACCAGCTGCTGTTGAATTTTCTCATGAAGTACATGCAA 53358

Qy       3909 AACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGT 3968
Db      53359 AACCA-CTTTGAACTTTGGAAGGTACTGGAACCGTCGTGTTTTACTGTCTTGTAAGTGTT 53417

Qy       3969 TAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTA-GAA 4027
Db      53418 AAAGAGGCAAAAAGATAAAAACTAACCAACCGTGAGTAGTAGGTTTGGGTCTTTTAGGGC 53477

Qy       4028 GCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTG-TTATCAGT 4086
Db      53478 ACCCAAGAATTCCTCTGTATCTTGTAATCTGTACTTATAACACTACTACTGTTTAACAAG 53537

Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAA-AC 4145
Db      53538 AATGCTAAATATGTAAT-CCGTAACATGATTTCTTTACAGAGAAAGCACAATTAAAACAA 53596

Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
Db      53597 AACCCTTACTAAGAAGGTGACAAGTTTGGCAGTTTTTGACATTTATATTAAGTAACACGT 53656

Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
Db      53657 TTCTCAATAAAGTA---TAATAGGTTTAGCGGATTAAAGTTAGCAAACACTAGAGAGCAG 53713

Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
Db      53714 AGTGTAAGTAGTTATCCAGAAAGTCAAACCTTTTTGTTTTGTTCTAAGCAGTCTCCCTAA 53773

Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
Db      53774 TCCAAGGCACTAGGAA--CAGTTAATGACCTCTGAAGTACTGGGATAAGCAAAGCAGAAA 53831

Qy       4386 ACTCTT--AAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTT 4443
Db      53832 CCCGGTGGGTGTCCTAAGTGTTCTCAGTAGAAAGGCGTACGCCTGAGCCCAGTGTGACTC 53891

Qy       4444 CTCA---TGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db      53892 CTCACGCTGTGTGCGACCTTCTGGAAGAGACTCATTCACAAAAAGGACTCAGATGGGCAG 53951

Qy       4501 AAGTTTTTTTTTTTTTCTTC--ATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTA 4558
Db      53952 AATGTCCATCAGATGGGACTCAGATGTCTCTCCTGACCAGTGATGGCTTGGATGGATCCC 54011

Qy       4559 TTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCT--T 4616
Db      54012 GCCCATACCTACTTTTAAAGTCTGTGACTTTTAAGGATGCTTCAACATCAGCACCTTACT 54071

Qy       4617 CTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTC-GAGACCATAAAGATATTCTT 4675
Db      54072 TTTTCTCTCTTGTCTCAGACGAGAAAGAACTGCAAACCCTGAGACCACAATGGTGCTGTT 54131

Qy       4676 TAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCA 4735
Db      54132 GAATGAAGGCTATGTGGGCATCAGCTTGGCTCTTCCCTTCCCACCATTAACTACAGCTAC 54191

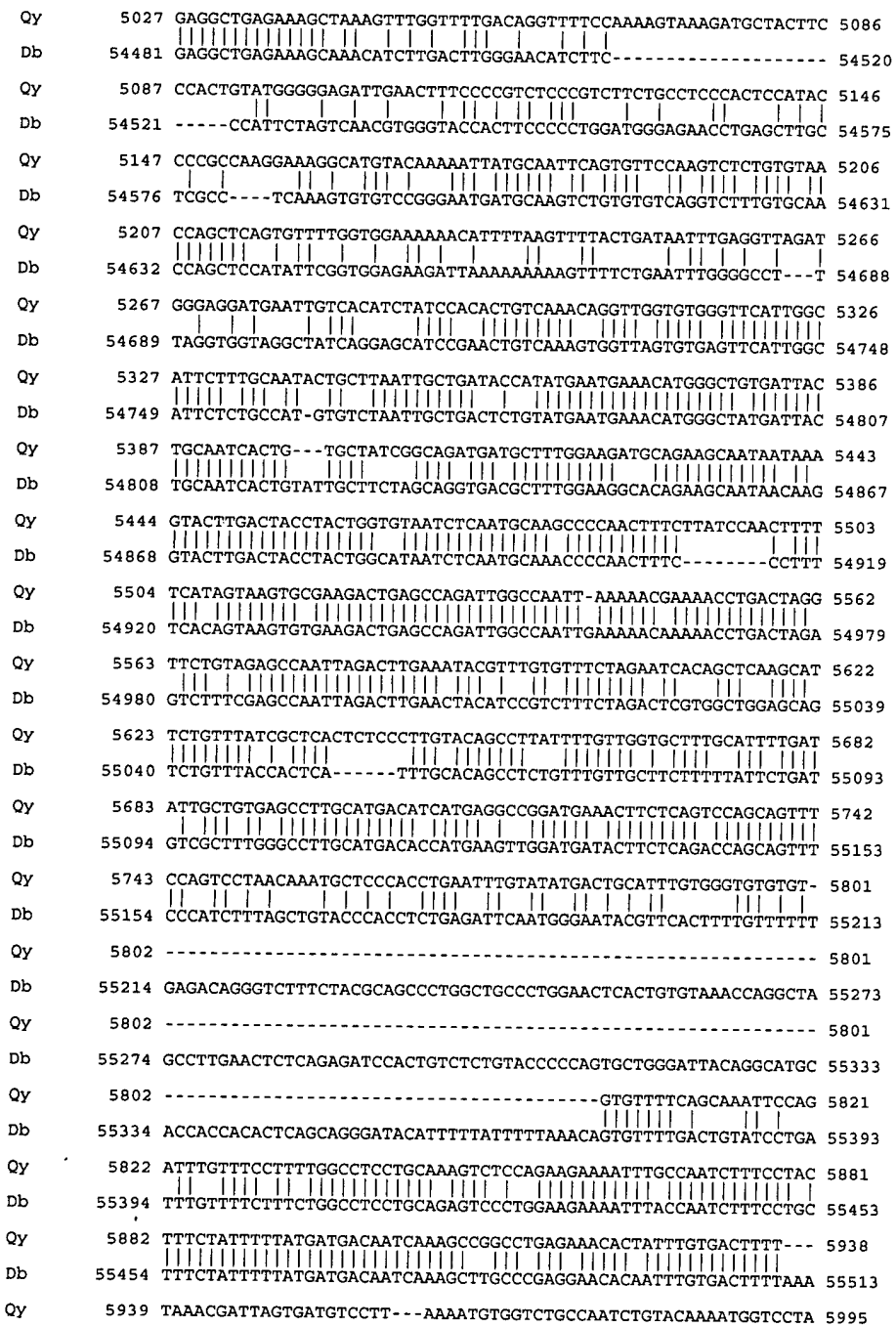
Qy       4736 GGATGACTAGATCCTGGGTTTCCATCCTT-------GAGATTCTGAAGTATGAAGTCTGA 4788
Db      54192 AGTTACTAGCCTCAATGGTGTCAGACCTTTGCCCCAGAGATTTGGAATTACAAGGTCTGA 54251

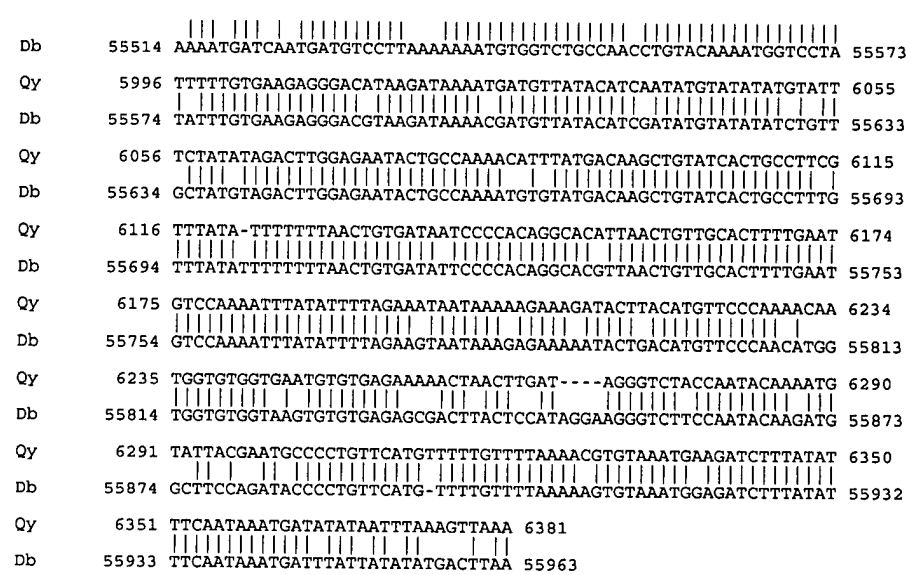
Qy       4789 GGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGG 4848
Db      54252 CGGGAGCAGGAAGC--TATATATATGAACTGCCTGGTGCTCTTGAATAGTCAGTGTTCAG 54309

Qy       4849 AAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAAC 4908
Db      54310 AAACACTGGCTTGGGTTACTGT---------TGGGGGAGGGCAACTTTGAAATTTGGAAC 54360

Qy       4909 AGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTG 4968
Db      54361 GGGGCTAGAAGTCAACCATGCAGGAAGGCTACTGTTTAAGTTCTTGGCTTCATGTCAATA 54420

Qy       4969 ACAT-TTAATGCCATCTAGCTAGCAATTGCGA-CCTTAATTTAACTTTCCAGTCTTAGCT 5026
Db      54421 ACATGTCAATGCCACGTATGCAGCTATTCCTACCCTTGATTTAAGTTTCCAGGCTTGGCT 54480
```





RESULT 41
US-10-741-601-156
; Sequence 156, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-156

Query Match 11.5%; Score 734.8; DB 7; Length 1047;
Best Local Similarity 98.3%; Pred. No. 4.7e-157;
Matches 761; Conservative 3; Mismatches 5; Indels 5; Gaps 2;



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Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGRCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACAT 772
              ||||||||||||||||||||||||||||||:||||||||||||||||  || |
Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGGTACTT 1027


RESULT 42
US-10-741-600-477
; Sequence 477, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-477

  Query Match            11.5%;  Score 734.8;  DB 8;  Length 1047;
  Best Local Similarity   98.3%;  Pred. No. 4.7e-157;
  Matches  761;  Conservative    3;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493


Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGRCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
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Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

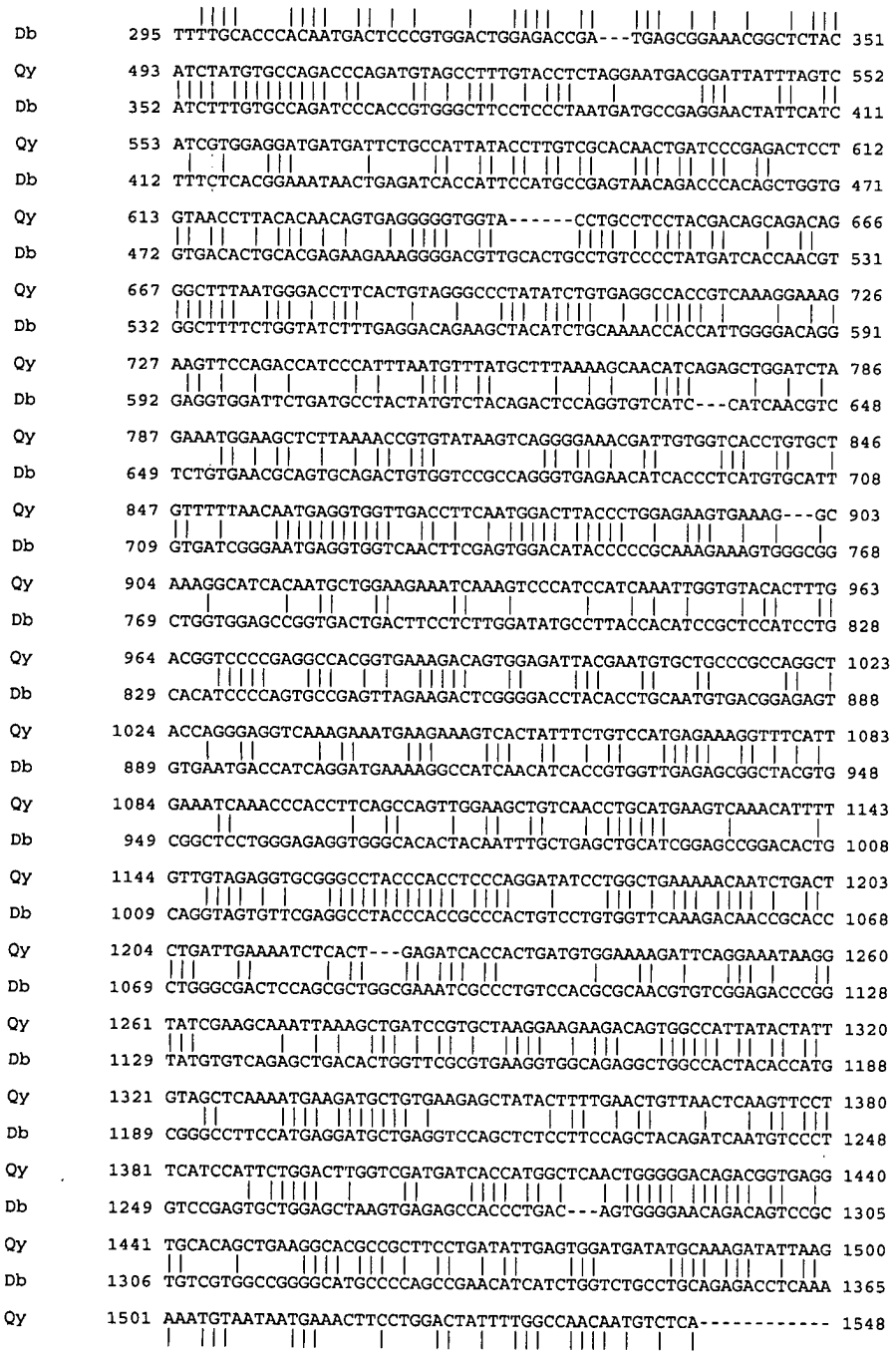
Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACAT 772
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Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGGTACTT 1027

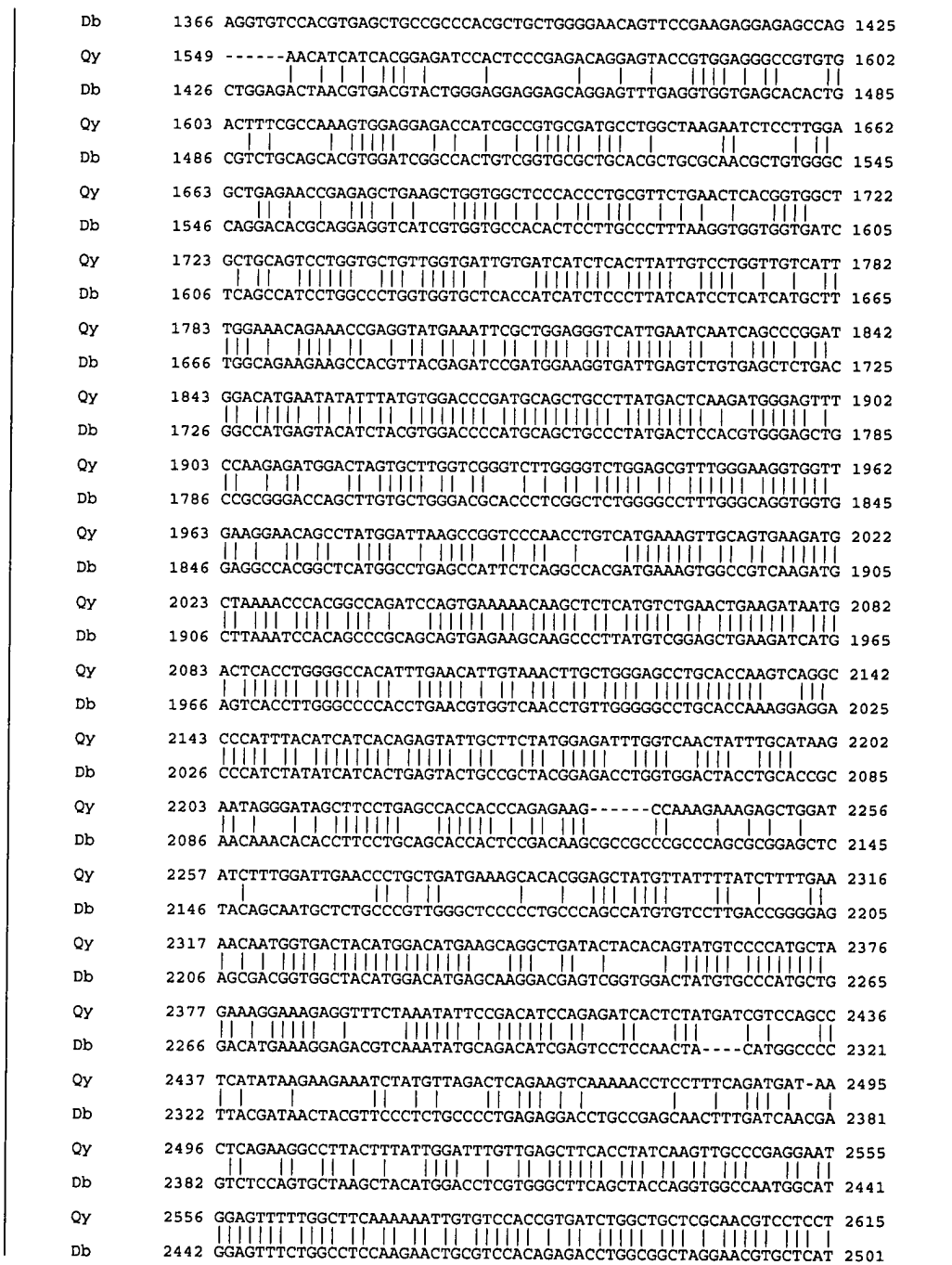

RESULT 43
US-09-866-510-21
; Sequence 21, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
;  APPLICANT: KAZLAUSKAS, ANDRIUS
;  APPLICANT:  IKUNO, YASUSHI
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
;  FILE REFERENCE: ERM-104.01
;  CURRENT APPLICATION NUMBER: US/09/866,510
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: 60/250,747
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: 60/289,103
;  PRIOR FILING DATE: 2001-05-07
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 3321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3318)
US-09-866-510-21

  Query Match            10.4%;  Score 667.6;  DB 3;  Length 3321;
  Best Local Similarity   55.5%;  Pred. No. 2.2e-141;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||  ||    |  ||  |   | ||| ||    | | |    |||| ||    |||
Db        235 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 294

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
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Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
Db       2502 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2561

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
Db       2562 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTATGAAGTGGATGGCTCCGGAGAG 2621

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
Db       2622 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2681

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
Db       2682 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2741

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
Db       2742 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2801

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
Db       2802 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 2861

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
Db       2862 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 2921

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
Db       2922 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 2951


RESULT 44
US-10-027-400-3
; Sequence 3, Application US/10027400
; Publication No. US20030017535A1
;   GENERAL INFORMATION:
;        APPLICANT: WILLIAMS, Lewis T.
;                   ESCOBEDO, Jaime A.
;        TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew
;             STREET: One Market, Steuart Street Tower, 20th Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94105
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/027,400
;             FILING DATE: 19-Dec-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/461,917
;             FILING DATE: 05-JUN-1995
;             APPLICATION NUMBER: US 07/151,414
;             FILING DATE: 02-FEB-1988
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Dow, Karen B.
;             REGISTRATION NUMBER: 29,684
;             REFERENCE/DOCKET NUMBER: 2307K-267-2-4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/326-2400
;             TELEFAX: 415/326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5427 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  187..3507
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-027-400-3

  Query Match             10.4%;  Score 667.6;  DB 5;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 2.9e-141;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

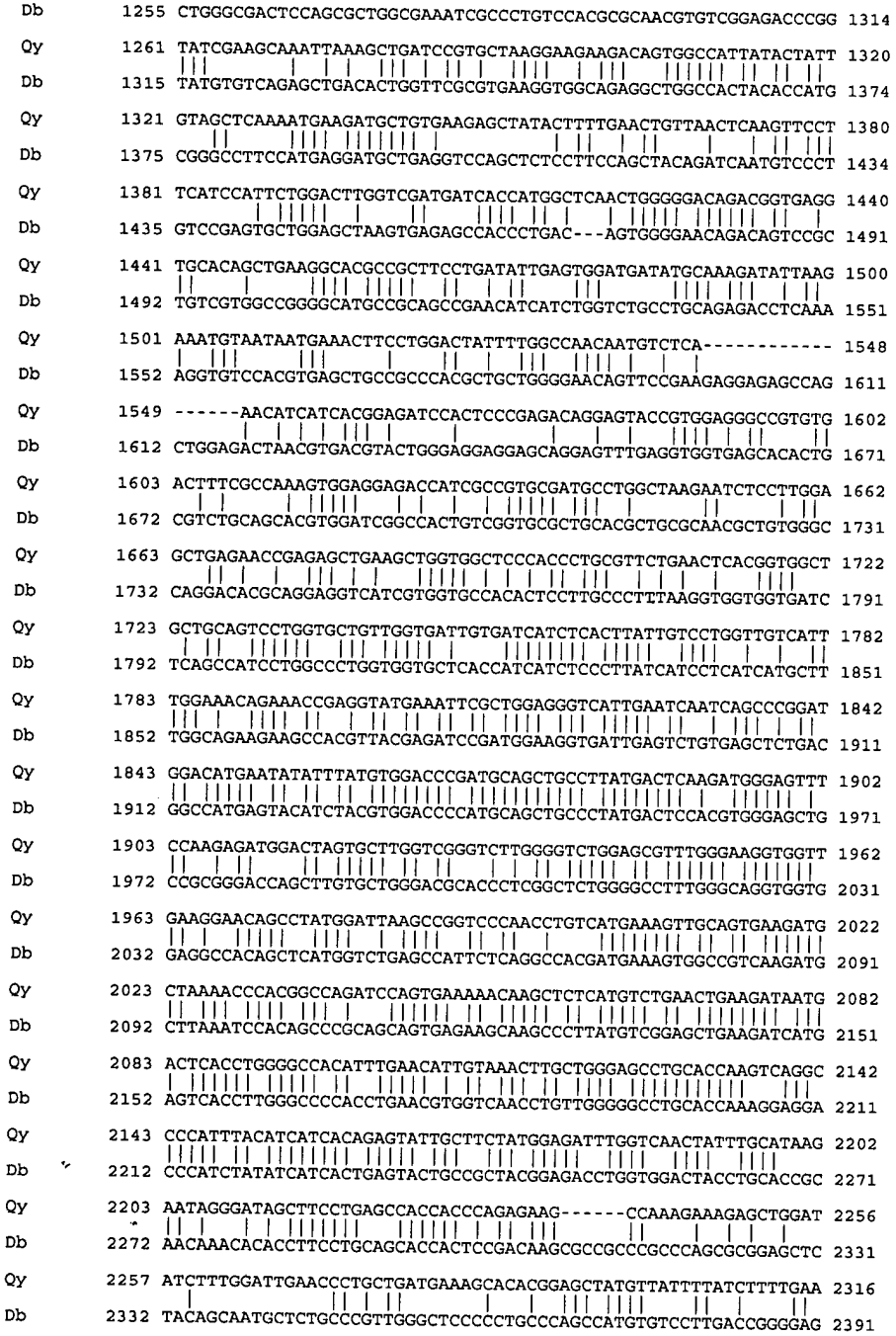
Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
Db       1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
Db       1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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RESULT 45
US-09-866-510-13
; Sequence 13, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT APPLICATION NUMBER: US/09/866,510
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 3321

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3270)
US-09-866-510-13

  Query Match            10.4%;  Score 666;  DB 3;  Length 3321;
  Best Local Similarity  55.5%;  Pred. No. 5e-141;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||    |  ||  |   | ||| ||    | | | |    |||| ||    |||
Db        235 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 294

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
              ||||    ||||  || | |     |    ||||  ||   |||  | |   |  | |||
Db        295 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 351

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||||  ||     || | |||  | |||   |        |||    ||  ||
Db        352 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 411

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              | . |   |||      |     ||  || || || ||  |||  || ||  ||
Db        412 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 471

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | |||  | |   | ||||  ||       |||| | |||| ||   |  ||
Db        472 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 531

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||    |   |   ||| |||||  |  |||||  |    |  | |
Db        532 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 591

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  |  |     | |   |||| ||     |  | |   ||||     |  |  |
Db        592 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 648

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
              || | ||  |  | ||| |||          || || |  ||     |||  ||   |
Db        649 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 708

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |    ||||||||||  || |  | ||||| |||||  |  |||  |  |    |
Db        709 GTGATCGGGAATGAGGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 768

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
              |     |  ||   ||     ||   |      |  | |   |   | ||   ||
Db        769 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 828

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
              |||||   |||  | |  |||||   ||     |||  ||   ||      || |
Db        829 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 888

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
              |  ||    | ||    |||    |||  ||  | ||   |||||  || | | |
Db        889 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 948

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
                ||          |  ||    |  ||  ||   | ||||||     |      |
Db        949 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1008

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
              ||||  | |  ||||||||||||| ||||    |   ||| |  ||| ||||  |  ||
Db       1009 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1068

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              |||   ||     | ||   || ||| ||          |   ||  |   ||| |   ||
Db       1069 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1128

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              |||       |  | |  ||| | || |  ||||  | |||   ||||||  || || ||

Db       1129 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1188

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
                ||    |||| |||||| |          | ||  | ||    |  | || |||
Db       1189 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1248

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
                    | |||||  |    ||    |||| || |   | |||||  |||||| ||  |
Db       1249 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1305

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||    |    |||| ||| |  ||  | ||    |||       |||| |||  | ||
Db       1306 TGTCGTGGCCGGGGCATGCCCCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1365

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
              |  |||     |||     |   ||  |  |||  ||||  |  |  |
Db       1366 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1425

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
                   | | | |||  |       |     |   |  |  ||||  | ||    ||
Db       1426 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1485

Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
              | |     | |||||   | |  |  | |||||  |||  |      ||      | ||
Db       1486 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1545

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
                || |  |  ||| | |   ||||| | | | ||  |||  | | |  |  ||||
Db       1546 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1605

Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
              | ||  ||||||  |||  |||||  |     |||||||| |||||  ||||  |  |  ||
Db       1606 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 1665

Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
              |||  |  |||| ||   | ||  ||  ||  ||  |||| ||| |||||  ||  | ||| | ||
Db       1666 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 1725

Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
              || |||||  || ||  || ||||||||  ||||||||||  ||||||||  |  ||||||  |
Db       1726 GGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGGAGCTG 1785

Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
              ||  | ||    || |||||  || ||  | || |||||  || ||||||  |||||||
Db       1786 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 1845

Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
              ||  |  || ||  ||||  | ||||  || ||  |    ||||||||  || || ||||||
Db       1846 GAGGCCACGGCTCATGGCCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 1905

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082
              || ||| |||| ||| |   ||||||  || |||||  || |||||  || ||||||||  |||
Db       1906 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 1965

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142
              | |||||| ||||| ||  |||||  | || ||| || |||| ||||||||||    |||
Db       1966 AGTCACCTTGGGCCCCACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGA 2025

Qy       2143 CCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAG 2202
              ||||| || |||||||| ||||| |||  |||  |||||  ||||  ||||  ||||
Db       2026 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2085

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256
              || |   | | |||||||   ||||||  | ||  |||       ||    |  |  |
Db       2086 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2145

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316
                |          || | ||    |   |  |||  ||||     ||  |    ||
Db       2146 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2205

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376
              | | | |||| ||||||||||||||    |||  ||  |      | |||||  ||||||||
Db       2206 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2265
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Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
Db       2266 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2321

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
Db       2322 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2381

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
Db       2382 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2441

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
Db       2442 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2501

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
Db       2502 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2561

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
Db       2562 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2621

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
Db       2622 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2681

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
Db       2682 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2741

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
Db       2742 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2801

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
Db       2802 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 2861

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
Db       2862 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 2921

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
Db       2922 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 2951
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RESULT 46
US-09-955-363-1
; Sequence 1, Application US/09955363
; Patent No. US20020173621A1
;   GENERAL INFORMATION:
;        APPLICANT: Sledziewski Ph.D., Andrzej Z
;                   Bell, Lillian A.
;                   Kindsvogel Ph.D., Wayne R.
;        TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;                            AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
;                            FUSIONS
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed and Berry
;             STREET: 6300 Columbia Center
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.24
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/955,363
;             FILING DATE: 18-Sep-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 07/634,510
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 07/347,291
;             FILING DATE: 02-MAY-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki J.D., David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 990008.446C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-622-4900
;             TELEFAX: 206-682-6031
;             TELEX: 3723836
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 4465 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: N
;        ANTI-SENSE: N
;        ORIGINAL SOURCE:
;             ORGANISM: Homo sapiens
;             DEVELOPMENTAL STAGE: Adult
;             TISSUE TYPE: Skin
;             CELL TYPE: fibroblasts
;        IMMEDIATE SOURCE:
;             CLONE: pR-rX1
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  354..3671
;             OTHER INFORMATION:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-955-363-1

  Query Match           10.4%;  Score 666;  DB 3;  Length 4465;
  Best Local Similarity  55.5%;  Pred. No. 6e-141;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
Db        588 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 647

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
Db        648 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 704

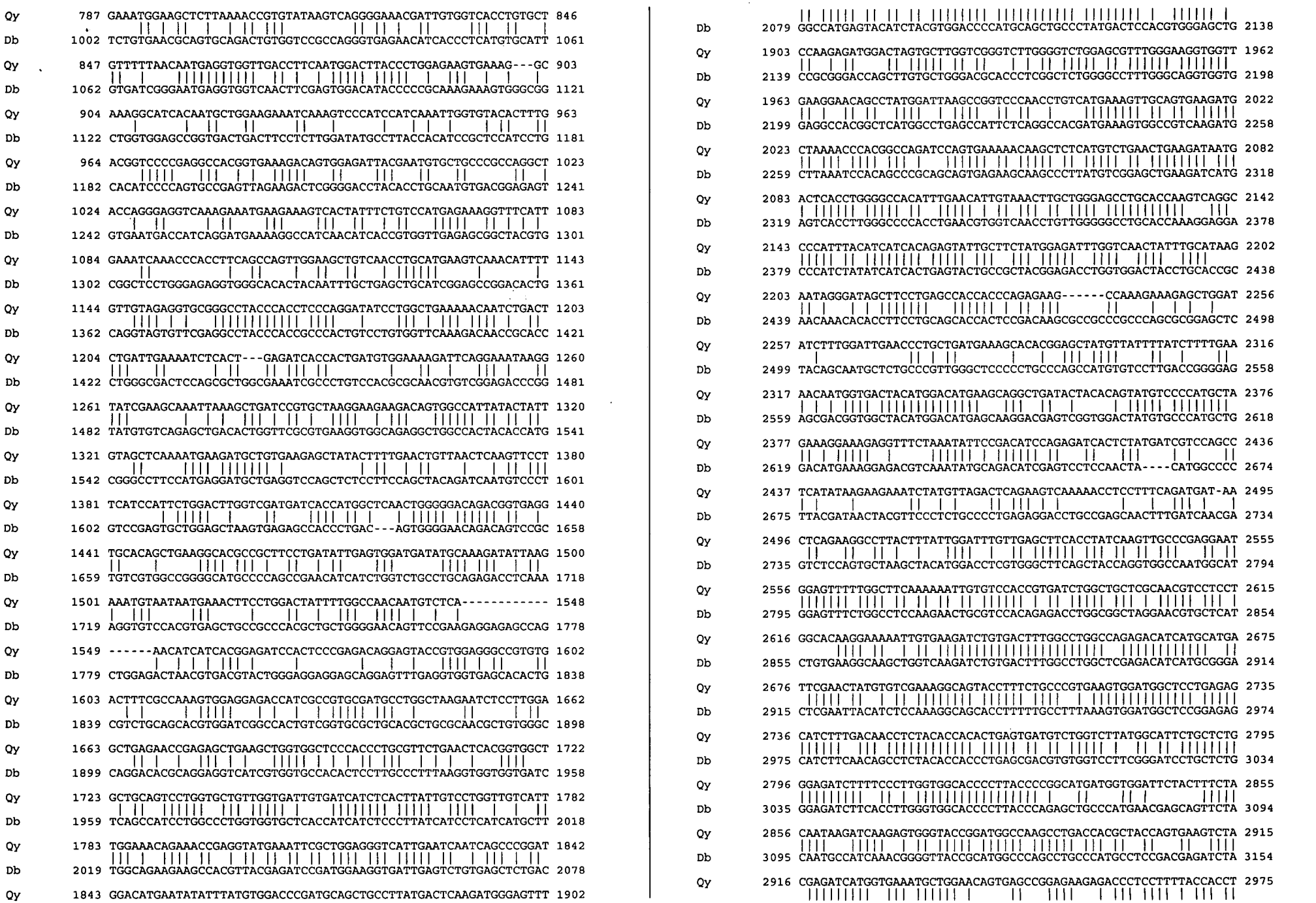
Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
Db        705 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 764

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
Db        765 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 824

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
Db        825 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 884

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
Db        885 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 944

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
Db        945 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 1001
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Db       3155 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3214

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3215 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3274

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3275 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3304


RESULT 47
US-10-007-926A-209
; Sequence 209, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
;  APPLICANT: BERTUCCI, FRANCOIS
;  APPLICANT:  HOULGATTE, REMI
;  APPLICANT:  BIRNBAUM, DANIEL
;  APPLICANT:  NGUYEN, CATHERINE
;  APPLICANT:  VIENS, PATRICE
;  APPLICANT:  FERT, VINCENT
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
;  TITLE OF INVENTION:  USING ARRAYS OF CANDIDATE GENES
;  FILE REFERENCE: 1546-R-00
;  CURRENT APPLICATION NUMBER: US/10/007,926A
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/254,090
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 468
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 209
;   LENGTH: 5570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: platelet-derived growth factor receptor,
;   OTHER INFORMATION: beta polypeptide (PDGFRB) gene.
US-10-007-926A-209

  Query Match             10.4%;  Score 666;  DB 6;  Length 5570;
  Best Local Similarity   55.5%;  Pred. No. 6.8e-141;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

Db        591 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 650

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        651 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 707

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552

Db        708 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 767

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612

Db        768 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 827

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666

Db        828 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 887

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726

Db        888 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 947

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786

Db        948 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 1004

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846

Db       1005 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 1064

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903

Db       1065 GTGATCGGGAATGAGGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 1124

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963

Db       1125 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1184

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023

Db       1185 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1244

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083

Db       1245 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1304

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143

Db       1305 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1364

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203

Db       1365 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1424

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260

Db       1425 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1484

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320

Db       1485 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1544

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380

Db       1545 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1604

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440

Db       1605 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1661

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500

Db       1662 TGTCGTGGCCGGGGCATGCCCCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1721

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548

Db       1722 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1781

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602

Db       1782 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1841

Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662

Db       1842 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1901

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722

Db       1902 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1961

Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782

Db       1962 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 2021

Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842

Db       2022 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 2081

Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
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Db       2082 GGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGGAGCTG 2141

Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962

Db       2142 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2201

Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022

Db       2202 GAGGCCACGGCTCATGGCCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2261

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082

Db       2262 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 2321

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142

Db       2322 AGTCACCTTGGGCCCCACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGA 2381

Qy       2143 CCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAG 2202

Db       2382 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2441

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256

Db       2442 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2501

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316

Db       2502 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2561

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376

Db       2562 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2621

Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436

Db       2622 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2677

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495

Db       2678 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2737

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555

Db       2738 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2797

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615

Db       2798 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2857

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675

Db       2858 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2917

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735

Db       2918 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2977

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795

Db       2978 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 3037

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855

Db       3038 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 3097

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Db       3098 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 3157

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975

Db       3158 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3217

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035

Db       3218 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3277

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065

Db       3278 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3307


RESULT 48
US-10-101-510-28
; Sequence 28, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
;  APPLICANT: WAN, JACKSON
;  APPLICANT:  WANG, YIXIN
;  TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
;  FILE REFERENCE: 15117.0012
;  CURRENT APPLICATION NUMBER: US/10/101,510
;  CURRENT FILING DATE:  2002-03-20
;  PRIOR APPLICATION NUMBER: 60/276,947
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 805
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 5570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-28

  Query Match            10.4%;  Score 666;  DB 6;  Length 5570;
  Best Local Similarity   55.5%;  Pred. No. 6.8e-141;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432

Db        591 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 650

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492

Db        651 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 707

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552

Db        708 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 767

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612

Db        768 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 827

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666

Db        828 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 887

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726

Db        888 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 947

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786

Db        948 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 1004

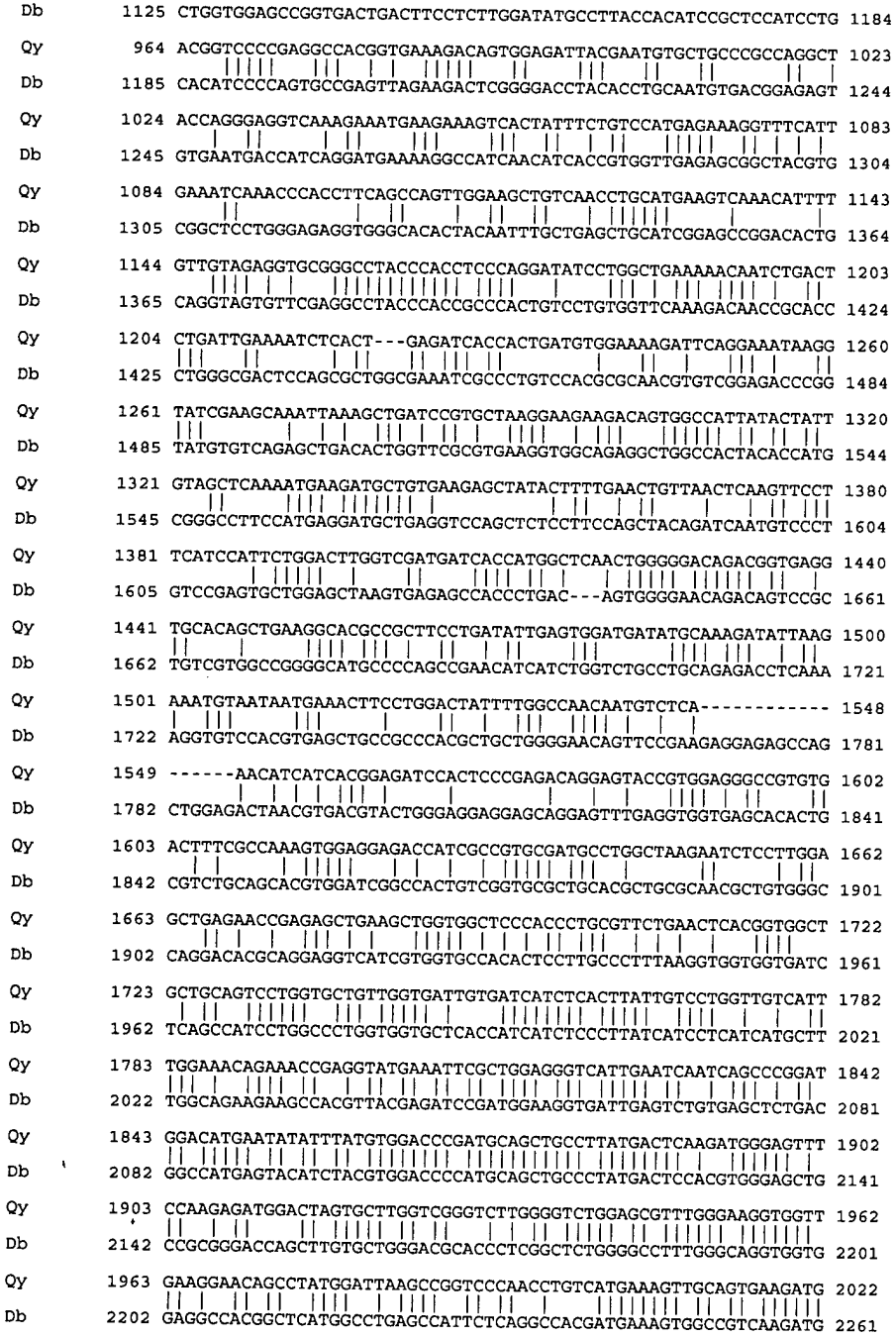
Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846

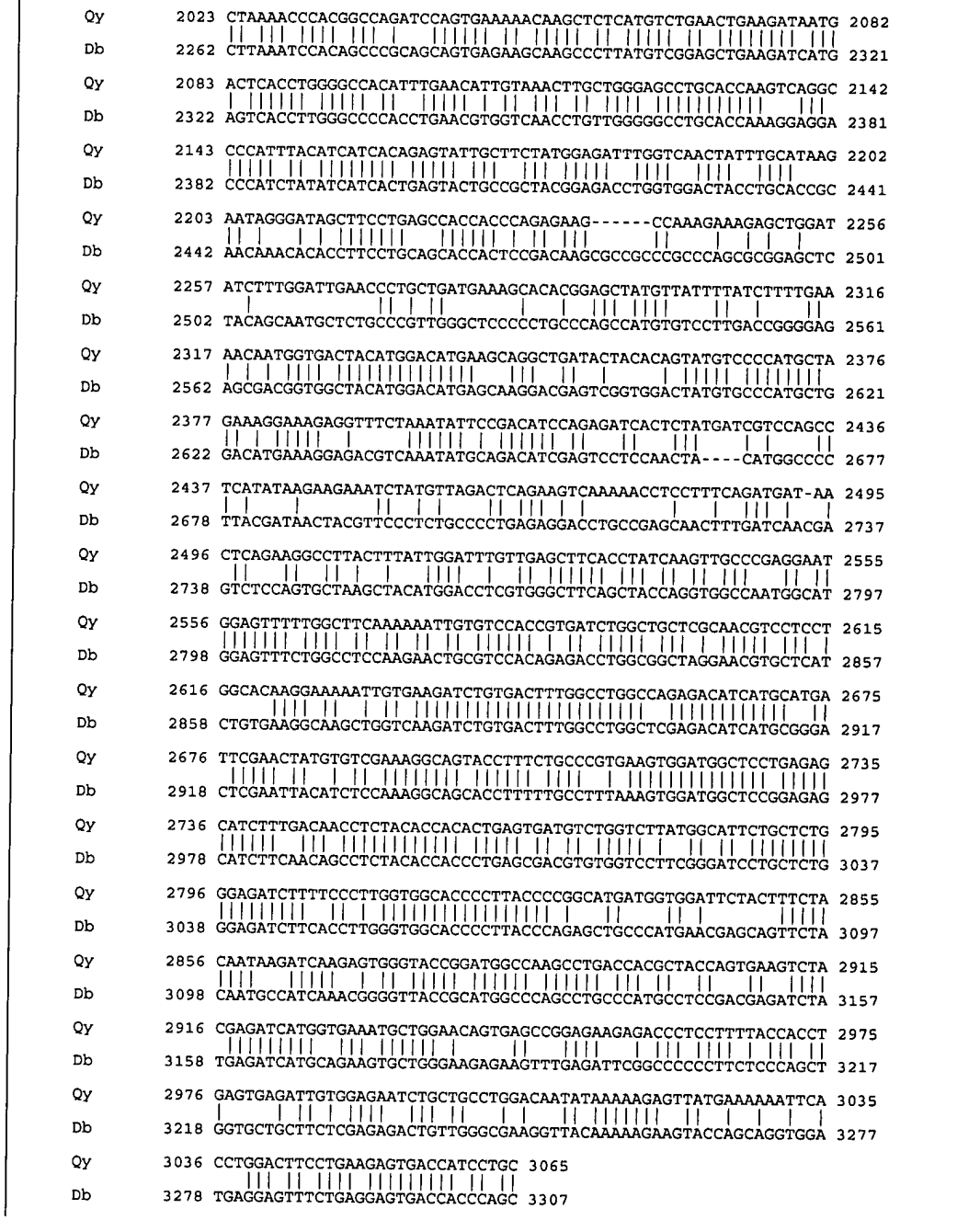
Db       1005 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 1064

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903

Db       1065 GTGATCGGGAATGAGGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 1124

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
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RESULT 49
US-10-641-643-1193
; Sequence 1193, Application US/10641643
; Publication No. US20040077003A1
;  GENERAL INFORMATION:
;       APPLICANT: Cocks, Benjamin G.
;                  Susan G. Stuart
;                  Jeffrey J. Seilhamer
;       TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                           GENE EXPRESSION
;       NUMBER OF SEQUENCES: 1508
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;            STREET: 3174 PORTER DRIVE
;            CITY: PALO ALTO
;            STATE: CALIFORNIA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/641,643
;            FILING DATE: 14-Aug-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Zeller, Karen J.
;            REGISTRATION NUMBER: 37,071
;            REFERENCE/DOCKET NUMBER: PA-0001 US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650) 855-0555
;            TELEFAX: (650) 845-4166
;  INFORMATION FOR SEQ ID NO: 1193:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5570 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;            LIBRARY: GENBANK
;            CLONE: g189731
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1193 :
US-10-641-643-1193

  Query Match             10.4%;  Score 666;  DB 7;  Length 5570;
  Best Local Similarity   55.5%;  Pred. No. 6.8e-141;
  Matches 1515;  Conservative    0;  Mismatches 1165;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||     |  ||  |   | ||| ||     | | | |    ||||  ||    |||
Db        591 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 650

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
                ||||    ||||  || | |     |   ||||  ||   |||  | |   |  | |||
Db        651 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 707

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||||| ||    || | |||  | |||   |        |||    ||  ||
Db        708 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 767

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
                |   |||       |      ||  || || || ||   ||| || ||  ||
Db        768 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 827

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | ||| | |   | ||||  ||       |||| | |||| ||   |  ||
Db        828 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 887

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||     |   |  ||| |||||  |  |||||  |    |  | |
Db        888 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 947

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  | |     | |   |||| ||      |  | |   ||||     |  |  |
Db        948 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 1004

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
                || | ||  |  | || |||          || || |  ||      |||  ||   |
Db        1005 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 1064

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |   ||||||||||  ||  |  |||||  |||||  |  |||  |  |    |
Db        1065 GTGATCGGGAATGAGGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 1124

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
                |      |  ||   ||      ||   |      |   | |  |    | ||   ||
Db        1125 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1184

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
                |||||   |||  | |  |||||   ||    |||   ||   ||       ||  |
Db        1185 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1244

Qy        1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
                |  ||    | ||    |||    |||  ||  | ||   |||||  || | | |
Db        1245 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1304

Qy        1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
                ||          | ||    | ||  ||   | ||||||      |       |
Db        1305 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1364

Qy        1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
               |||| | |   |||||||||||| ||||    |    ||| | ||| |||| |  ||
Db        1365 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1424

Qy        1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
               |||  ||     | ||   || ||| ||       |   ||  |  |||  |   ||
Db        1425 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1484

Qy        1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
               |||       |  | |  ||| | || |  ||||  | |||   |||||| || || ||
Db        1485 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1544

Qy        1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
                ||     |||| |||||||  |           | ||  | ||    |  | ||| |||
Db        1545 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1604

Qy        1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
                | |||||  |    ||   |||| || |   | |||||  ||||||  ||  |
Db        1605 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1661

Qy        1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
                ||    |  |||| ||| |  ||  | ||    |||       |||| |||  | ||
Db        1662 TGTCGTGGCCGGGGCATGCCCCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1721

Qy        1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
               | |||   |||       |    ||  |  |||  |||| |  |  |
Db        1722 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1781

Qy        1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
                    | | | |||  |    |    |  |  |  |||| | ||   ||
Db        1782 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1841

Qy        1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
                | |     | |||||   | |  |  | |||||  |||  |       ||     | ||
Db        1842 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1901

Qy        1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
                || |  | |||  | |   ||||| | | | ||  |||  | | |  |    ||||
Db        1902 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1961
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Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
Db       1962 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 2021

Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
Db       2022 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 2081

Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
Db       2082 GGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGGAGCTG 2141

Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
Db       2142 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2201

Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
Db       2202 GAGGCCACGGCTCATGGCCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2261

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082
Db       2262 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 2321

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142
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Db       2382 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2441

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256
Db       2442 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2501

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316
Db       2502 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2561

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376
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Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
Db       2622 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2677

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
Db       2678 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2737

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
Db       2738 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2797

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
Db       2798 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2857

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
Db       2858 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2917

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
Db       2918 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2977

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
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; Publication No. US20050095592A1
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;  APPLICANT: The Government of the United States of America as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Jazaeri, Amir A.
;  APPLICANT:  Boyd, Jeff
;  APPLICANT:  Liu, Edison T.
;  TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TAR
;  FILE REFERENCE: 4239-64452
;  CURRENT APPLICATION NUMBER: US/10/505,680
;  CURRENT FILING DATE:  2004-08-12
;  PRIOR APPLICATION NUMBER: 60/357,031
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 822
;  SOFTWARE: PatentIn version 3.1
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;   LENGTH: 5570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-505-680-581

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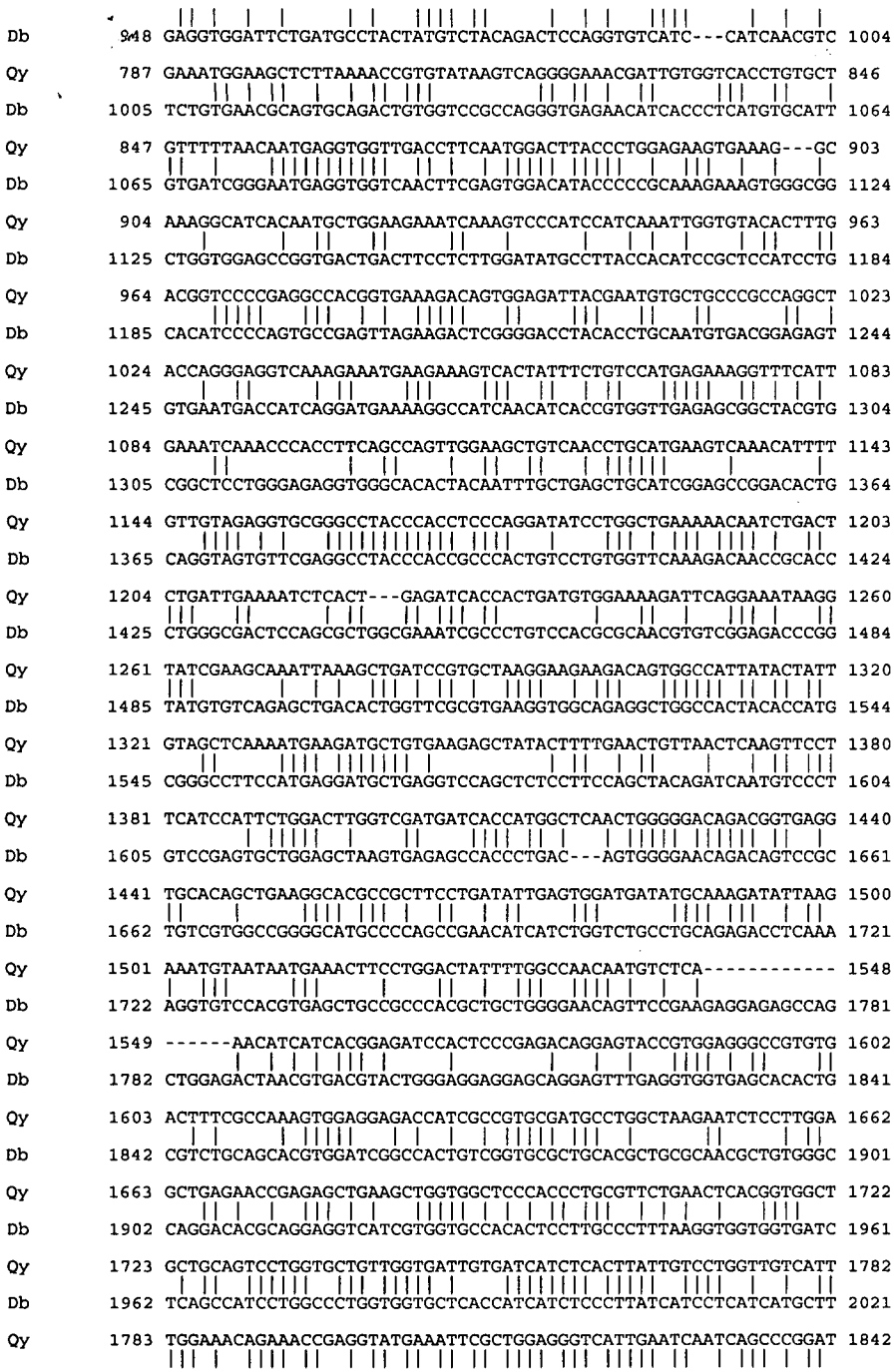
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GenCore version 5.1.8
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SUMMARIES

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3	6364.4	99.2	6633	13	US-10-517-905-1	Sequence 1, Appli
4	6364.4	99.2	6633	17	US-11-148-770-30	Sequence 30, Appl
5	6362.8	99.2	6633	13	US-10-517-905-3	Sequence 3, Appli
6	6362.8	99.2	6633	13	US-10-517-905-20	Sequence 20, Appl
7	6359.6	99.2	6633	13	US-10-517-905-24	Sequence 24, Appl
8	6348.4	99.0	6639	13	US-10-517-905-9	Sequence 9, Appli
9	6334.8	98.8	6624	13	US-10-517-905-7	Sequence 7, Appli
10	6330.4	98.7	6621	13	US-10-517-905-5	Sequence 5, Appli
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16	4765.6	74.3	6375	18	US-11-075-047A-116	Sequence 116, App
17	4765.6	74.3	6375	18	US-11-177-894-24	Sequence 24, Appl
18	3260.6	50.8	6264	17	US-11-136-527-3722	Sequence 3722, Ap
19	3105.6	48.4	81210	10	US-10-995-561-13295	Sequence 13295, A
20	3101.6	48.4	134174	17	US-11-121-086-99	Sequence 99, Appl
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	100	169.8	2.6	594	7	US-09-925-065A-182068 Sequence 182068,
c	101	169.8	2.6	606	12	US-10-301-480-272669 Sequence 272669,
c	102	169.8	2.6	606	12	US-10-301-480-272670 Sequence 272670,
c	103	169.8	2.6	606	12	US-10-301-480-886078 Sequence 886078,
c	104	169.8	2.6	606	12	US-10-301-480-886079 Sequence 886079,
	105	169.8	2.6	632	7	US-09-925-065A-54167 Sequence 54167, A
	106	169.8	2.6	632	7	US-09-925-065A-54168 Sequence 54168, A
	107	169.8	2.6	632	11	US-10-301-480-155405 Sequence 155405,
	108	169.8	2.6	632	11	US-10-301-480-155406 Sequence 155406,
	109	169.8	2.6	632	12	US-10-301-480-768814 Sequence 768814,
	110	169.8	2.6	632	12	US-10-301-480-768815 Sequence 768815,
	111	169	2.6	2648	17	US-11-136-527-220 Sequence 220, App
	112	168	2.6	201	10	US-10-995-561-48258 Sequence 48258, A
	113	166.4	2.6	372	17	US-11-000-688-357 Sequence 357, App
	114	164.4	2.6	3676	17	US-11-136-527-3587 Sequence 3587, Ap
	115	164.4	2.6	5210	17	US-11-136-527-1017 Sequence 1017, Ap
	116	159.4	2.5	4574	13	US-10-960-414-172 Sequence 172, App
	117	159.4	2.5	4574	18	US-11-072-175-132 Sequence 132, App
	118	157.2	2.5	560	7	US-09-925-065A-575974 Sequence 575974,
	119	151.6	2.4	600	17	US-11-136-527-4415 Sequence 4415, Ap
	120	143.6	2.2	600	17	US-11-136-527-7760 Sequence 7760, Ap
	121	143.6	2.2	1152	17	US-11-136-527-3664 Sequence 3664, Ap
	122	141	2.2	574	7	US-09-925-065A-182066 Sequence 182066,
	123	141	2.2	579	12	US-10-301-480-272668 Sequence 272668,
	124	141	2.2	579	12	US-10-301-480-886077 Sequence 886077,
	125	139.4	2.2	201	10	US-10-995-561-48274 Sequence 48274, A
	126	132.8	2.1	600	17	US-11-136-527-7609 Sequence 7609, Ap
	127	128	2.0	600	17	US-11-136-527-7610 Sequence 7610, Ap
c	128	126.6	2.0	617	7	US-09-925-065A-892119 Sequence 892119,
	129	125	1.9	600	17	US-11-136-527-4838 Sequence 4838, Ap
	130	124.6	1.9	201	10	US-10-995-561-48364 Sequence 48364, A
c	131	121.2	1.9	699	17	US-11-136-527-1734 Sequence 1734, Ap
	132	121.2	1.9	4364	18	US-11-245-147-172 Sequence 172, App
	133	121.2	1.9	4364	18	US-11-245-147-233 Sequence 233, App
	134	119.8	1.9	1383	7	US-09-925-065A-81830 Sequence 81830, A
	135	119.8	1.9	1383	7	US-09-925-065A-81831 Sequence 81831, A
	136	119.8	1.9	1383	11	US-10-301-480-183070 Sequence 183070,
	137	119.8	1.9	1383	11	US-10-301-480-183071 Sequence 183071,
	138	119.8	1.9	1383	12	US-10-301-480-796479 Sequence 796479,
	139	119.8	1.9	1383	12	US-10-301-480-796480 Sequence 796480,
	140	118	1.8	3801	17	US-11-136-527-2337 Sequence 2337, Ap
	141	117.8	1.8	143	10	US-10-995-561-8979 Sequence 8979, Ap
	142	117.8	1.8	201	10	US-10-995-561-48410 Sequence 48410, A
	143	117	1.8	608	7	US-09-925-065A-575973 Sequence 575973,
	144	116	1.8	4541	11	US-10-501-035-75 Sequence 75, Appl
c	145	114.4	1.8	592	7	US-09-925-065A-801787 Sequence 801787,
	146	112.6	1.8	2298	17	US-11-172-410-18 Sequence 18, Appl
	147	112.6	1.8	2583	17	US-11-172-410-20 Sequence 20, Appl
	148	112.6	1.8	2831	17	US-11-172-410-1 Sequence 1, Appli
	149	112.6	1.8	2855	17	US-11-136-527-2869 Sequence 2869, Ap
	150	111.8	1.7	2043	13	US-10-469-469-140 Sequence 140, App
	151	110.4	1.7	3417	17	US-11-049-536-1 Sequence 1, Appli
	152	110.4	1.7	3417	18	US-11-199-739-1 Sequence 1, Appli
	153	110.4	1.7	3845	13	US-10-960-414-201 Sequence 201, App
	154	109.6	1.7	201	10	US-10-995-561-48317 Sequence 48317, A
	155	109.6	1.7	6193	17	US-11-136-527-2331 Sequence 2331, Ap
	156	106.8	1.7	4590	17	US-11-136-527-2788 Sequence 2788, Ap
	157	106.2	1.7	2676	17	US-11-136-527-2568 Sequence 2568, Ap
	158	106	1.7	4703	17	US-11-136-527-68 Sequence 68, Appl
	159	105.8	1.6	201	10	US-10-995-561-48382 Sequence 48382, A
	160	105.8	1.6	3527	10	US-10-770-726-35 Sequence 35, Appl
	161	104.8	1.6	2748	17	US-11-136-527-2493 Sequence 2493, Ap
	162	104.6	1.6	2015	9	US-10-511-937-2828 Sequence 2828, Ap
	163	104.6	1.6	2015	10	US-10-775-169-106 Sequence 106, App
	164	104.6	1.6	2015	12	US-10-497-299A-3 Sequence 3, Appli
	165	104	1.6	201	10	US-10-995-561-48303 Sequence 48303, A
	166	103.4	1.6	600	17	US-11-136-527-6965 Sequence 6965, Ap
	167	101.4	1.6	600	17	US-11-136-527-7756 Sequence 7756, Ap
	168	101.4	1.6	1538	17	US-11-136-527-3660 Sequence 3660, Ap
	169	100.4	1.6	1183	17	US-11-136-527-3335 Sequence 3335, Ap
	170	100.4	1.6	1183	17	US-11-136-527-7431 Sequence 7431, Ap
	171	100.4	1.6	2331	10	US-10-947-249-4 Sequence 4, Appli
	172	100.4	1.6	2391	10	US-10-947-249-6 Sequence 6, Appli
	173	99.8	1.6	2032	9	US-10-511-937-403 Sequence 403, App
	174	99	1.5	201	10	US-10-995-561-48320 Sequence 48320, A
	175	98	1.5	5484	10	US-10-955-054A-86 Sequence 86, Appl
	176	98	1.5	5484	11	US-10-912-971-11 Sequence 11, Appl
	177	98	1.5	5484	14	US-11-248-122-1 Sequence 1, Appli
	178	98	1.5	5484	17	US-11-113-202-15 Sequence 15, Appl
	179	97.2	1.5	1400	17	US-11-136-527-7409 Sequence 7409, Ap
	180	97.2	1.5	4016	17	US-11-136-527-3313 Sequence 3313, Ap
	181	96.8	1.5	3227	18	US-11-245-147-112 Sequence 112, App
	182	96.8	1.5	4986	18	US-11-245-147-231 Sequence 231, App
	183	96.8	1.5	4987	9	US-10-505-928-433 Sequence 433, App
	184	96.8	1.5	4987	14	US-11-251-465-4 Sequence 4, Appli
	185	96.8	1.5	5014	14	US-11-251-465-5 Sequence 5, Appli
	186	96.8	1.5	5015	18	US-11-245-147-232 Sequence 232, App
	187	96.2	1.5	4543	17	US-11-175-405-1 Sequence 1, Appli
	188	96	1.5	3674	9	US-10-473-173-2 Sequence 2, Appli
	189	96	1.5	4691	17	US-11-000-688-210 Sequence 210, App
	190	96	1.5	4723	10	US-10-496-711-23 Sequence 23, Appl
	191	95.2	1.5	980	13	US-10-469-469-270 Sequence 270, App
	192	95.2	1.5	1403	13	US-10-469-469-272 Sequence 272, App
	193	95.2	1.5	4620	18	US-11-072-175-52 Sequence 52, Appl
c	194	95	1.5	514	7	US-09-925-065A-500114 Sequence 500114,
	195	94.8	1.5	1400	17	US-11-136-527-7486 Sequence 7486, Ap
	196	94.8	1.5	1682	11	US-10-329-258-21 Sequence 21, Appl
	197	94.8	1.5	2157	17	US-11-136-527-3390 Sequence 3390, Ap
	198	94.8	1.5	2187	17	US-11-230-995-4 Sequence 4, Appli
	199	94.8	1.5	3608	9	US-10-196-749-433 Sequence 433, App
	200	94.8	1.5	3608	13	US-10-194-487-433 Sequence 433, App
	201	94.8	1.5	3608	13	US-10-195-883-433 Sequence 433, App
	202	94.8	1.5	3608	13	US-10-195-888-433 Sequence 433, App
	203	94.8	1.5	3608	13	US-10-195-889-433 Sequence 433, App
	204	94.8	1.5	3608	18	US-11-245-147-234 Sequence 234, App
	205	94.8	1.5	4189	17	US-11-136-527-2933 Sequence 2933, Ap
	206	94.6	1.5	3768	17	US-11-202-516-3 Sequence 3, Appli
	207	94.6	1.5	4530	10	US-10-770-726-18 Sequence 18, Appl
	208	94.6	1.5	4530	11	US-10-826-585-27 Sequence 27, Appl
	209	94.6	1.5	4530	11	US-10-826-585-38 Sequence 38, Appl
	210	94.6	1.5	4530	13	US-10-521-313A-1 Sequence 1, Appli
	211	94.6	1.5	4530	17	US-11-113-202-9 Sequence 9, Appli
	212	94.6	1.5	4530	17	US-11-155-288-29 Sequence 29, Appl
	213	94.6	1.5	4624	14	US-11-223-945-44 Sequence 44, Appl
	214	94.4	1.5	1611	13	US-10-469-469-274 Sequence 274, App
	215	94.4	1.5	2455	11	US-10-330-773-748 Sequence 748, App
	216	94.4	1.5	4145	18	US-11-233-510-23 Sequence 23, Appl
	217	94.4	1.5	4189	18	US-11-036-196-1904 Sequence 1904, Ap
	218	94.4	1.5	4989	11	US-10-510-903-9 Sequence 9, Appli
	219	94.4	1.5	4989	17	US-11-090-351-3 Sequence 3, Appli
	220	94.4	1.5	4989	17	US-11-113-202-17 Sequence 17, Appl
	221	94.4	1.5	4989	17	US-11-000-688-205 Sequence 205, App
	222	94.4	1.5	5180	10	US-10-496-711-24 Sequence 24, Appl
	223	93.6	1.5	170	7	US-09-925-065A-575969 Sequence 575969,
	224	93.6	1.5	170	7	US-09-925-065A-575970 Sequence 575970,
	225	93	1.5	4149	18	US-11-208-414-1 Sequence 1, Appli
	226	93	1.5	4149	18	US-11-208-414-2 Sequence 2, Appli
	227	93	1.5	4149	18	US-11-208-414-8 Sequence 8, Appli
	228	92.8	1.4	2442	13	US-10-469-469-276 Sequence 276, App
	229	92.8	1.4	5229	10	US-10-995-561-21 Sequence 21, Appl
	230	92.8	1.4	5232	10	US-10-995-561-22 Sequence 22, Appl
	231	92.6	1.4	2019	17	US-11-136-527-2281 Sequence 2281, Ap
	232	92.6	1.4	4060	17	US-11-136-527-2581 Sequence 2581, Ap
	233	92.2	1.4	600	17	US-11-136-527-6211 Sequence 6211, Ap

	234	92.2	1.4	1858	17	US-11-136-527-2115 Sequence 2115, Ap
	235	90.8	1.4	4815	17	US-11-113-202-7 Sequence 7, Appli
	236	90.8	1.4	5616	11	US-10-826-585-19 Sequence 19, Appl
	237	90.8	1.4	5616	17	US-11-113-202-5 Sequence 5, Appli
	238	90.8	1.4	5616	17	US-11-145-566-2 Sequence 2, Appli
	239	90.6	1.4	1605	13	US-10-782-413-80 Sequence 80, Appl
	240	90.6	1.4	2672	10	US-10-989-718-1 Sequence 1, Appli
	241	90.6	1.4	2681	17	US-11-000-688-1036 Sequence 1036, Ap
c	242	90.6	1.4	5187	17	US-11-091-883-205 Sequence 205, App
	243	89.6	1.4	1759	17	US-11-230-995-2 Sequence 2, Appli
	244	89	1.4	1614	9	US-10-473-173-1 Sequence 1, Appli
	245	89	1.4	2541	18	US-11-218-020-8 Sequence 8, Appli
	246	89	1.4	2647	11	US-10-501-035-123 Sequence 123, App
	247	89	1.4	2650	11	US-10-912-971-13 Sequence 13, Appl
	248	88.8	1.4	4811	17	US-11-136-527-2105 Sequence 2105, Ap
	249	88.6	1.4	5333	17	US-11-136-527-2117 Sequence 2117, Ap
	250	88.2	1.4	4975	10	US-10-770-726-19 Sequence 19, Appl
	251	88.2	1.4	4975	17	US-11-113-202-11 Sequence 11, Appl
	252	88.2	1.4	4975	17	US-11-113-202-13 Sequence 13, Appl
	253	87.8	1.4	2255	17	US-11-136-527-714 Sequence 714, App
	254	87.6	1.4	3899	11	US-10-330-773-506 Sequence 506, App
	255	87.6	1.4	3944	11	US-10-330-773-504 Sequence 504, App
	256	87	1.4	4042	17	US-11-136-527-2417 Sequence 2417, Ap
	257	87	1.4	4224	17	US-11-136-527-2386 Sequence 2386, Ap
	258	86.6	1.4	1846	17	US-11-136-527-2609 Sequence 2609, Ap
	259	85.6	1.3	600	17	US-11-136-527-5830 Sequence 5830, Ap
	260	85.6	1.3	2682	18	US-11-245-147-37 Sequence 37, Appl
	261	85.2	1.3	1400	17	US-11-136-527-6253 Sequence 6253, Ap
	262	85.2	1.3	7902	17	US-11-136-527-2157 Sequence 2157, Ap
	263	83.6	1.3	4062	17	US-11-128-061-469 Sequence 469, App
	264	83.6	1.3	4062	17	US-11-128-049-469 Sequence 469, App
	265	83.4	1.3	201	10	US-10-995-561-48414 Sequence 48414, A
	266	83.4	1.3	4172	17	US-11-154-035-1 Sequence 1, Appli
	267	83.4	1.3	4514	17	US-11-154-035-2 Sequence 2, Appli
	268	83	1.3	600	17	US-11-128-061-4429 Sequence 4429, Ap
	269	83	1.3	600	17	US-11-128-049-4429 Sequence 4429, Ap
	270	83	1.3	2521	17	US-11-128-061-787 Sequence 787, App
	271	83	1.3	2521	17	US-11-128-049-787 Sequence 787, App
	272	82.6	1.3	3370	18	US-11-245-147-219 Sequence 219, App
	273	82.2	1.3	4335	17	US-11-136-527-2301 Sequence 2301, Ap
	274	81.8	1.3	201	10	US-10-995-561-10396 Sequence 10396, A
	275	81.8	1.3	201	10	US-10-995-561-10410 Sequence 10410, A
	276	81.8	1.3	201	10	US-10-995-561-10425 Sequence 10425, A
	277	81.8	1.3	3952	14	US-11-223-945-41 Sequence 41, Appl
c	278	80.6	1.3	1524	17	US-11-136-527-1235 Sequence 1235, Ap
	279	80.4	1.3	2208	17	US-11-136-527-2767 Sequence 2767, Ap
	280	79.4	1.2	600	17	US-11-136-527-7029 Sequence 7029, Ap
	281	79.4	1.2	2454	9	US-10-511-937-2817 Sequence 2817, Ap
	282	79.4	1.2	2454	18	US-11-218-020-6 Sequence 6, Appli
c	283	79	1.2	197096	17	US-11-121-086-107 Sequence 107, App
	284	78.4	1.2	3805	10	US-10-510-524-2 Sequence 2, Appli
	285	78.4	1.2	3805	10	US-10-955-054A-144 Sequence 144, App
	286	78.4	1.2	3805	18	US-11-245-147-170 Sequence 170, App
	287	78.4	1.2	3805	18	US-11-245-147-214 Sequence 214, App
	288	78.4	1.2	4234	10	US-10-955-054A-133 Sequence 133, App
	289	78.2	1.2	3386	11	US-10-330-773-509 Sequence 509, App
	290	78.2	1.2	3416	11	US-10-912-971-15 Sequence 15, Appl
	291	77.6	1.2	2298	9	US-10-505-928-354 Sequence 354, App
	292	77.6	1.2	2298	9	US-10-511-937-434 Sequence 434, App
	293	77.2	1.2	1400	17	US-11-136-527-7271 Sequence 7271, Ap
	294	77.2	1.2	3528	17	US-11-136-527-3175 Sequence 3175, Ap
	295	77.2	1.2	3775	17	US-11-128-061-560 Sequence 560, App
	296	77.2	1.2	3775	17	US-11-128-049-560 Sequence 560, App
	297	77.2	1.2	6383	9	US-10-511-937-2838 Sequence 2838, Ap
	298	76.8	1.2	4400	17	US-11-136-527-1982 Sequence 1982, Ap
	299	75.4	1.2	1623	11	US-10-330-773-745 Sequence 745, App
	300	75.2	1.2	1611	17	US-11-004-762-2 Sequence 2, Appli
	301	75.2	1.2	2001	17	US-11-004-762-4 Sequence 4, Appli
	302	74.6	1.2	1254	10	US-10-966-483-32 Sequence 32, Appl
	303	74.6	1.2	1254	17	US-11-021-441-16 Sequence 16, Appl
	304	74.6	1.2	1437	10	US-10-966-483-35 Sequence 35, Appl
	305	74.6	1.2	1437	17	US-11-021-441-19 Sequence 19, Appl
	306	74.6	1.2	3105	10	US-10-966-483-19 Sequence 19, Appl
	307	74.6	1.2	3105	17	US-11-021-441-3 Sequence 3, Appli
	308	74.6	1.2	3921	18	US-11-072-175-1 Sequence 1, Appli
	309	74.6	1.2	3921	18	US-11-245-147-223 Sequence 223, App
	310	74.6	1.2	3935	17	US-11-233-796-1 Sequence 1, Appli
	311	74.6	1.2	3963	10	US-10-966-483-1 Sequence 1, Appli
	312	74.4	1.2	2094	11	US-10-330-773-490 Sequence 490, App
	313	74.4	1.2	4523	18	US-11-245-147-211 Sequence 211, App
	314	74.2	1.2	3052	10	US-10-770-726-34 Sequence 34, Appl
	315	74.2	1.2	4453	17	US-11-000-688-1248 Sequence 1248, Ap
	316	73.6	1.1	2981	10	US-10-949-720-399 Sequence 399, App
	317	73.6	1.1	3945	18	US-11-245-147-213 Sequence 213, App
	318	73.6	1.1	3955	10	US-10-821-234-349 Sequence 349, App
	319	73.6	1.1	4235	10	US-10-949-720-392 Sequence 392, App
c	320	72	1.1	566	17	US-11-136-527-857 Sequence 857, App
	321	72	1.1	566	17	US-11-136-527-4953 Sequence 4953, Ap
c	322	69.8	1.1	995	12	US-10-301-480-548473 Sequence 548473,
c	323	69.8	1.1	995	12	US-10-301-480-1161882 Sequence 1161882,
	324	69.8	1.1	2867	18	US-11-072-512-689 Sequence 689, App
	325	69.2	1.1	3107	18	US-11-245-147-218 Sequence 218, App
	326	68	1.1	2231	11	US-10-330-773-493 Sequence 493, App
	327	68	1.1	2613	11	US-10-330-773-495 Sequence 495, App
	328	67.8	1.1	4554	17	US-11-136-527-255 Sequence 255, App
	329	67.6	1.1	600	17	US-11-136-527-6664 Sequence 6664, Ap
	330	67.2	1.0	3942	18	US-11-245-147-216 Sequence 216, App
	331	67.2	1.0	3949	18	US-11-072-175-2 Sequence 2, Appli
	332	67.2	1.0	4711	17	US-11-000-688-440 Sequence 440, App
	333	67.2	1.0	4711	17	US-11-169-041-28 Sequence 28, Appl
	334	67.2	1.0	6057	18	US-11-245-147-215 Sequence 215, App
	335	67.2	1.0	6058	10	US-10-770-726-17 Sequence 17, Appl
	336	66.8	1.0	2952	14	US-11-302-678-3 Sequence 3, Appli
	337	66.8	1.0	3149	14	US-11-302-678-1 Sequence 1, Appli
	338	66.8	1.0	3149	18	US-11-245-147-220 Sequence 220, App
	339	66.6	1.0	579	10	US-10-775-169-298 Sequence 298, App
	340	66	1.0	201	10	US-10-995-561-48421 Sequence 48421, A
	341	65.8	1.0	2591	9	US-10-511-937-603 Sequence 603, App
	342	65.2	1.0	815	7	US-09-925-065A-94936 Sequence 94936, A
	343	65.2	1.0	815	7	US-09-925-065A-94937 Sequence 94937, A
	344	65.2	1.0	815	7	US-09-925-065A-94938 Sequence 94938, A
	345	65.2	1.0	815	11	US-10-301-480-196178 Sequence 196178,
	346	65.2	1.0	815	11	US-10-301-480-196179 Sequence 196179,
	347	65.2	1.0	815	11	US-10-301-480-196180 Sequence 196180,
	348	65.2	1.0	815	12	US-10-301-480-809587 Sequence 809587,
	349	65.2	1.0	815	12	US-10-301-480-809588 Sequence 809588,
	350	65.2	1.0	815	12	US-10-301-480-809589 Sequence 809589,
	351	65.2	1.0	3573	17	US-11-136-527-3438 Sequence 3438, Ap
	352	65.2	1.0	182190	17	US-11-121-086-102 Sequence 102, App
	353	64.6	1.0	1400	17	US-11-136-527-6247 Sequence 6247, Ap
	354	64.6	1.0	3807	17	US-11-136-527-2151 Sequence 2151, Ap
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	356	64	1.0	201	10	US-10-995-561-10419 Sequence 10419, A
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	368	64	1.0	3583	13	US-10-243-345-103 Sequence 103, App
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	370	64	1.0	3583	13	US-10-245-083-103 Sequence 103, App
	371	64	1.0	3583	13	US-10-247-015-103 Sequence 103, App
	372	64	1.0	3641	17	US-11-113-424-19 Sequence 19, Appl
	373	64	1.0	3692	17	US-11-113-424-21 Sequence 21, Appl
	374	63.4	1.0	123	18	US-11-051-720-1109 Sequence 1109, Ap
	375	63.4	1.0	600	17	US-11-136-527-6705 Sequence 6705, Ap
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	377	60.8	0.9	600	17	US-11-136-527-6589 Sequence 6589, Ap
	378	58.8	0.9	4176	17	US-11-122-329-124 Sequence 124, App
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	458	51.8	0.8	1656	12	US-10-644-807-33
	459	51.8	0.8	4061	13	US-10-745-586-152
	460	51.8	0.8	4339	10	US-10-909-125-801
	461	51.8	0.8	6152	17	US-11-196-400-1
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	476	51	0.8	1230	7	US-09-925-065A-77683
	477	51	0.8	1230	7	US-09-925-065A-77684
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	489	51	0.8	6200	10	US-10-895-011-1
	490	51	0.8	6200	11	US-10-722-371-1
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ALIGNMENTS

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RESULT 1
US-11-177-894-23
; Sequence 23, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 6378
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: PDGFRA nucleotide sequence
US-11-177-894-23
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  Query Match             99.2%;  Score 6364.4;  DB 18;  Length 6378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

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Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801

Qy       1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861

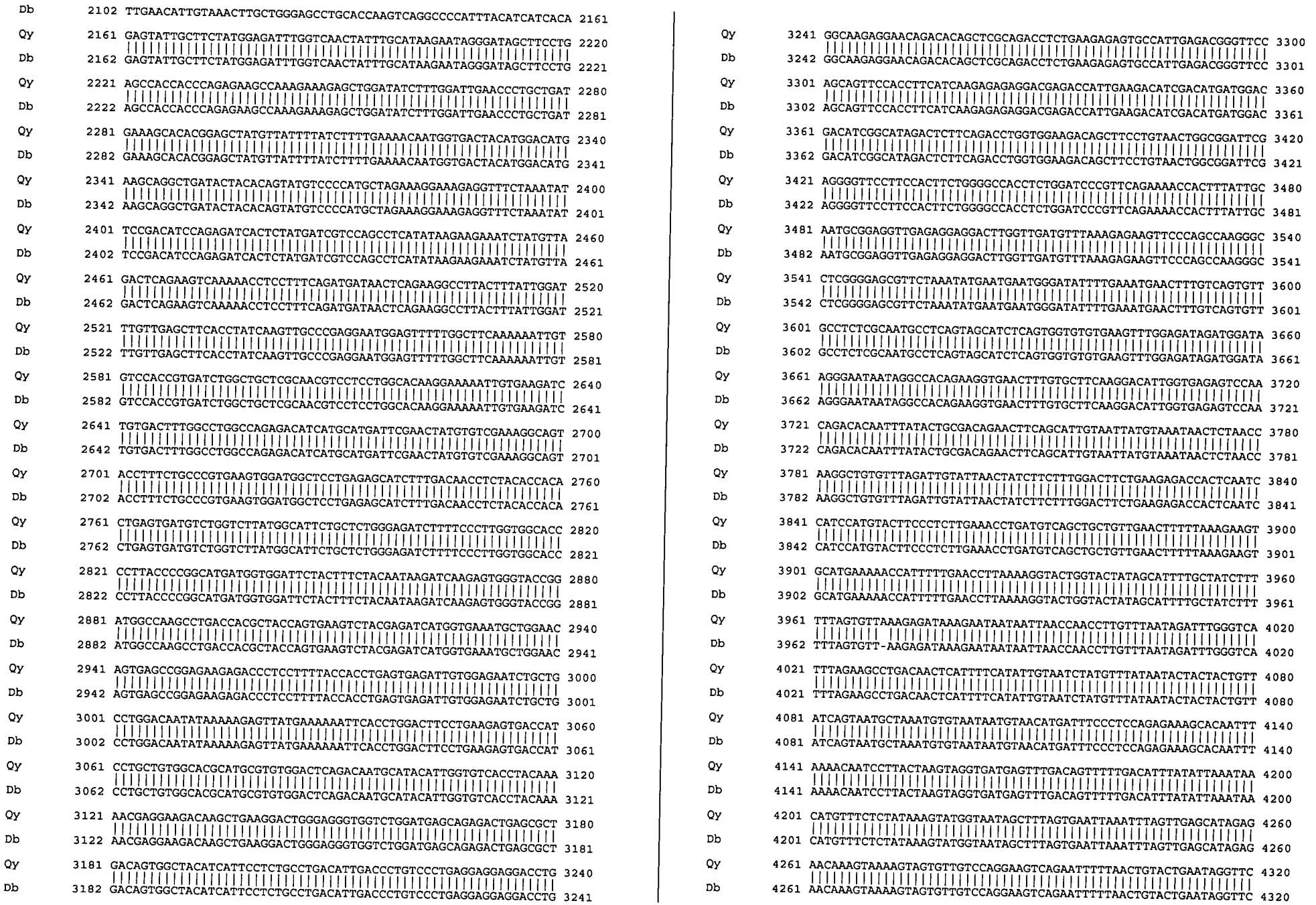
Qy       1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921

Qy       1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981

Qy       1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041

Qy       2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101

Qy       2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db 2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db 2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db 2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db 2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy 2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db 2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db 2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821
Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db 2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db 2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001
Qy 3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db 3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061
Qy 3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db 3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
Qy 3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db 3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db 3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601
Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Qy 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Db 4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
Qy 4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
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Db       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500

Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
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Db       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
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Db       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Db       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Db       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Db       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
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Db       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Db       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
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Db       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360

Qy       6361 GATATATAATTTAAAGTT 6378
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Db       6361 GATATATAATTTAAAGTT 6378
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RESULT 2
US-11-233-510-27
; Sequence 27, Application US/11233510
; Publication No. US20060063190A1
; GENERAL INFORMATION:

; APPLICANT: Fischer, Timothy J.
; APPLICANT: Whitehead, Clark M.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Marcelpoil, Raphael
; APPLICANT: Morel, Didier
; TITLE OF INVENTION: Methods and Compositions for Evaluating
; TITLE OF INVENTION: Breast Cancer Prognosis
; FILE REFERENCE: 46143/296738
; CURRENT APPLICATION NUMBER: US/11/233,510
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 60/612,073
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/611,965
; PRIOR FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)...(3409)
US-11-233-510-27

Query Match 99.2%; Score 6364.4; DB 18; Length 6378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          2 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 61

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 121

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 181

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Db        182 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 241

Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        242 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 301

Qy        301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 361

Qy        361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 421

Qy        421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 481

Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 541

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 601

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 661

Qy        661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 721

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 781

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 841

Qy        841 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGTGCTGTTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 901

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 961

Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1021

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1081

Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1141

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1201

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1261

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1321

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1381

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1441

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1501

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1561

Qy       1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1621

Qy       1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1681

Qy       1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1741

Qy       1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Db      1742 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1801
Qy      1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db      1802 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1861
Qy      1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db      1862 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1921
Qy      1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db      1922 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1981
Qy      1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db      1982 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2041
Qy      2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db      2042 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2101
Qy      2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db      2102 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2161
Qy      2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db      2162 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2221
Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db      2222 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2281
Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db      2282 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2341
Qy      2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db      2342 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2401
Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db      2402 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2461
Qy      2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db      2462 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2521
Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db      2522 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2581
Qy      2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
Db      2582 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2641
Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
Db      2642 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2701
Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db      2702 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2761
Qy      2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
Db      2762 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2821
Qy      2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
Db      2822 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2881
Qy      2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db      2882 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2941
Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
Db      2942 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3001
Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
Db      3002 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3061
Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
Db      3062 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3121
Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
Db      3122 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3181
Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db      3182 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3241
Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db      3242 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3301
Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db      3302 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3361
Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db      3362 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3421
Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db      3422 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3481
Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db      3482 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3541
Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
Db      3542 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3601
Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db      3602 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3661
Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db      3662 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3721
Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db      3722 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3781
Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db      3782 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3841
Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db      3842 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3901
Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db      3902 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3961
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Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3962 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020

Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080

Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140

Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200

Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260

Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320

Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380

Qy      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440

Qy      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500

Qy      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560

Qy      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620

Qy      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680

Qy      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740

Qy      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800

Qy      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860

Qy      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920

Qy      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980

Qy      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040

Qy      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100

Qy      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160

Qy      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220

Qy      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280

Qy      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340

Qy      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400

Qy      5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460

Qy      5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520

Qy      5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580

Qy      5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640

Qy      5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700

Qy      5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
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Qy      5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820

Qy      5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880

Qy      5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940

Qy      5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000

Qy      6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060

Qy      6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120

Qy      6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240

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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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Db       6361 GATATATAATTTAAAGTT 6378


RESULT 3
US-10-517-905-1
; Sequence 1, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 6633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (395)..(3664)
US-10-517-905-1

  Query Match             99.2%;  Score 6364.4;  DB 13;  Length 6633;
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  Matches 6376;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436

Qy        181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
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Qy        241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
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Db        497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556

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Qy        481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

Qy        541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856

Qy        601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
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Db        857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916

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Db        917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976

Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Db        977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036

Qy        781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096

Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Db       1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156

Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276

Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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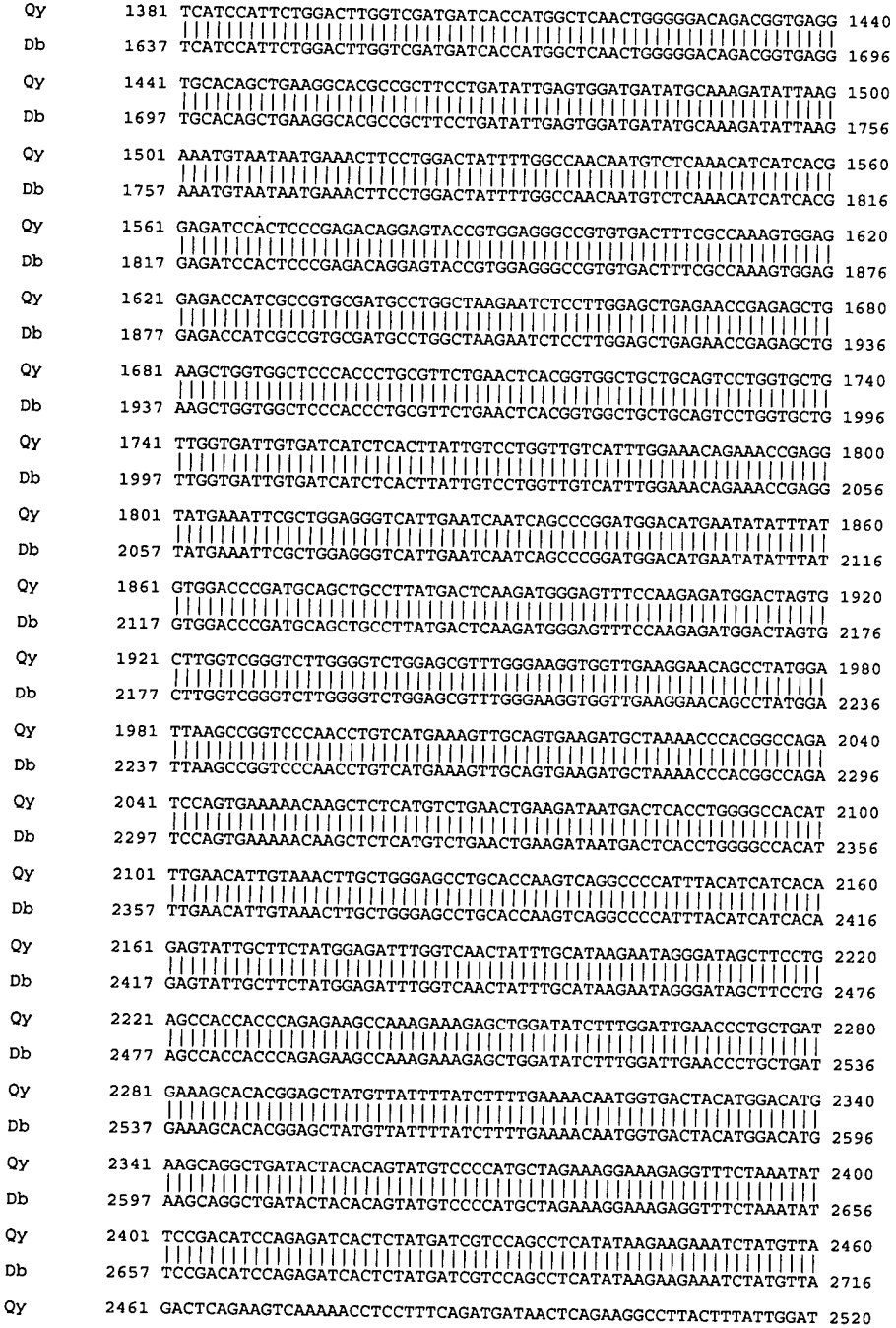
Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396

Qy       1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1456

Qy       1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1457 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1516

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636
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Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db 1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696
Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db 1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756
Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db 1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816
Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db 1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876
Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db 1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936
Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db 2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
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Db 2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
Db 2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476
Qy 2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
Db 2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536
Qy 2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
Db 2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596
Qy 2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
Db 2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656
Qy 2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
Db 2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716
Qy 2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
Db 2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776
Qy 2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
Db 2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836
Qy 2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
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Qy 2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
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Qy 2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
Db 3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
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Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db       3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036

Qy       3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Db       4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096

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             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275

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Db       4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335

Qy       4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
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Db       4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395

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Qy       4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
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Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
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Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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RESULT 4
US-11-148-770-30
; Sequence 30, Application US/11148770
; Publication No. US20060019280A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LEI L.
; APPLICANT: FRAZIER, MARSHA L.
; TITLE OF INVENTION: MUTATIONS IN KIT CONFER IMATINIB RESISTANCE IN
; TITLE OF INVENTION: GASTROINTESTINAL STROMAL TUMORS
; FILE REFERENCE: UTXC:869US
; CURRENT APPLICATION NUMBER: US/11/148,770
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/578,403
; PRIOR FILING DATE: 2004-06-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-148-770-30

Query Match 99.2%; Score 6364.4; DB 17; Length 6633;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6376; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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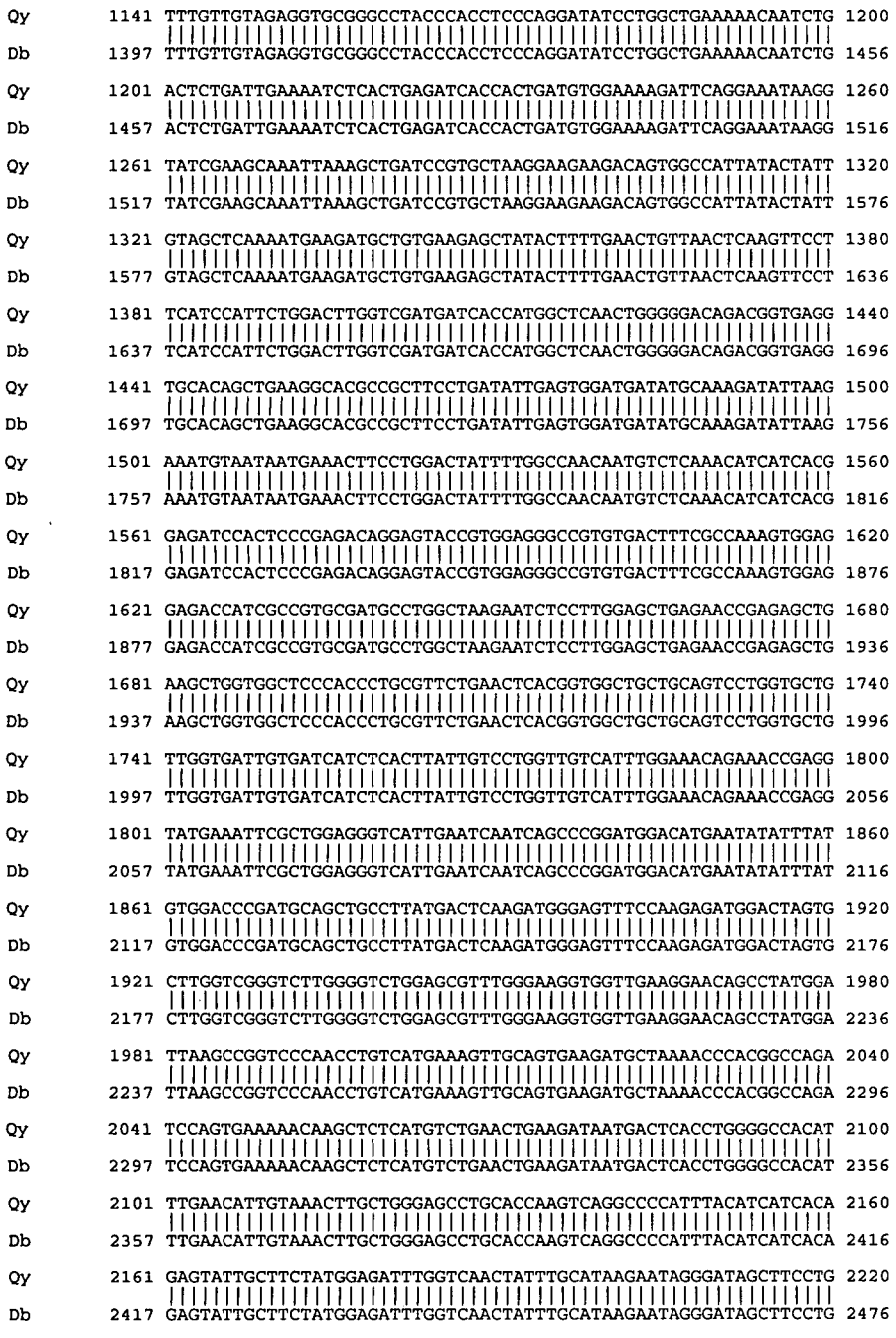
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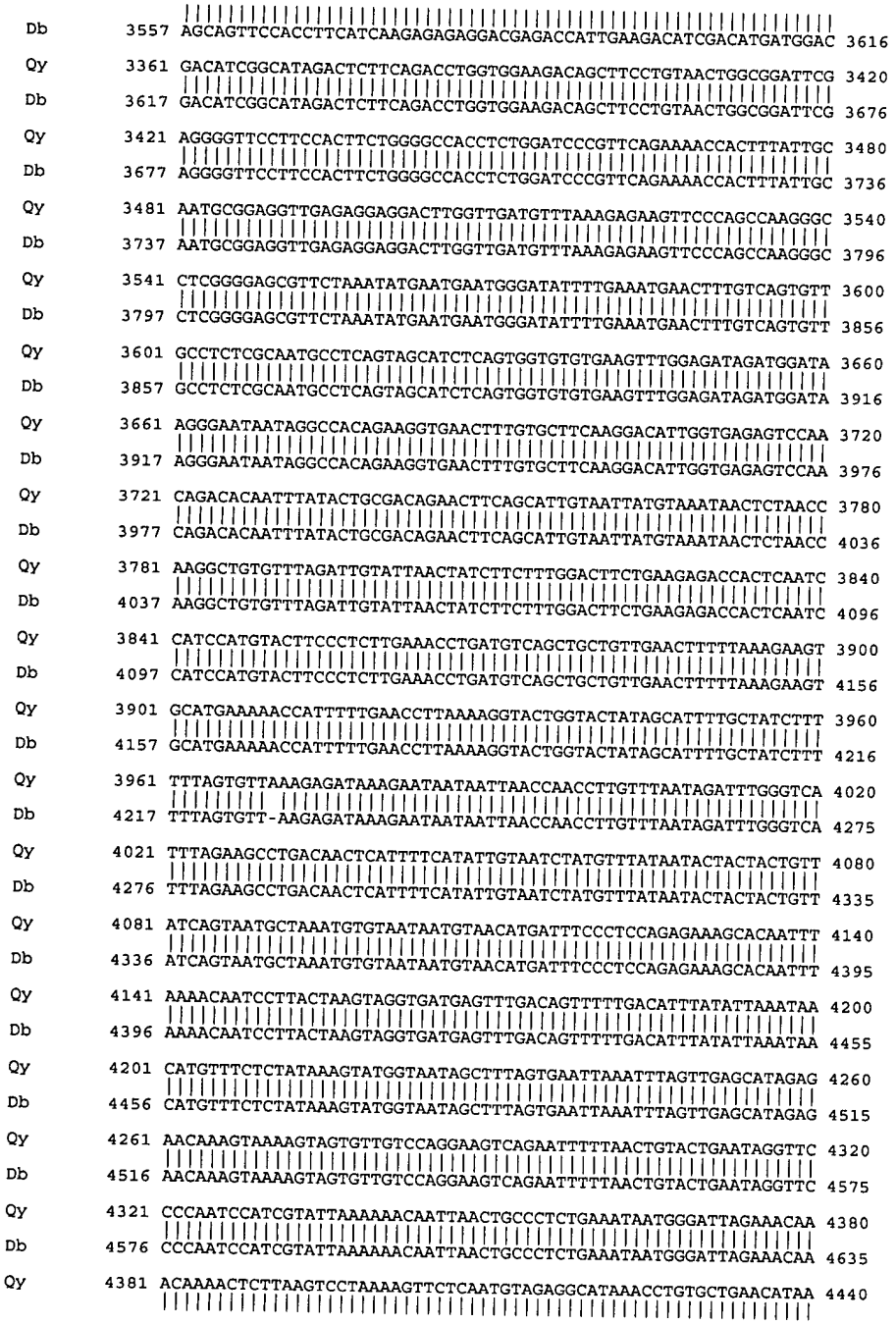
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Db       1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216

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RESULT 5
US-10-517-905-3
; Sequence 3, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3664)
US-10-517-905-3

Query Match 99.2%; Score 6362.8; DB 13; Length 6633;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6375; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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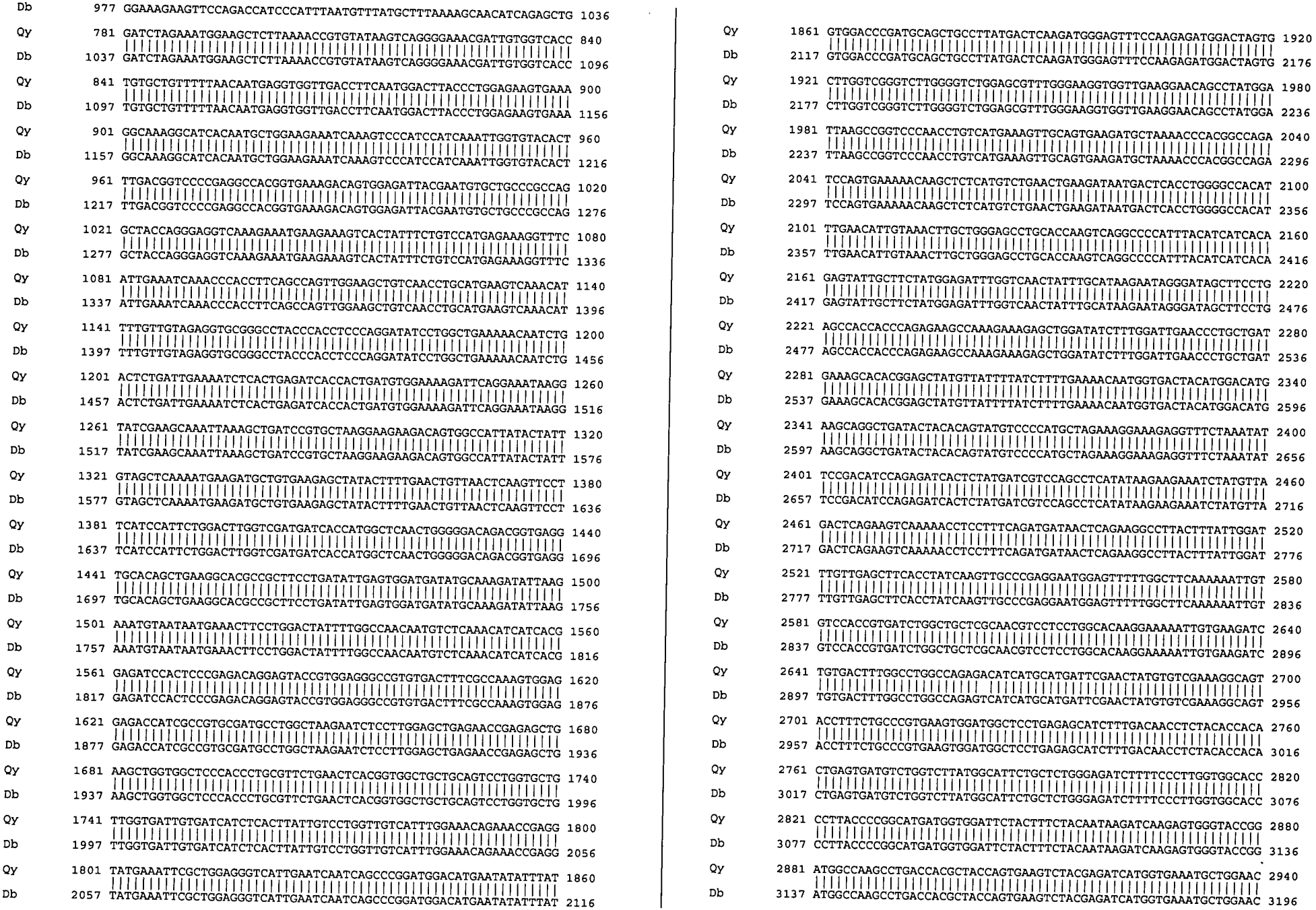
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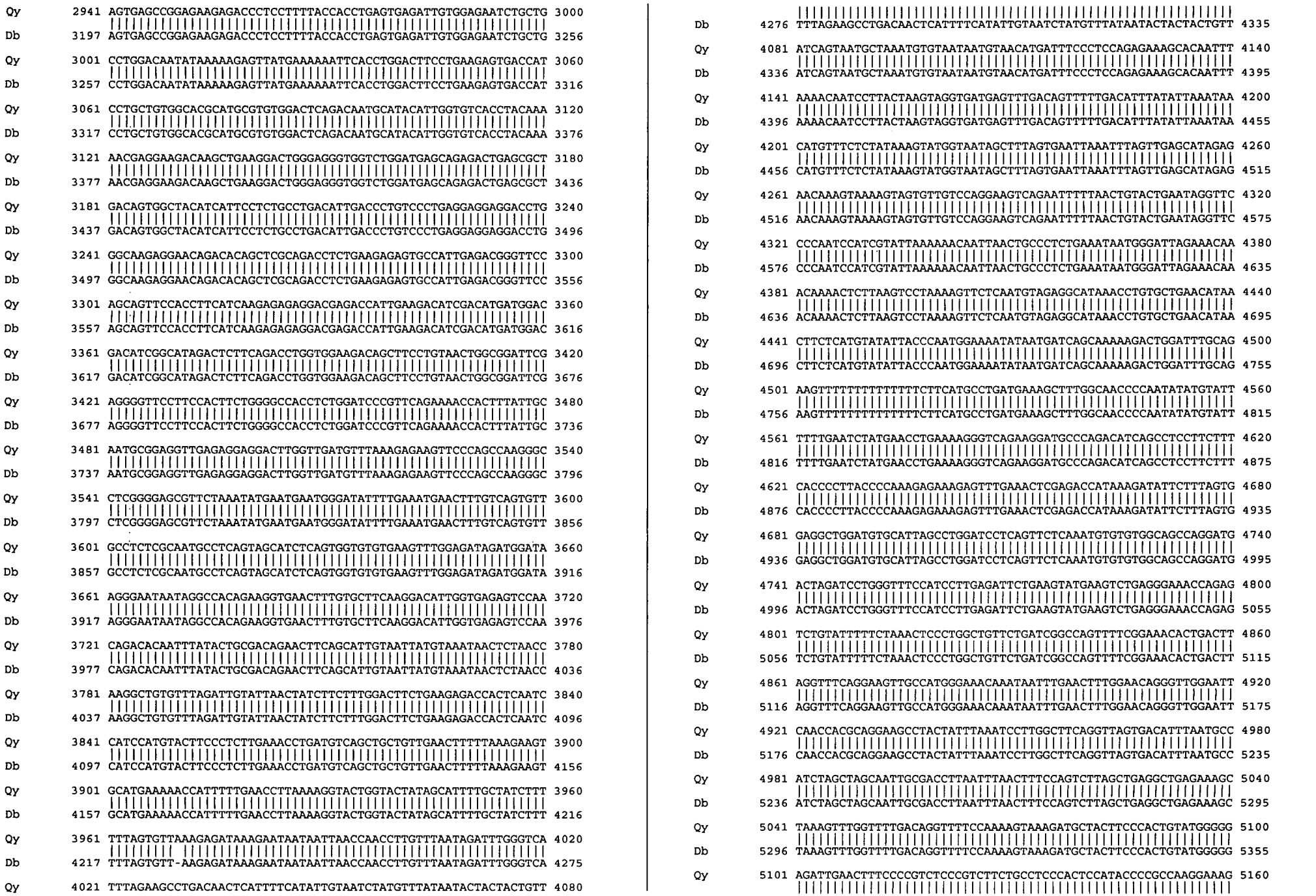
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RESULT 6
US-10-517-905-20
; Sequence 20, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3664)
US-10-517-905-20

Query Match 99.2%; Score 6362.8; DB 13; Length 6633;
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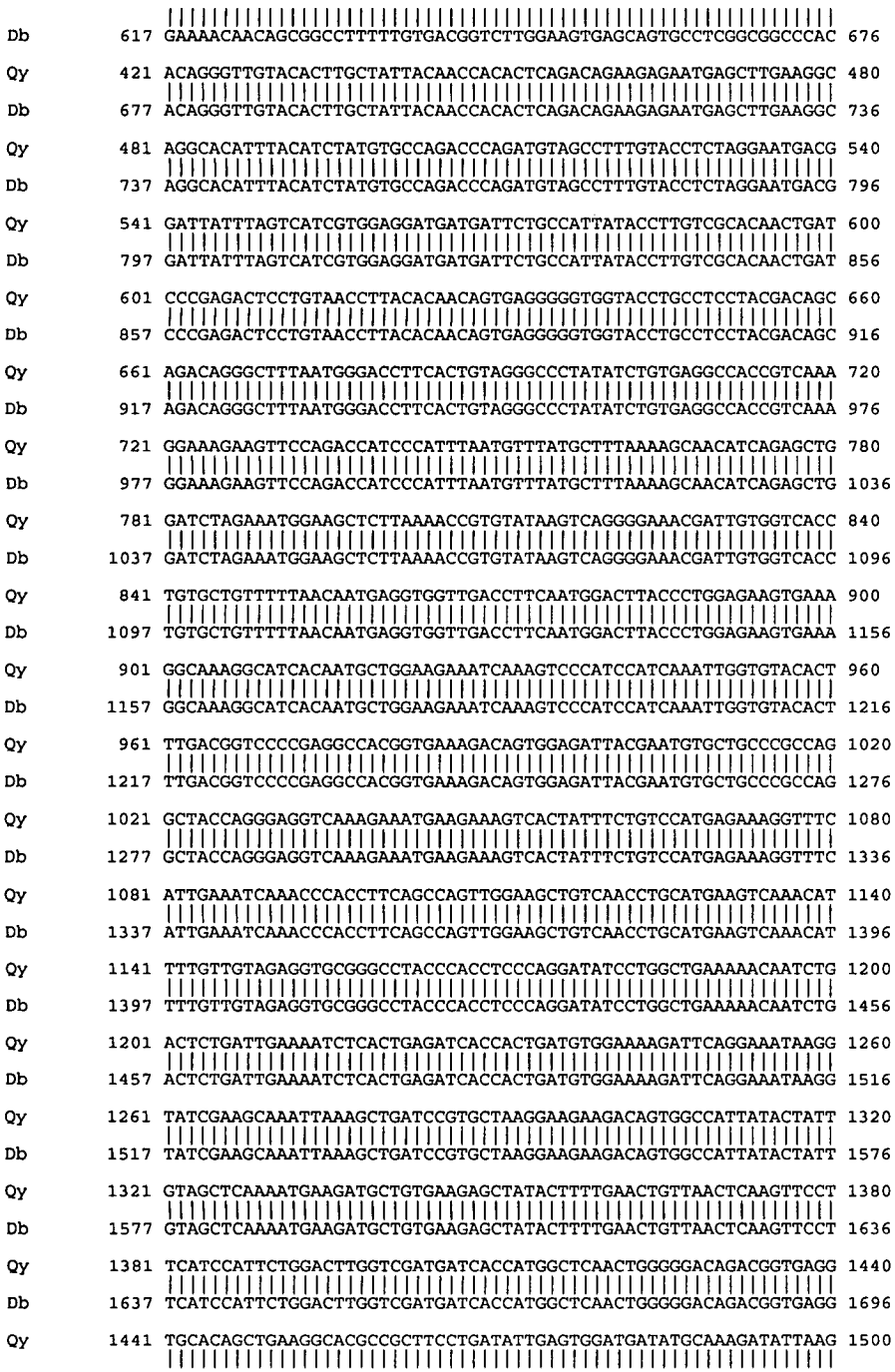
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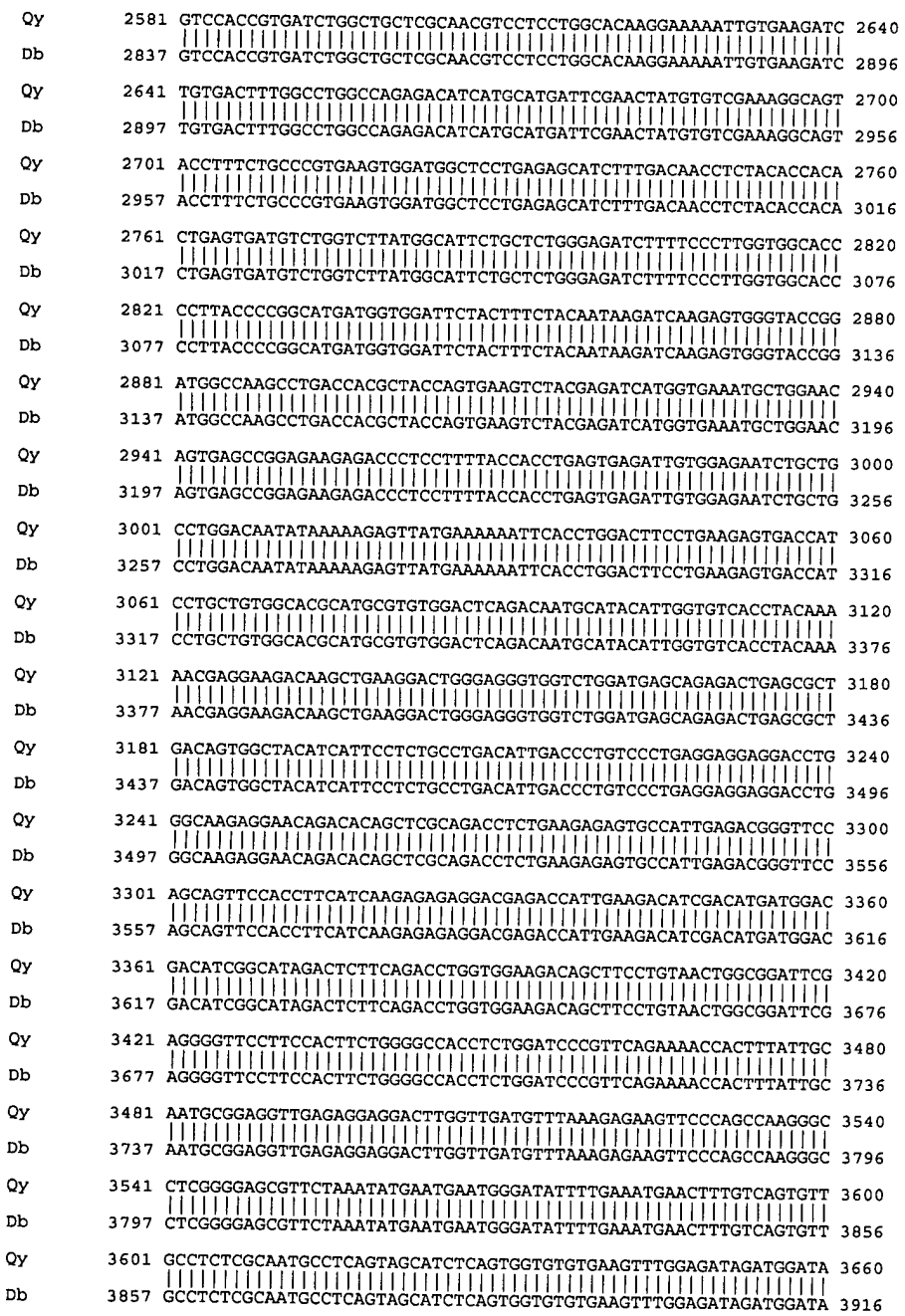
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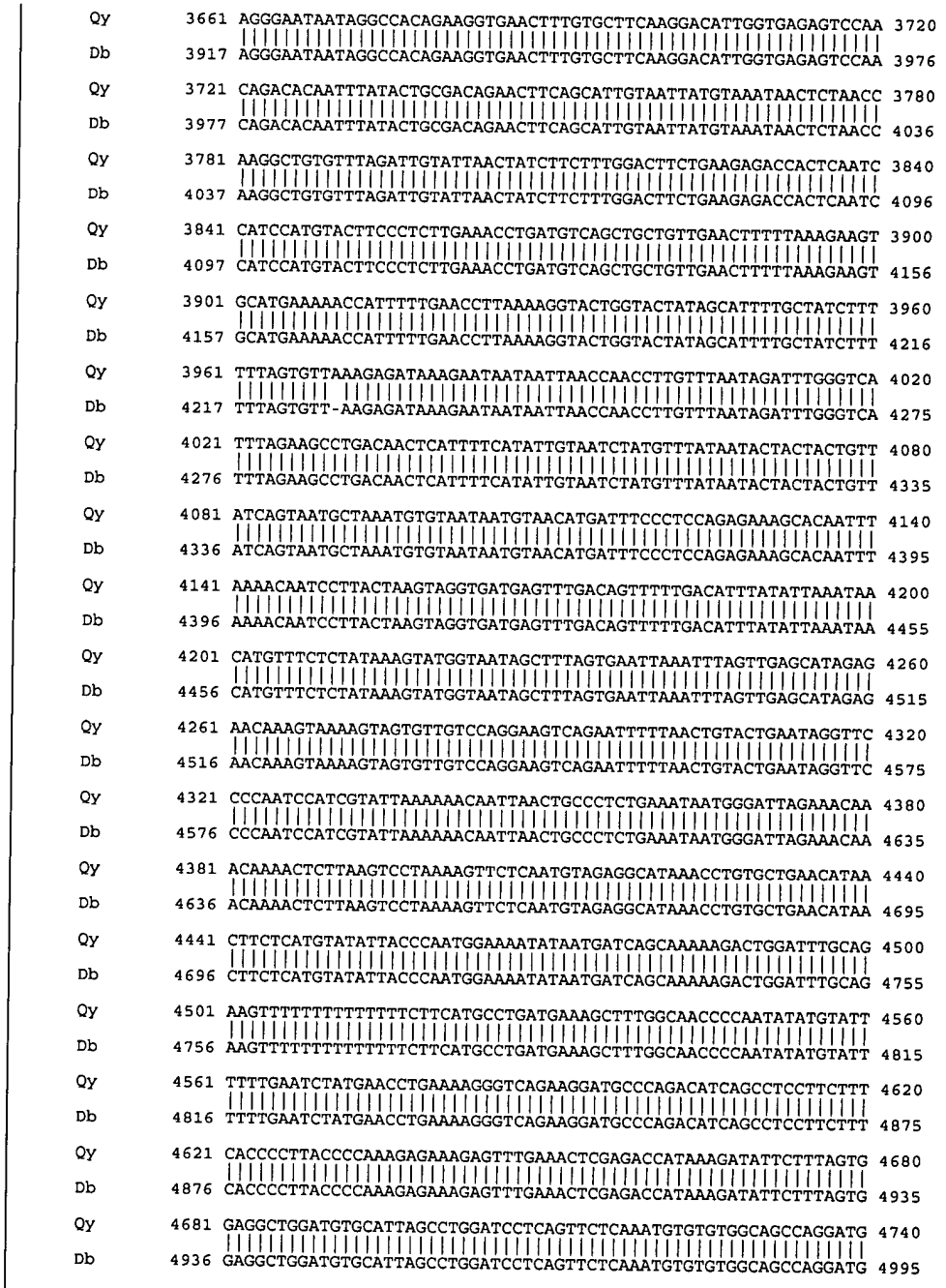
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Db 2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476
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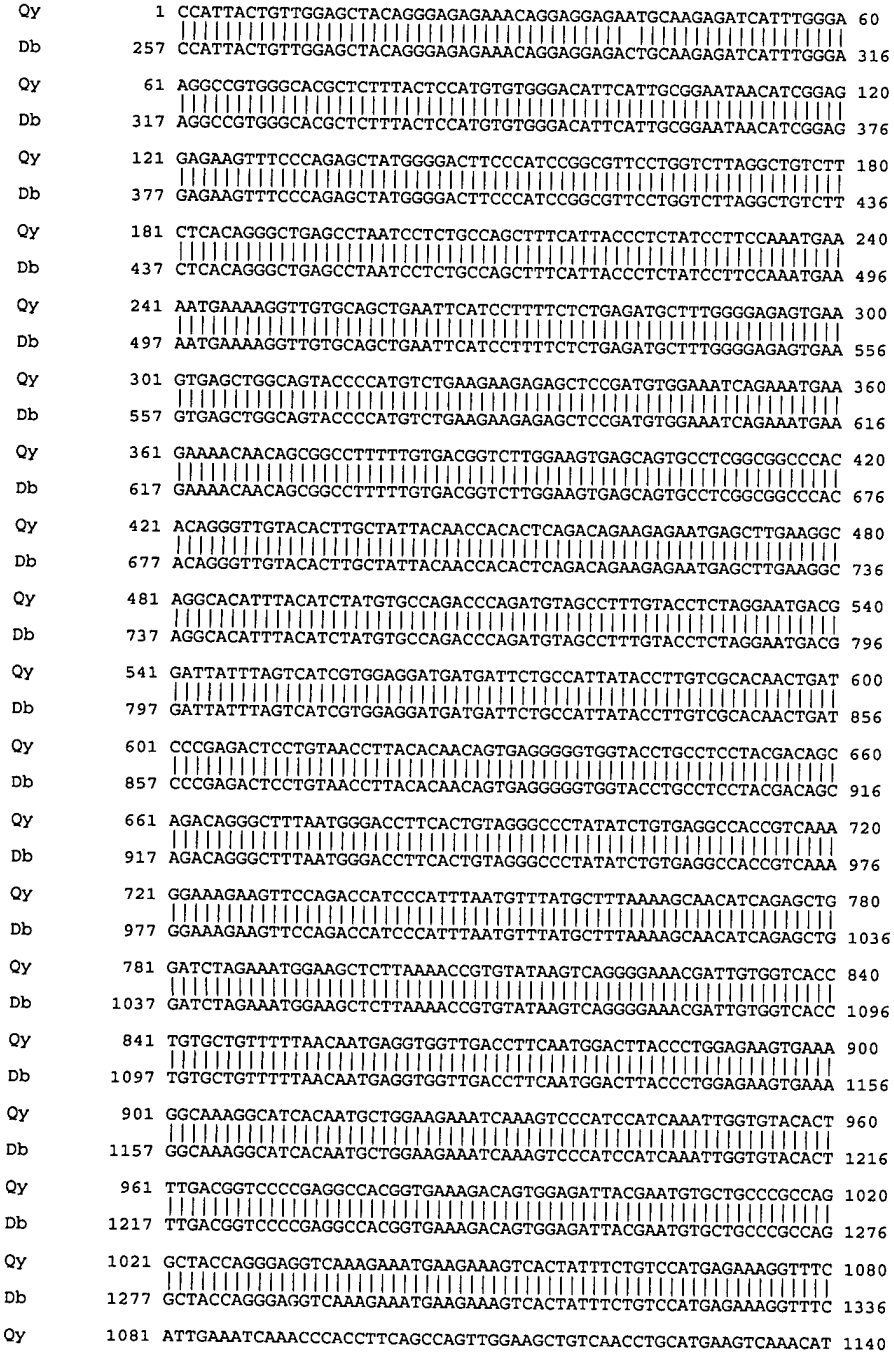
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RESULT 7
US-10-517-905-24
; Sequence 24, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 6633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3664)
US-10-517-905-24

Query Match 99.2%; Score 6359.6; DB 13; Length 6633;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6373; Conservative 0; Mismatches 4; Indels 1; Gaps 1;


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Db 377 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 436
Qy 181 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 240
Db 437 CTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAA 496
Qy 241 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 300
Db 497 AATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAA 556
Qy 301 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 360
Db 557 GTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAA 616
Qy 361 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 420
Db 617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676
Qy 421 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 480
Db 677 ACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGC 736
Qy 481 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 540
Db 737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796
Qy 541 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 600
Db 797 GATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGAT 856
Qy 601 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 660
Db 857 CCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGC 916
Qy 661 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 720
Db 917 AGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAA 976
Qy 721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
Db 977 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 1036
Qy 781 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 840
Db 1037 GATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACC 1096
Qy 841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
Db 1097 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 1156
Qy 901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
Db 1157 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 1216
Qy 961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
Db 1217 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1276
Qy 1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
Db 1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336
Qy 1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
Db 1337 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1396
Qy 1141 TTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTG 1200
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Qy 1201 ACTCTGATTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
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Qy 1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
Db 1517 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1576
Qy 1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
Db 1577 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1636
Qy 1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
Db 1637 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1696
Qy 1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
Db 1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756
Qy 1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
Db 1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816
Qy 1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
Db 1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876
Qy 1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
Db 1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936
Qy 1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
Db 1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996
Qy 1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
Db 1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056
Qy 1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
Db 2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116
Qy 1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
Db 2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176
Qy 1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
Db 2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236
Qy 1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
Db 2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296
Qy 2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
Db 2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356
Qy 2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
Db 2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416
Qy 2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220

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Db      2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476

Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536

Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596

Qy      2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656

Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716

Qy      2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776

Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836

Qy      2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2837 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2896

Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
             |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Db      2897 TGTGACTTTGGCCTGGCCAAAATCATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2956

Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2957 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3016

Qy      2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3017 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3076

Qy      2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3077 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3136

Qy      2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3137 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3196

Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3197 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3256

Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Db      3257 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3316

Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3317 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3376

Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3377 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3436

Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3437 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3496

Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3497 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3556

Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3557 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3616

Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3617 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3676

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3677 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3736

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3737 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3796

Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3797 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3856

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3857 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3916

Qy      3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3917 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3976

Qy      3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3977 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4036

Qy      3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4037 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4096

Qy      3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
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Db      4097 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4156

Qy      3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4157 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4216

Qy      3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4217 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4275

Qy      4021 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4276 TTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTT 4335

Qy      4081 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4336 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4395

Qy      4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4396 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4455

Qy      4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4456 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4515

Qy      4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4516 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4575

Qy      4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4576 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4635
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Qy       4381 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4440
Db       4636 ACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAA 4695

Qy       4441 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4500
Db       4696 CTTCTCATGTATATTACCCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAG 4755

Qy       4501 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4560
Db       4756 AAGTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4815

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
Db       4816 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4875

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
Db       4876 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4935

Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
Db       4936 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4995

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
Db       4996 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5055

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
Db       5056 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5115

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
Db       5116 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5175

Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
Db       5176 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 5235

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
Db       5236 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5295

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
Db       5296 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5355

Qy       5101 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5160
Db       5356 AGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAG 5415

Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Db       5416 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5475

Qy       5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db       5476 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5535

Qy       5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Db       5536 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5595

Qy       5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db       5596 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5655

Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db       5656 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5715

Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
Db       5716 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5775

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
Db       5776 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5835

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
Db       5836 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5895

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
Db       5896 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5955

Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
Db       5956 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 6015

Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
Db       6016 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6075

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
Db       6076 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6135

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
Db       6136 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6195

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
Db       6196 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6255

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Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Qy       6361 GATATATAATTTAAAGTT 6378
Db       6616 GATATATAATTTAAAGTT 6633
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RESULT 8
US-10-517-905-9
; Sequence 9, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred

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;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 6639
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (395)..(3664)
US-10-517-905-9

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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
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Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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Db       1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816

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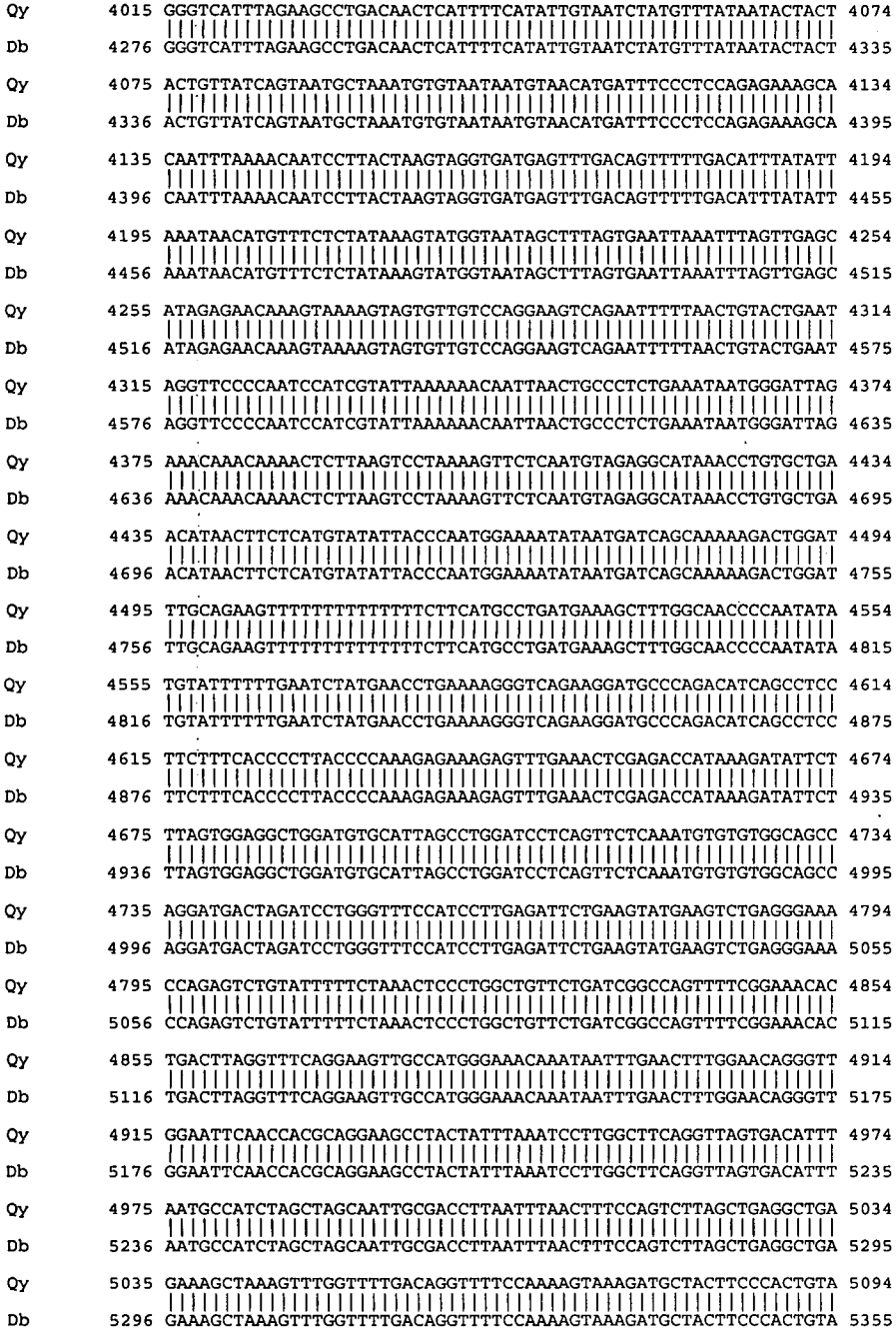
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Qy       2095 CCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATC 2154
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Qy 5155 GGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCA 5214
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Qy 5215 GTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGAT 5274
Db 5476 GTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGAT 5535
Qy 5275 GAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTG 5334
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Qy 5395 CTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTA 5454
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Qy 5755 AATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAA 5814
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Qy 5875 TTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC 5934
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Qy 6115 GTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAAT 6174
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Qy 6175 GTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAA 6234

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Qy      1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
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Db      1697 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1756

Qy      1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1757 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1816

Qy      1561 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1817 GAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAG 1876

Qy      1621 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1877 GAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTG 1936

Qy      1681 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1740
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Db      1937 AAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTG 1996

Qy      1741 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 1800
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Db      1997 TTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGG 2056

Qy      1801 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 1860
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Db      2057 TATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTAT 2116

Qy      1861 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 1920
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Db      2117 GTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTG 2176

Qy      1921 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 1980
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Db      2177 CTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGA 2236

Qy      1981 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2040
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Db      2237 TTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGA 2296

Qy      2041 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2100
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Db      2297 TCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACAT 2356

Qy      2101 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2160
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Db      2357 TTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACA 2416

Qy      2161 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2220
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Db      2417 GAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTG 2476

Qy      2221 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2280
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Db      2477 AGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGAT 2536

Qy      2281 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2340
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Db      2537 GAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATG 2596

Qy      2341 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2400
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Db      2597 AAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATAT 2656

Qy      2401 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2460
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Db      2657 TCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTA 2716

Qy      2461 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2717 GACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGAT 2776

Qy      2521 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2777 TTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGT 2836

Qy      2581 GTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATC 2640
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Qy      2641 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2700
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Db      2897 TGTGACTTTGGCCTGGCCAGAGACATCATGC---------CCTATGTGTCGAAAGGCAGT 2947

Qy      2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
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Db      2948 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3007

Qy      2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3008 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 3067

Qy      2821 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3068 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3127

Qy      2881 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 2940
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Db      3128 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3187

Qy      2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3188 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3247

Qy      3001 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3060
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Db      3248 CCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCAT 3307

Qy      3061 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3308 CCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAA 3367

Qy      3121 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3368 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3427

Qy      3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3428 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3487

Qy      3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3488 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3547

Qy      3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3548 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3607

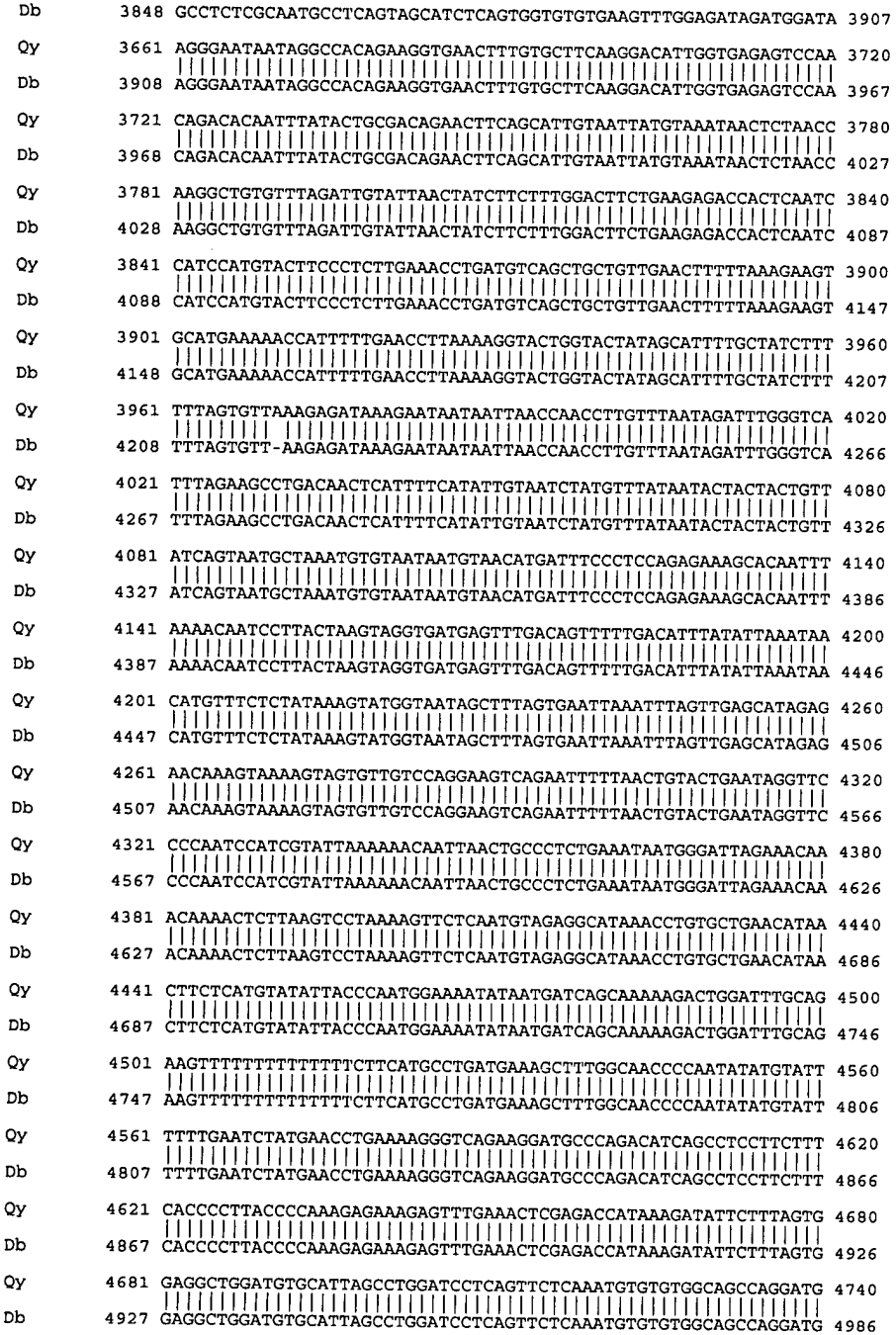
Qy      3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
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Db      3608 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3667

Qy      3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
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Db      3668 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3727

Qy      3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
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Db      3728 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3787

Qy      3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Db      3788 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3847

Qy      3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
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Db 3848 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3907
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3908 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3967
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3968 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4027
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
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Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
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RESULT 10
US-10-517-905-5
; Sequence 5, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3652)
US-10-517-905-5

Query Match 98.7%; Score 6330.4; DB 13; Length 6621;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 6364; Conservative 0; Mismatches 1; Indels 13; Gaps 2;

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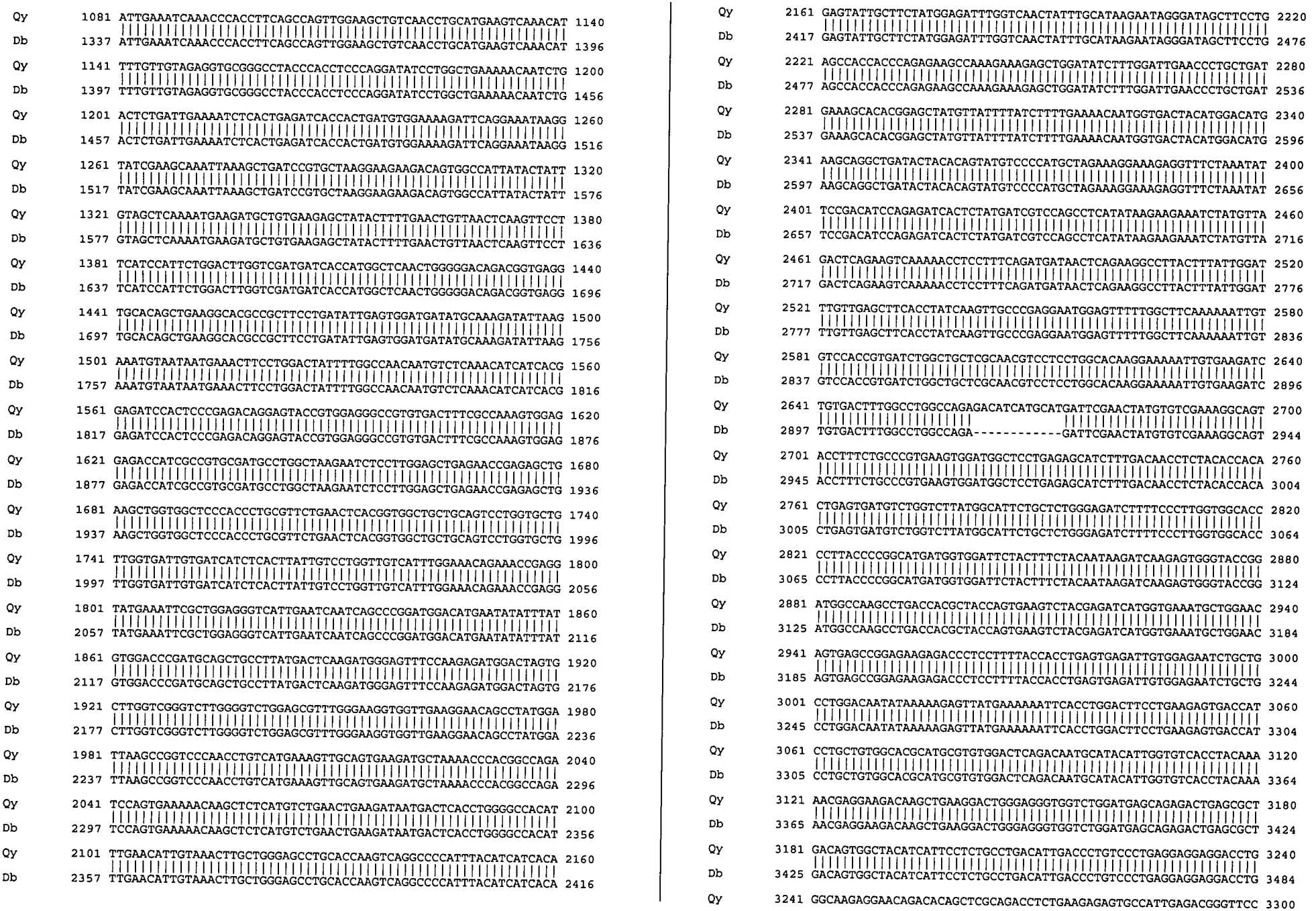
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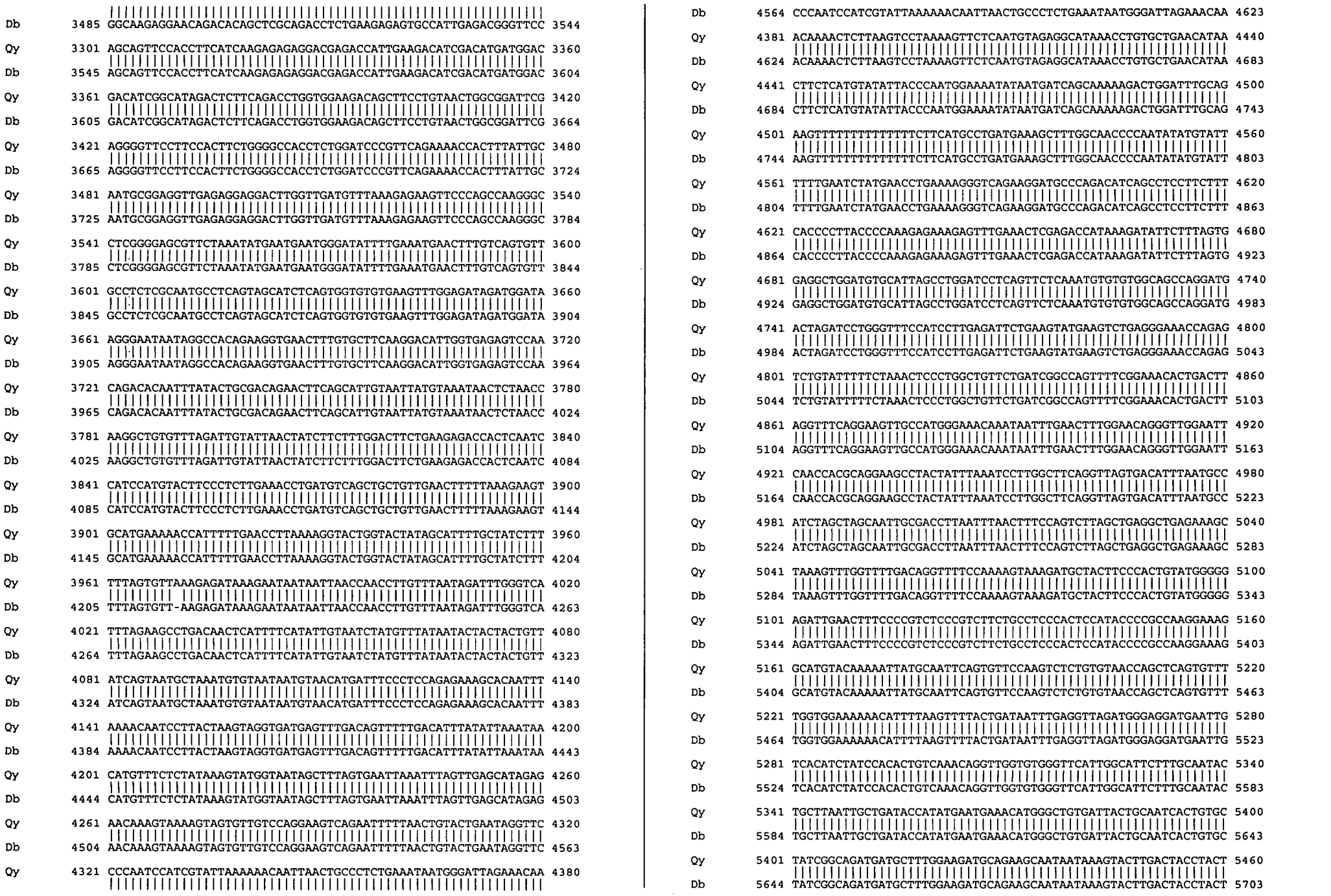
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Db       1277 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1336
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Qy 1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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Qy 5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
Db 5404 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5463
Qy 5221 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5280
Db 5464 TGGTGGAAAAAACATTTTAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTG 5523
Qy 5281 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5340
Db 5524 TCACATCTATCCACACTGTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATAC 5583
Qy 5341 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5400
Db 5584 TGCTTAATTGCTGATACCATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGC 5643
Qy 5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
Db 5644 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5703

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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5704 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5763

Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5764 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5823

Qy       5581 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5824 ACTTGAAATACGTTTGTGTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTC 5883

Qy       5641 TCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCA 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5701 TGACATCATGAGGCCGGATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCT 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       5761 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6004 CCCACCTGAATTTGTATATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCA 6063

Qy       5821 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6064 GATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTA 6123

Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6124 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 6183

Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6184 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6243

Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6244 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6303

Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6304 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6363

Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6364 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6423

Qy       6181 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6240
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Db       6424 AATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGT 6483

Qy       6241 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6300
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Db       6484 GGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAAT 6543

Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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RESULT 11
US-10-995-561-312
; Sequence 312, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 312
;   LENGTH: 6633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-312

  Query Match             98.7%;  Score 6326.6;  DB 10;  Length 6633;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 6356;  Conservative   15;  Mismatches    4;  Indels    6;  Gaps    3;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  ||||||||| |||||||||||||| |
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Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
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Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
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Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
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Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGC 778
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Qy        779 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 TGGATCTAGAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCA 1093
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Qy       839 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 898
Db      1094 CCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGA 1153

Qy       899 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 958
Db      1154 AAGGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACA 1213

Qy       959 CTTTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCC 1018
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Qy      1019 AGGCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTT 1078
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Qy      1319 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1378
Db      1574 TTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTC 1633

Qy      1379 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1438
Db      1634 CTTCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGA 1693

Qy      1439 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1498
Db      1694 GGTGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTA 1753

Qy      1499 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1558
Db      1754 AGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCA 1813

Qy      1559 CGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1618
Db      1814 CGGAGATCCACYCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGG 1873

Qy      1619 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1678
Db      1874 AGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGC 1933

Qy      1679 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1738
Db      1934 TGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGC 1993

Qy      1739 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 1798
Db      1994 TGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGA 2053

Qy      1799 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTT 1858
Db      2054 GGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCRGATGGACATGAATATATTT 2113

Qy      1859 ATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAG 1918
Db      2114 ATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAG 2173

Qy      1919 TGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATG 1978

Db      2174 TGCTTGGTCGGGTCTTGGGGTCTGGAGCRTTTGGGAAGGTGGTTGAAGGAACAGCCTATG 2233

Qy      1979 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2038
Db      2234 GATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCA 2293

Qy      2039 GATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCAC 2098
Db      2294 GATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCAC 2353

Qy      2099 ATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCA 2158
Db      2354 ATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCA 2413

Qy      2159 CAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCC 2218
Db      2414 CAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCC 2473

Qy      2219 TGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTG 2278
Db      2474 TGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTG 2533

Qy      2279 ATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACA 2338
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Qy      2339 TGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAAT 2398
Db      2594 TGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAAT 2653

Qy      2399 ATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGT 2458
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Qy      2459 TAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGG 2518
Db      2714 TAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGG 2773

Qy      2519 ATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATT 2578
Db      2774 ATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATT 2833

Qy      2579 GTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGA 2638
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Qy      2639 TCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCA 2698
Db      2894 TCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCA 2953

Qy      2699 GTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCA 2758
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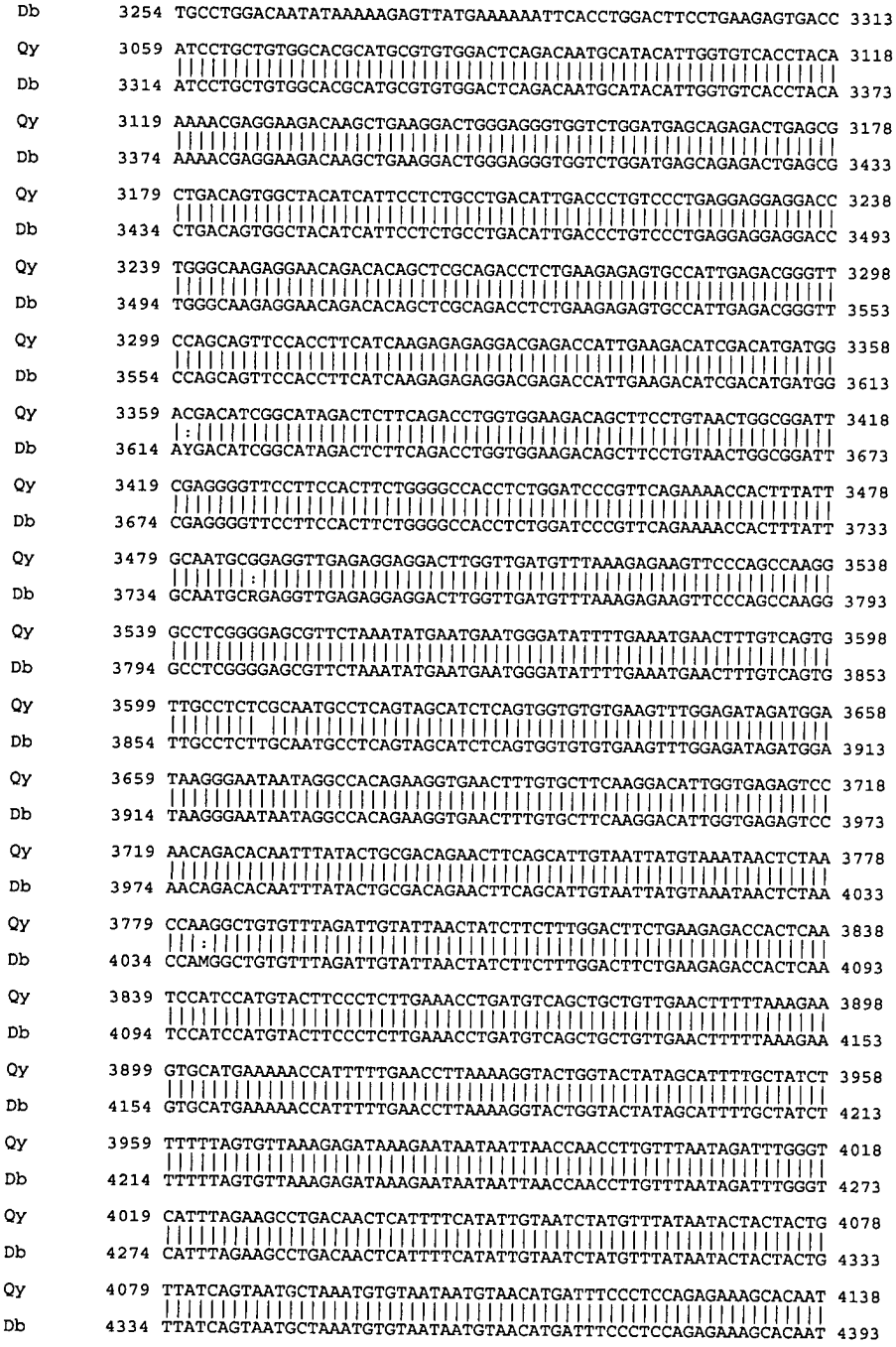
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Qy      2819 CCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACC 2878
Db      3074 CCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACC 3133

Qy      2879 GGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGA 2938
Db      3134 GGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGA 3193

Qy      2939 ACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGC 2998
Db      3194 ACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGC 3253

Qy      2999 TGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACC 3058
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Db 3254 TGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACC 3313
Qy 3059 ATCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACA 3118
Db 3314 ATCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACA 3373
Qy 3119 AAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCG 3178
Db 3374 AAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCG 3433
Qy 3179 CTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACC 3238
Db 3434 CTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACC 3493
Qy 3239 TGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTT 3298
Db 3494 TGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTT 3553
Qy 3299 CCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGG 3358
Db 3554 CCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGG 3613
Qy 3359 ACGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATT 3418
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RESULT 12
US-10-517-905-22
; Sequence 22, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 6618
; TYPE: DNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3649)
US-10-517-905-22

Query Match 98.6%; Score 6324.4; DB 13; Length 6618;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 6361; Conservative 0; Mismatches 1; Indels 16; Gaps 2;

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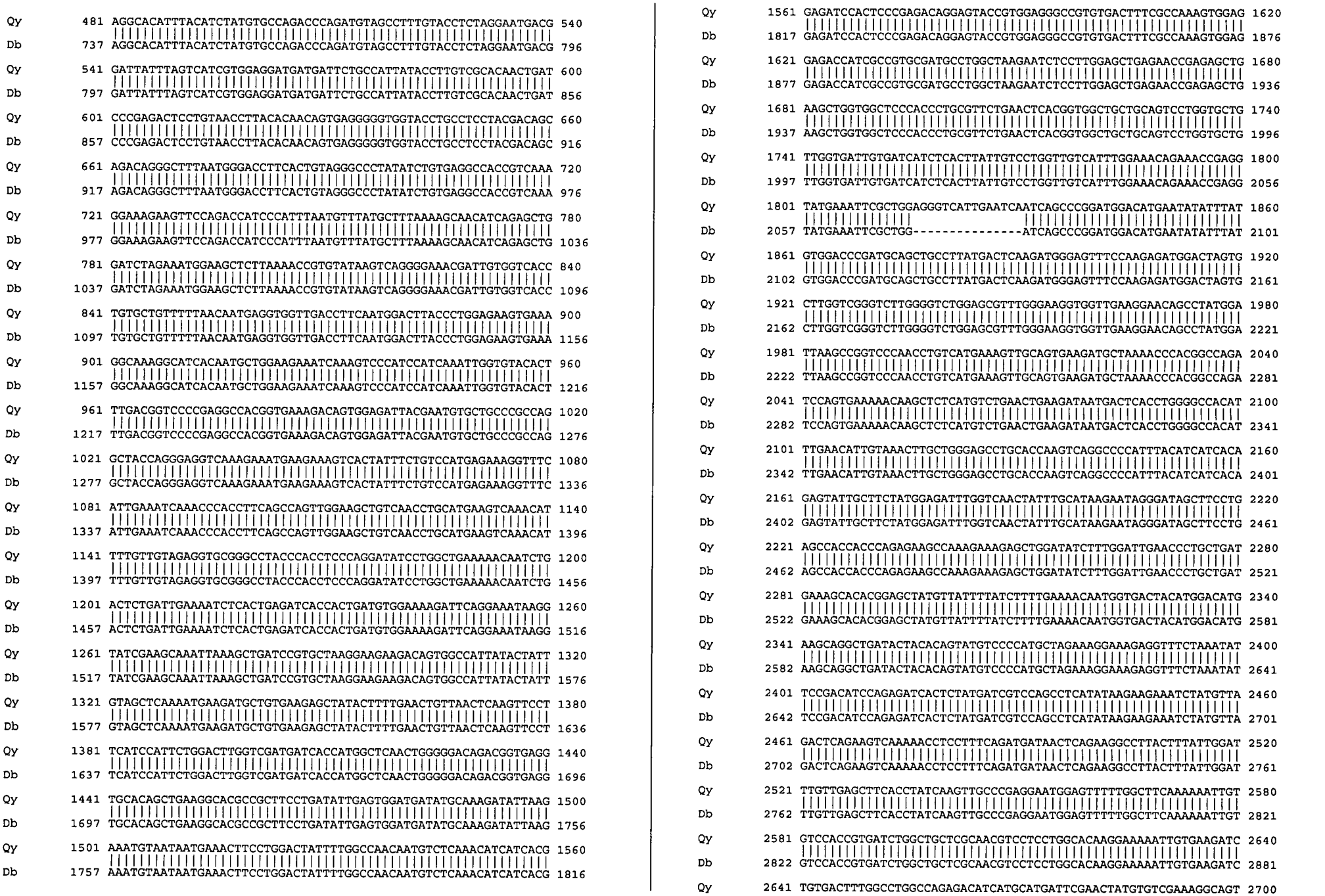
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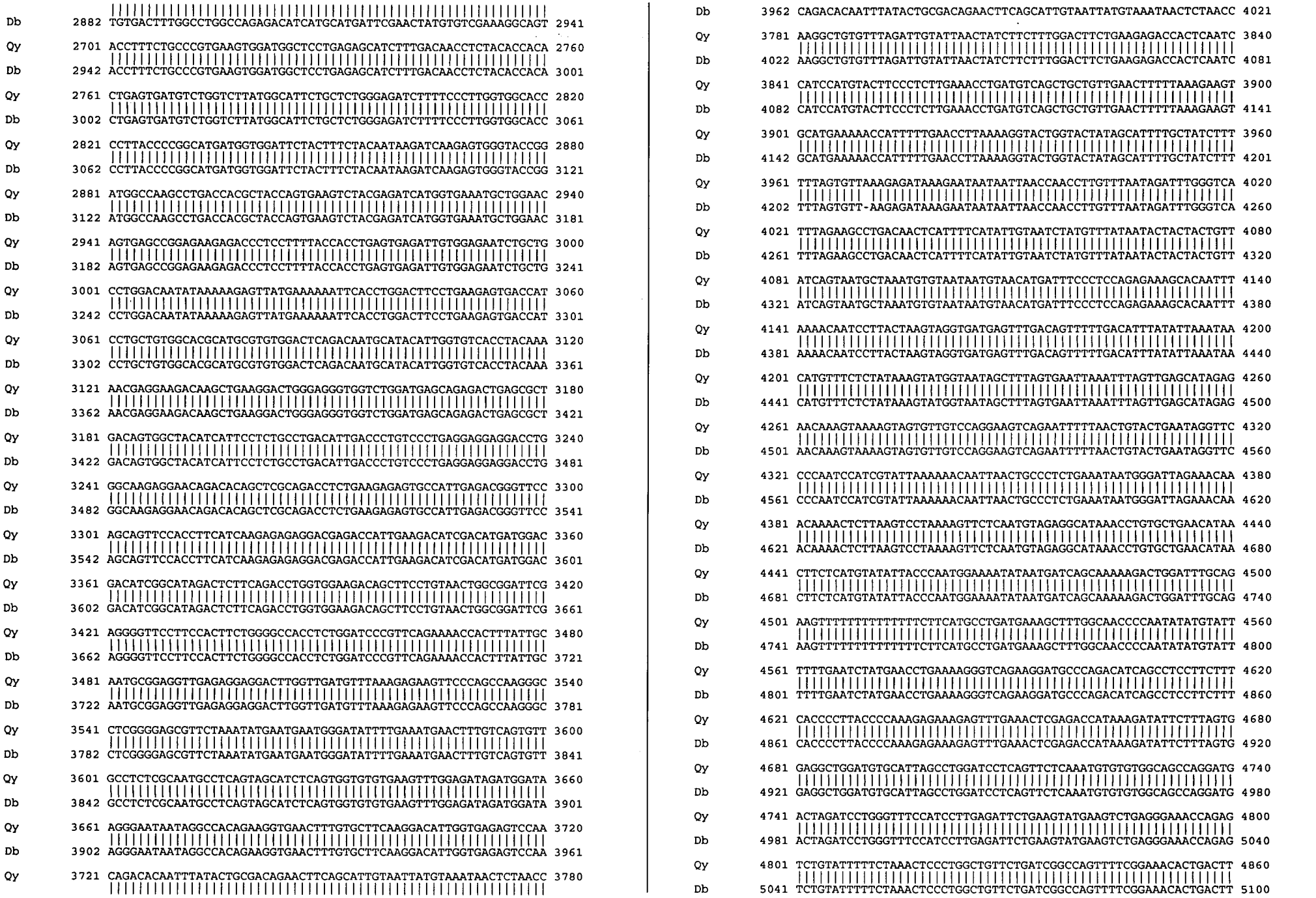
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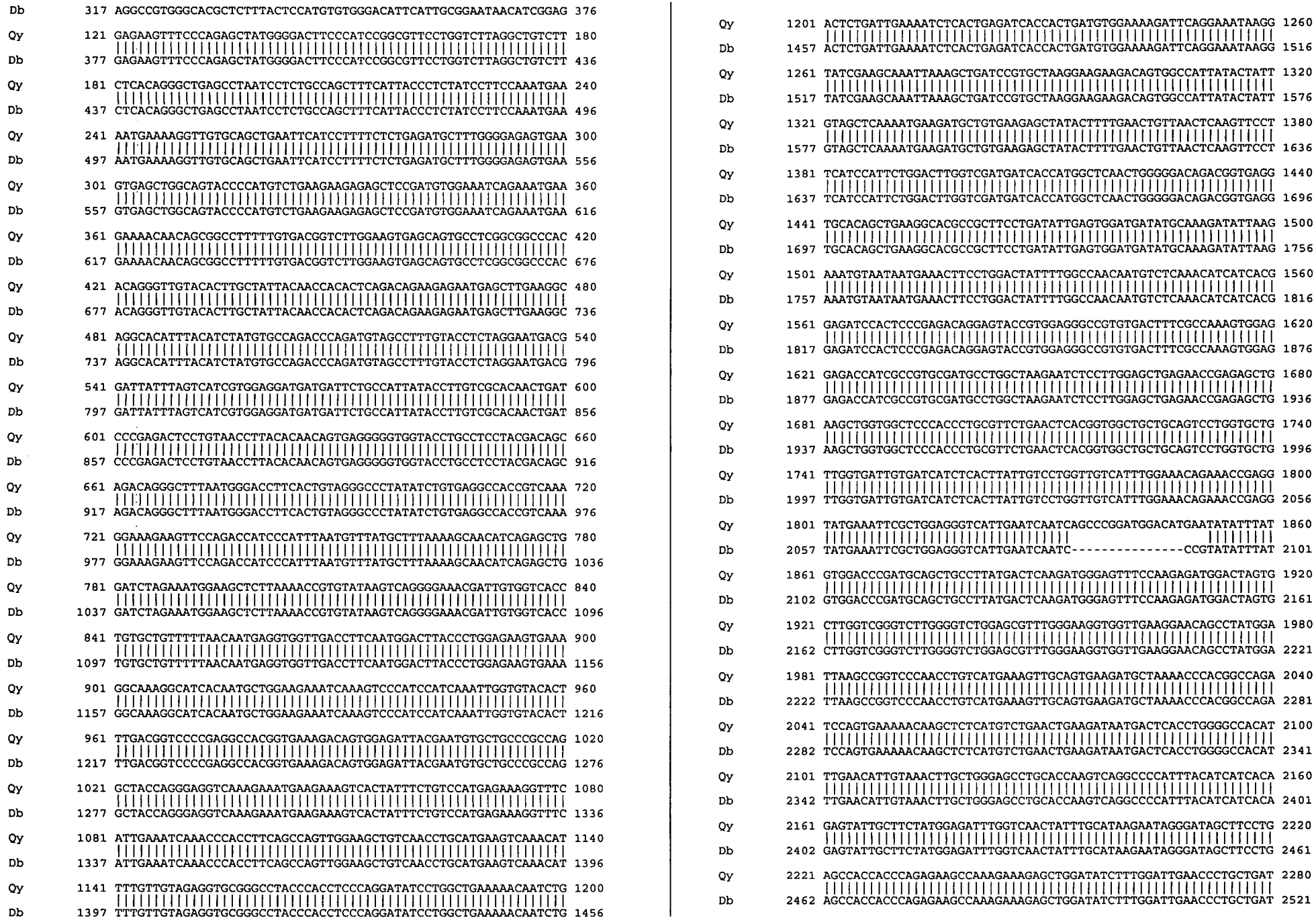
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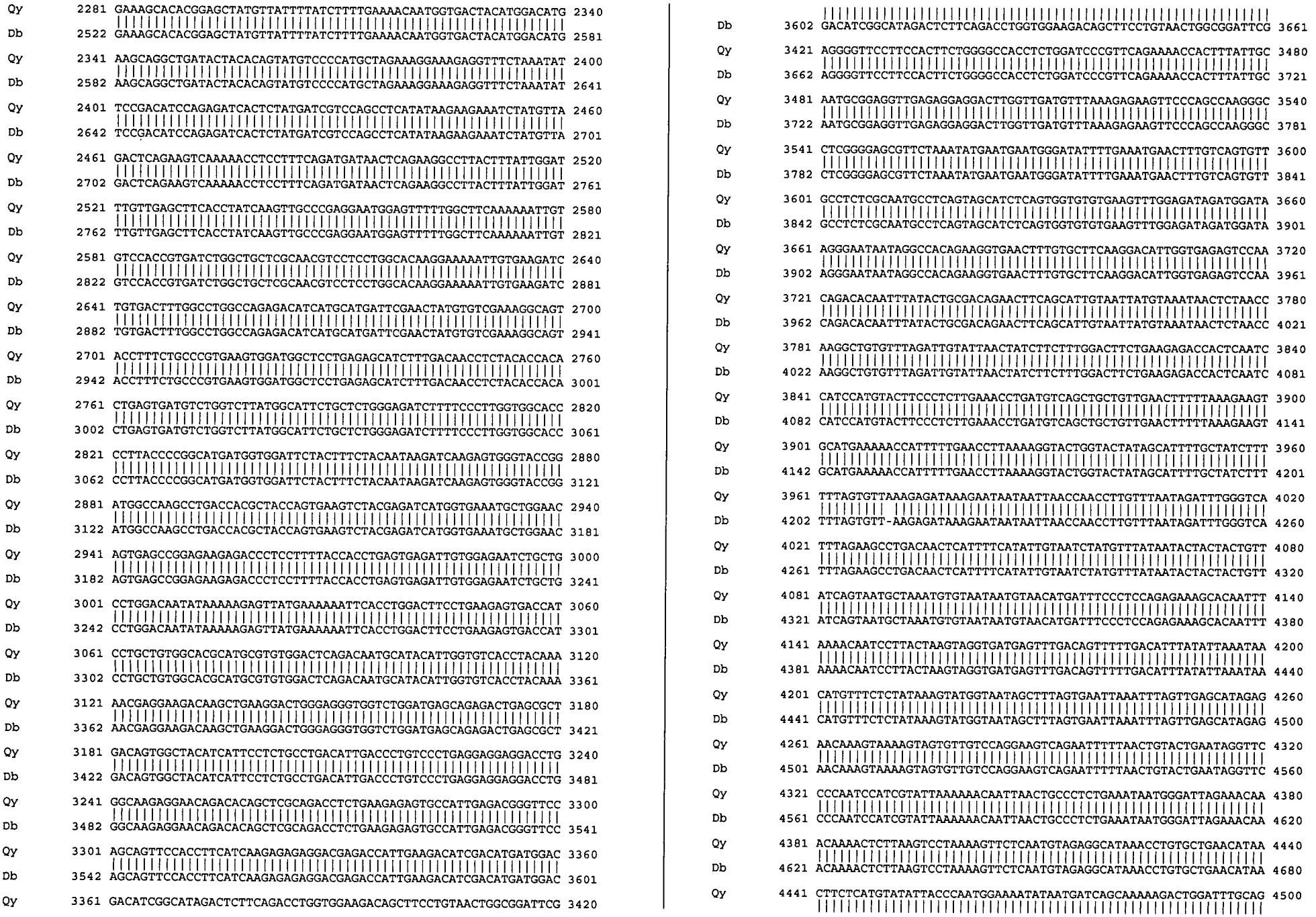
RESULT 13
US-10-517-905-11
; Sequence 11, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/389,107
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/438,899
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 6618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (395)..(3649)
US-10-517-905-11

Query Match 98.5%; Score 6319.6; DB 13; Length 6618;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 6358; Conservative 0; Mismatches 4; Indels 16; Gaps 2;

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Db 2882 TGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGT 2941
Qy 2701 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 2760
Db 2942 ACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACA 3001
Qy 2761 CTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACC 2820
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Db 3062 CCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGG 3121
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Db 3122 ATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAAC 3181
Qy 2941 AGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTG 3000
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Db 3362 AACGAGGAAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCT 3421
Qy 3181 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3240
Db 3422 GACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTG 3481
Qy 3241 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3300
Db 3482 GGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCC 3541
Qy 3301 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3360
Db 3542 AGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGAC 3601
Qy 3361 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3420
Db 3602 GACATCGGCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCG 3661
Qy 3421 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3480
Db 3662 AGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGC 3721
Qy 3481 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3540
Db 3722 AATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGC 3781
Qy 3541 CTCGGGGAGCGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTT 3600
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Qy 3601 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3660
Db 3842 GCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATA 3901
Qy 3661 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3720
Db 3902 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAA 3961
Qy 3721 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 3780
Db 3962 CAGACACAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACC 4021
Qy 3781 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 3840
Db 4022 AAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATC 4081
Qy 3841 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 3900
Db 4082 CATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGT 4141
Qy 3901 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 3960
Db 4142 GCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTT 4201
Qy 3961 TTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4020
Db 4202 TTTAGTGTT-AAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCA 4260
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Db 4321 ATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT 4380
Qy 4141 AAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAA 4200
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Qy 4201 CATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAG 4260
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Qy 4261 AACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTC 4320
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Qy 4321 CCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAA 4380
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Db       4741 AAGTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATT 4800

Qy       4561 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 TTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTT 4860

Qy       4621 CACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTG 4680
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Qy       4681 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATG 4980

Qy       4741 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 4800
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Db       4981 ACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAG 5040

Qy       4801 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 4860
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Db       5041 TCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTT 5100

Qy       4861 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 4920
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Db       5101 AGGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATT 5160

Qy       4921 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 4980
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Db       5161 CAACCACGCAGGAAGCCTACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCC 5220

Qy       4981 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5040
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Db       5221 ATCTAGCTAGCAATTGCGACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGC 5280

Qy       5041 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5100
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Db       5281 TAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGG 5340

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Qy       5161 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5220
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Db       5401 GCATGTACAAAAATTATGCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTT 5460

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Qy       5401 TATCGGCAGATGATGCTTTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACT 5460
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Qy       5461 GGTGTAATCTCAATGCAAGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAG 5520
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Qy       5521 ACTGAGCCAGATTGGCCAATTAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAG 5580
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Qy       5881 CTTTCTATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTA 5940
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Qy       5941 AACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTT 6000
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Qy       6001 GTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATGTATTTCTAT 6060
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Qy       6061 ATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTAT 6120
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Qy       6121 ATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAA 6180
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Qy       6301 GCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAAT 6360
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RESULT 14
US-10-517-905-26
; Sequence 26, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Michael, Heinrich Charles
; APPLICANT: Corless, Christopher Lee
; APPLICANT: Fletcher, Jonathan Alfred
; APPLICANT: Demetri, George D.
; TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
; FILE REFERENCE: 899-65892-02
; CURRENT APPLICATION NUMBER: US/10/517,905
; CURRENT FILING DATE: 2004-12-10

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;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
;   LENGTH: 6633
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (395)..(3664)
;   OTHER INFORMATION: Insertion of the sequence "GAGAGG" in PDGFRA insertion ER561-562
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2072)..(2086)
;   OTHER INFORMATION: Any N may equal either no nucleotide (i.e., a deletion) or any
;   OTHER INFORMATION: nucleotide (i.e., a, t, g, or c)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2074)..(2075)
;   OTHER INFORMATION: Insertion of the sequence "GAGAGG" in PDGFRA insertion ER561-562
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2090)..(2107)
;   OTHER INFORMATION: Any N may equal either no nucleotide (i.e., a deletion) or any
;   OTHER INFORMATION: nucleotide (i.e., a, t, g, or c)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2916)..(2937)
;   OTHER INFORMATION: Any N may equal either no nucleotide (i.e., a deletion) or any
;   OTHER INFORMATION: nucleotide (i.e., a, t, g, or c)
US-10-517-905-26

  Query Match             98.4%;  Score 6310.4;  DB 13;  Length 6633;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 6322;  Conservative    0;  Mismatches   55;  Indels    1;  Gaps    1;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGAATGCAAGAGATCATTTGGGA 60
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Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGATCATTTGGGA 316

Qy         61 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 120
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Db        317 AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAG 376

Qy        121 GAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTT 180
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Db        617 GAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCAC 676

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Db        737 AGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACG 796

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Qy        721 GGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTG 780
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Qy        841 TGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA 900
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Qy        901 GGCAAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACT 960
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Qy        961 TTGACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAG 1020
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Qy       1021 GCTACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTC 1080
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Qy       1081 ATTGAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACAT 1140
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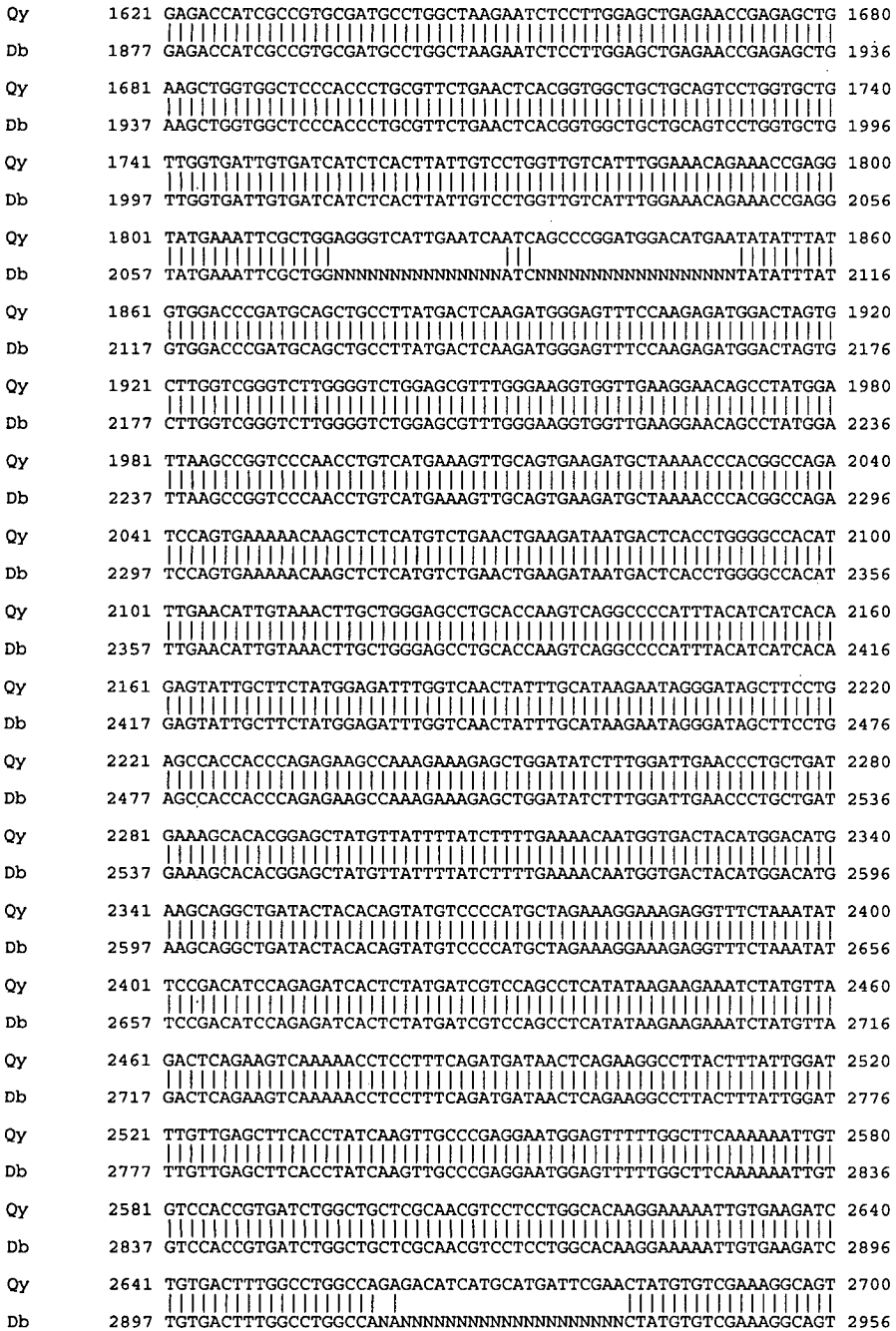
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Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACG 1560
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RESULT 15
US-11-076-427A-13
; Sequence 13, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
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Query Match 74.3%; Score 4765.6; DB 17; Length 6375;
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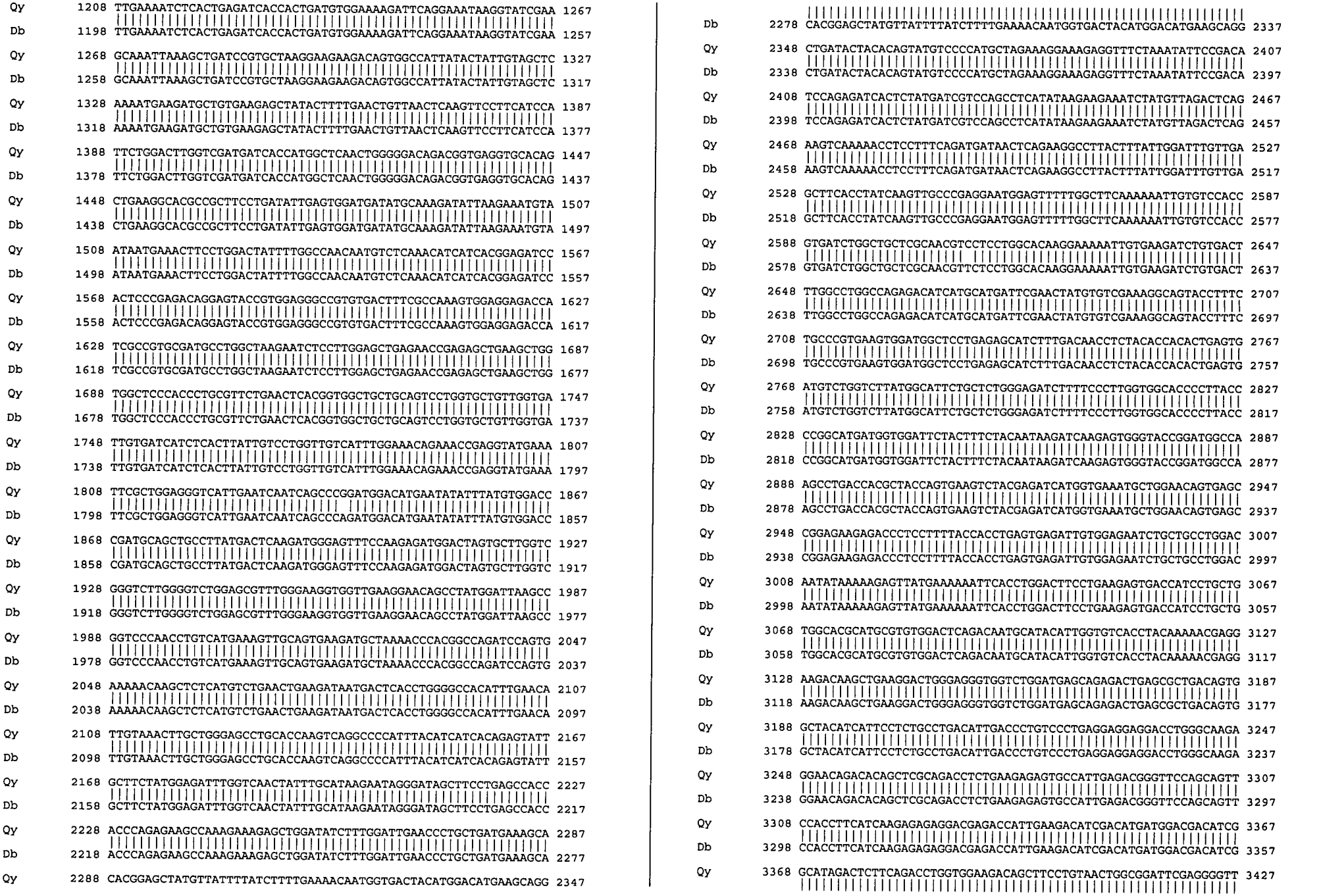
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Qy 2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
Db 2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217
Qy 2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
Db 2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277
Qy 2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGGACTACATGGACATGAAGCAGG 2347
Db 2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337
Qy 2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
Db 2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397
Qy 2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
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Qy 2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
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Qy 2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
Db 2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577
Qy 2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
Db 2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637
Qy 2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
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Qy 2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
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Qy 2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
Db 2758 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2817
Qy 2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
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Db 2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937
Qy 2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
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Qy 3008 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
Db 2998 AATATAAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3057
Qy 3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
Db 3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117
Qy 3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
Db 3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177
Qy 3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
Db 3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237
Qy 3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
Db 3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297
Qy 3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
Db 3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357
Qy 3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427

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Db       3358 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3417

Qy       3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db       3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy       3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Db       3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

Qy       3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
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Db       3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy       3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
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Qy       3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
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Qy       3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
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Db       3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777

Qy       3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

Qy       3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
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Db       3838 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3897

Qy       3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
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Db       3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956

Qy       3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
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Db       3957 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4016

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Db       4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

Qy       4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
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Db       4077 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAATTTAAAAAC 4136

Qy       4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
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Db       4137 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4196

Qy       4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Qy       4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
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Qy       4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Qy       4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
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Db       4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy       4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
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Db       4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496

Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
              || |||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||
Db       4497 TTNTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4556

Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
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Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
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Db       4617 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4676

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
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Db       4677 AGGCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGA 4735

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
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Qy       4802 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTA 4861
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Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
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RESULT 16
US-11-075-047A-116
; Sequence 116, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116
; LENGTH: 6375
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)..(3398)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4476)..(4476)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4499)..(4499)
; OTHER INFORMATION: n is a, c, g, or t
US-11-075-047A-116

Query Match 74.3%; Score 4765.6; DB 18; Length 6375;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 4880; Conservative 0; Mismatches 20; Indels 13; Gaps 9;

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Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
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Db         58 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 117
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Qy       128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Db       118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy       188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
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Db       178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy       248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy       308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
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Db       298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy       368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Qy       548 TAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGA 607
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Qy       608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
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Db       598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy       668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Db       658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy       728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy       788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
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Db       778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy       848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
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Qy       908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Db       898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy       968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
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Db       958 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1017

Qy      1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
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Db      1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy      1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
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Db      1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy      1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy      1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
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Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317

Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377

Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
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Qy      1448 CTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAGAAATGTA 1507
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Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1498 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1557

Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
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Db      1558 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1617

Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
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Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
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Db      1798 TTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACATGAATATATTTATGTGGACC 1857

Qy      1868 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1927
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Db      1858 CGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTC 1917

Qy      1928 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1987
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Db      1918 GGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCC 1977

Qy      1988 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1978 GGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTG 2037

Qy      2048 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2038 AAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACA 2097

Qy      2108 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2098 TTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATT 2157

Qy      2168 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2158 GCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACC 2217

Qy      2228 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2218 ACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGCA 2277

Qy      2288 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2347
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Db      2278 CACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGG 2337

Qy      2348 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2407
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Db      2338 CTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACA 2397

Qy      2408 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2467
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2398 TCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAG 2457

Qy      2468 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2527
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Db      2458 AAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGA 2517

Qy      2528 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2587
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2518 GCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACC 2577

Qy      2588 GTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2647
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      2578 GTGATCTGGCTGCTCGCAACGTTCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACT 2637

Qy      2648 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2707
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2638 TTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTC 2697

Qy      2708 TGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTG 2767
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Qy      2768 ATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACC 2827
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Qy      2828 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2887
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Db      2818 CCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCA 2877

Qy      2888 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2947
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Db      2878 AGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGC 2937

Qy      2948 CGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGAC 3007
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Qy      3008 AATATAAAAAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGCTG 3067
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Qy      3068 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3127
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Db      3058 TGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGTGTCACCTACAAAAACGAGG 3117

Qy      3128 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3187
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Db      3118 AAGACAAGCTGAAGGACTGGGAGGGTGGTCTGGATGAGCAGAGACTGAGCGCTGACAGTG 3177

Qy      3188 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3247
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Db      3178 GCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAGA 3237

Qy      3248 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3307
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Db      3238 GGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTT 3297

Qy      3308 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3367
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Db      3298 CCACCTTCATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGGACGACATCG 3357

Qy      3368 GCATAGACTCTTCAGACCTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTT 3427
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Qy      3428 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3487
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Db      3418 CCTTCCACTTCTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGG 3477

Qy      3488 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3547
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Db      3478 AGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGG 3537

Qy      3548 AG-CGTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3606
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Db      3538 AGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCT 3597

Qy      3607 CGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAA 3666
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Qy      3667 TAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACA 3726
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Qy      3727 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCT 3786
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Db      3718 CAATTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCT 3777

Qy      3787 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3778 GTGTTTAGATTGTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCA 3837

Qy      3847 TGTACTTCCCTCTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGA 3906
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Qy      3907 AAAACCATTTTTGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3966
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Db      3898 AAAACCATTTTTG-ACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGT 3956

Qy      3967 GTTAAAGAGATAAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGA 4026
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Qy      4027 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4086
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Db      4017 AGCCTGACAACTCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGT 4076

Qy      4087 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTT-AAAAC 4145
             |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||| |||||
Db      4077 AATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAATTTAAAAAC 4136

Qy      4146 AATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGT 4205
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Qy      4206 TTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAA 4265
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Qy      4266 AGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAA 4325
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Qy      4326 TCCATCGTATTAAAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAA 4385
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Qy      4386 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4445
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Db      4377 ACTCTTAAGTCCTAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCT 4436

Qy      4446 CATGTATATTACCCAATGGAAAATATAATGATCA--GCAAAAAGACTGGATTTGCAGAAG 4503
             |||||||||||||||||||||||||||||||||  ||| |||||||||||||||||||||
Db      4437 CATGTATATTACCCAATGGAAAATATAATGATCAGCGCANAAAGACTGGATTTGCAGAAG 4496
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Qy       4504 TT-TTTTTTTTTTTTCTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTT 4562
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Db       4497 TTNTTTTTTTTTTTTTCTTCTTGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTT 4556

Qy       4563 TTGAATCTATGAACCTGAAAAGGGTCA-GAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4621
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Db       4557 TTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAGACATCAGCCTCCTTCTTTC 4616

Qy       4622 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4681
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Db       4617 ACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGG 4676

Qy       4682 AGGCTGGATGTGCATTAGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGA 4741
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Db       4677 AGGCTGGAAGTGCATTAGCCT-GATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGTAGA 4735

Qy       4742 CTAGATCCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4801
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Db       4736 CTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGT 4795

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Db       4796 CTGTATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTA 4855

Qy       4862 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4914
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Db       4856 GGTTTCAGGAAGTTGCCATGGGAAACAAATAATTTGAACTTTGGAACAGGGTT 4908


RESULT 17
US-11-177-894-24
; Sequence 24, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 6375
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: PDGFRA nucleotide sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4476)..(4476)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4499)..(4499)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-177-894-24

  Query Match             74.3%;  Score 4765.6;  DB 18;  Length 6375;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 4880;  Conservative    0;  Mismatches   20;  Indels   13;  Gaps    9;

Qy         10 TTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGGGAAGGCCGT 67
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Db          1 TTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG---AGGCCGT 57

Qy         68 GGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGT 127
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Qy        128 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 187
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Db        118 TTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAG 177

Qy        188 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAA 237

Qy        248 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 AGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTGAAGTGAGCT 297

Qy        308 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACA 357

Qy        368 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 427
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Db        358 ACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGT 417

Qy        428 TGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACA 487
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Qy        488 TTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATT 547
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Qy        608 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACAGCAGACAGG 657

Qy        668 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 727
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Db        658 GCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAGA 717

Qy        728 AGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTAG 787
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Qy        788 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 847
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Db        778 AAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCTG 837

Qy        848 TTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAGGCAAAG 907
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Qy        908 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 967
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Db        898 GCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTGACGG 957

Qy        968 TCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCTACCA 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1028 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1087
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Db       1018 GGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATTGAAA 1077

Qy       1088 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTTGTTG 1137

Qy       1148 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACTCTGA 1197

Qy       1208 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TTGAAAATCTCACTGAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAA 1257

Qy       1268 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1327
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Db      1258 GCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATTGTAGCTC 1317
Qy      1328 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1387
Db      1318 AAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCTTCATCCA 1377
Qy      1388 TTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAG 1447
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Qy      1508 ATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCAAACATCATCACGGAGATCC 1567
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Qy      1568 ACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCA 1627
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Qy      1628 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1687
Db      1618 TCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGAGAGCTGAAGCTGG 1677
Qy      1688 TGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGA 1747
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RESULT 18
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; Sequence 3722, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3722
;   LENGTH: 6264
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-3722

  Query Match            50.8%;  Score 3260.6;  DB 17;  Length 6264;
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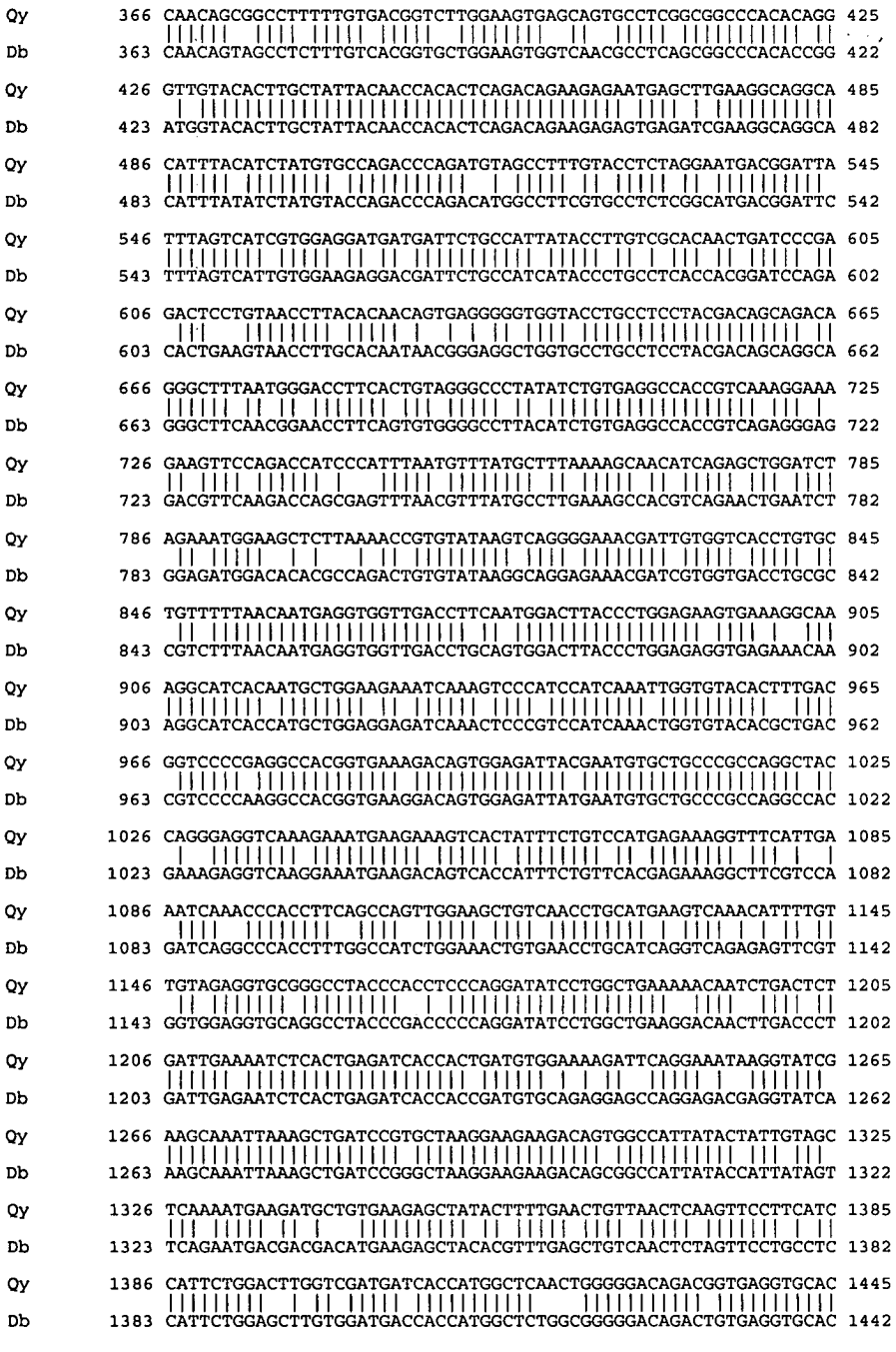
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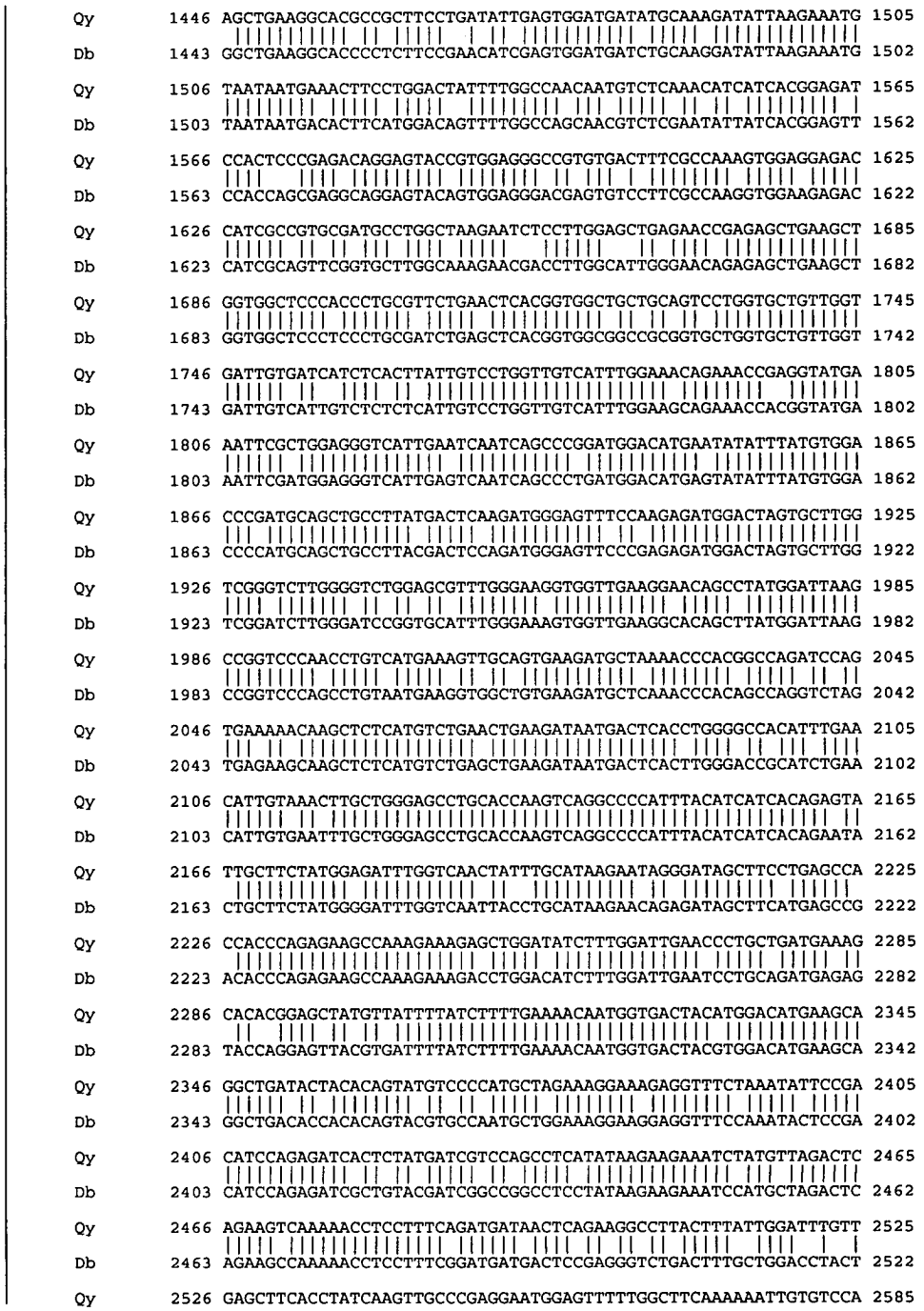
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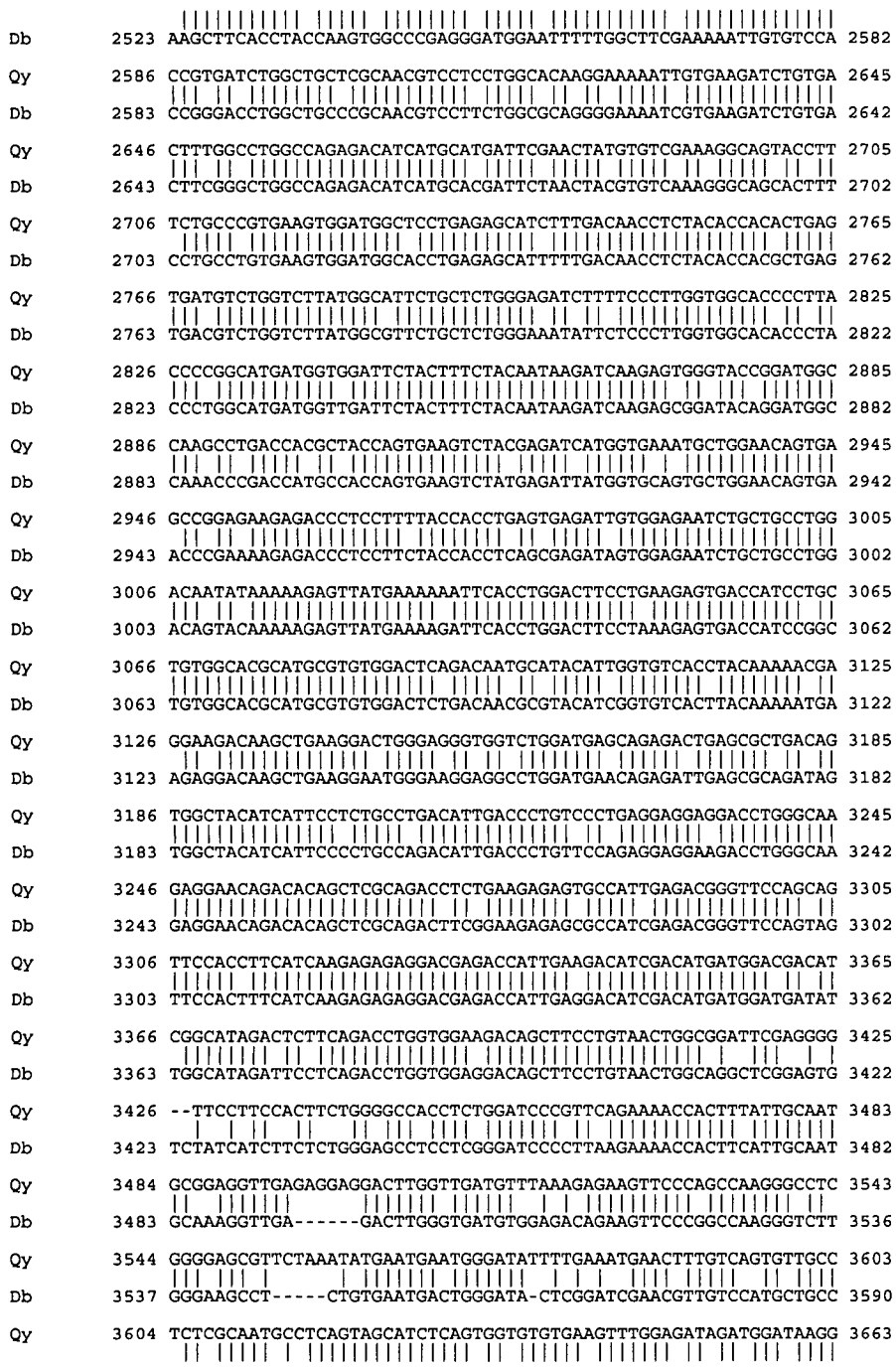
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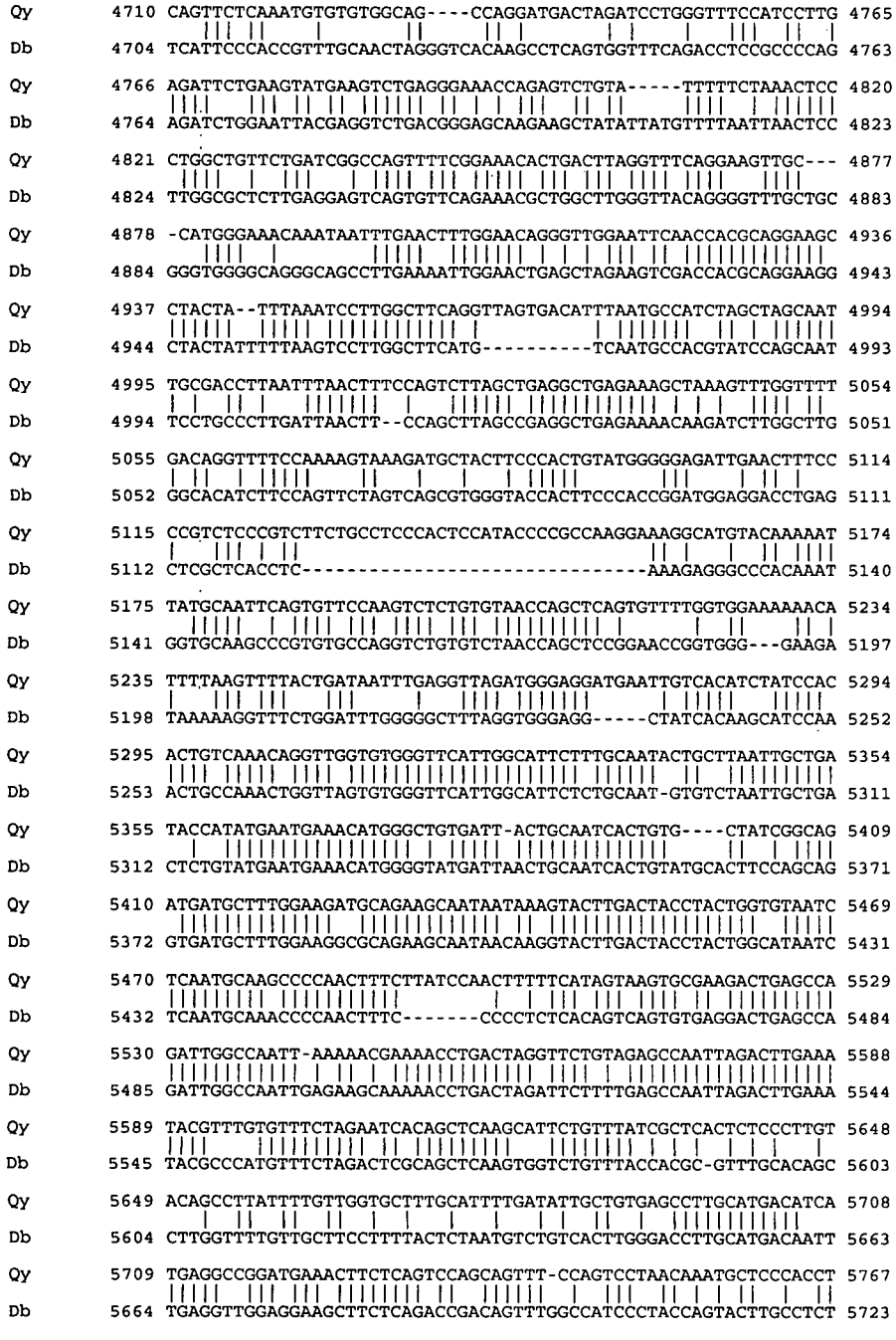
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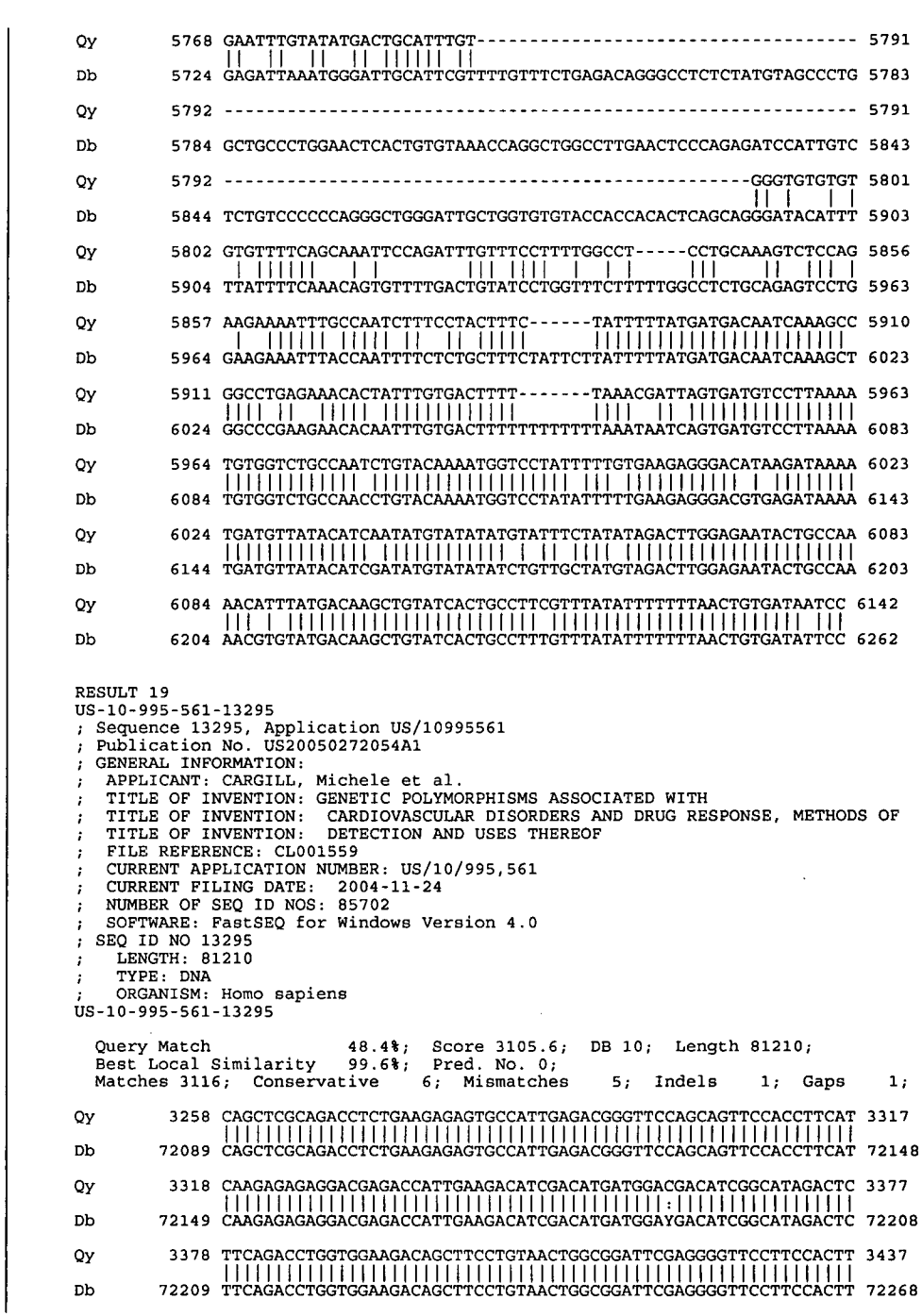
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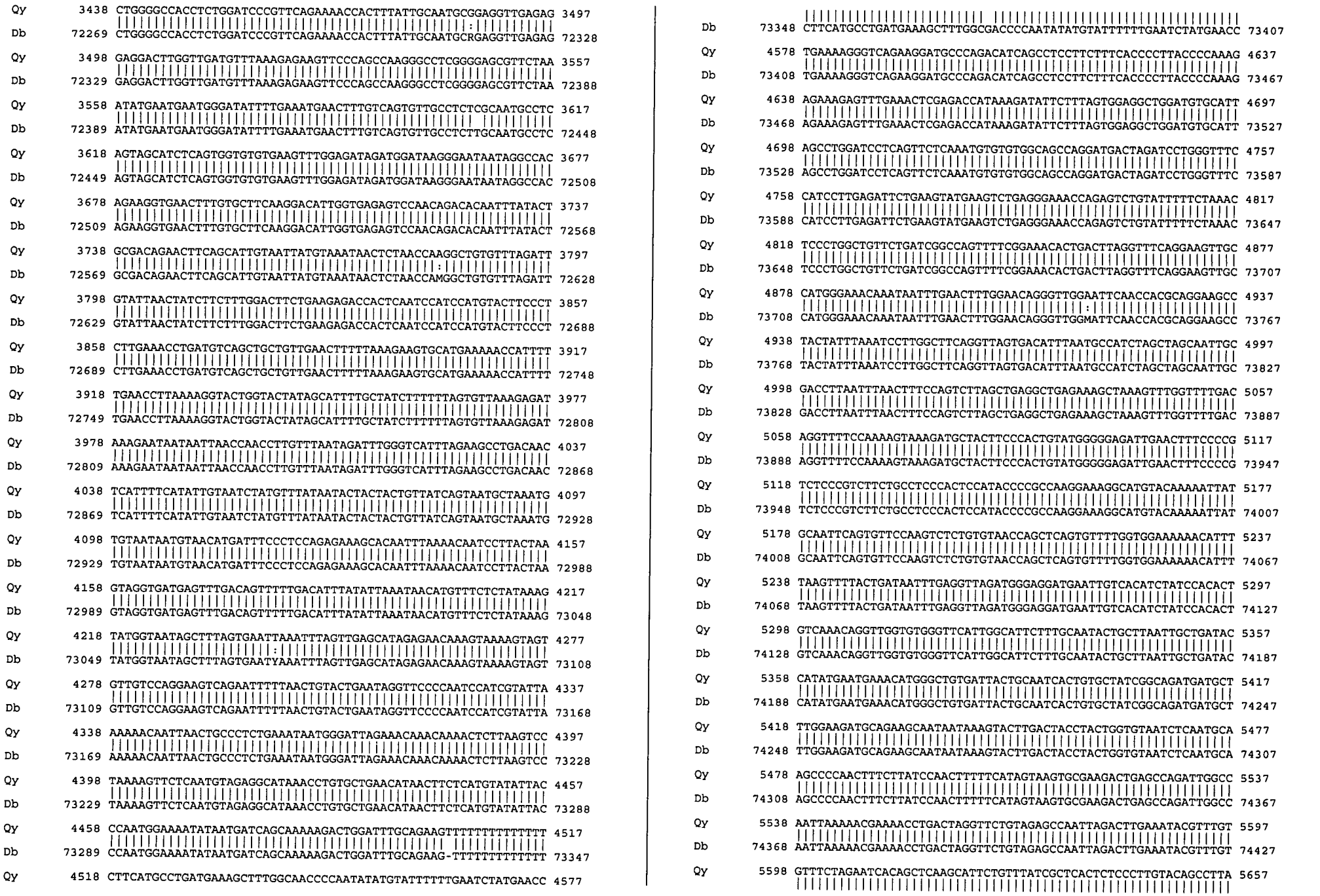

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Db 4008 TCCCTTAGGAGCCCAAGAACGAATGTTCTGTATCTTGTAATCTATACATATAACACCACT 4067
Qy 4075 ACTGTTATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCA 4134
Db 4068 ACTGTTAACAATAATGCTAAAGATGTAAT-CCCTAACCTGATTTCTTTACAGAGAAAGCA 4126
Qy 4135 CAATT-----TAAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAG-----TTTTTGA 4184
Db 4127 CAATTAATTAGAACAAAACCCTTACTAAGTAGATGACGAGTTTGGCAGTTTTTTTTTTAA 4186
Qy 4185 CATTTATATTAAATAACATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAAT 4244
Db 4187 CATTTATATTAAGTAACATGTTTCTCAATAAAATA---TAATAGGTTTAGTGGTTTAAAG 4243
Qy 4245 TTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAATT---TTT 4301
Db 4244 TTAGCAAGCCCTAGAGAGCAGAGTGTAAGTAGTGTTGTCCAGAAGGCCAACCTTTTGTTG 4303
Qy 4302 AACTGTACTGAATAGGTTCCCCAATCCATCGTATTAAAAAACAATTAACTGCCCTCTGAA 4361
Db 4304 TAGTGTTCTAAGCTGTTTCCCTAATCCAAGGCCCTAAGAA--CAGTTAATCGCCTCTGAG 4361
Qy 4362 ATAATGGGATTAGAAACAAACAAAA-------CTCTTAAGTCCTAAAAGTTCTCAATGTA 4414
Db 4362 TTACTGGGATTAGAAATAAGCAAAACAGAACCCCCGGGTGTCCTAAATGTTCTTAGTAGA 4421
Qy 4415 GAGGCATAAACCTGTGCTGAACATAACTTCTCA---TGTATATTACCCAATGGAAAATAT 4471
Db 4422 AAGGCTTAAGTCTGAGCCCAGTGTGACTTCTCATGCTGTGTGTGACCTTGTGGAAAAGAA 4481
Qy 4472 AATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTCTTCATGCCTGATG 4531
Db 4482 CCGTCCACAAAAAGGACTCCGGTGGGCAGAAGTATCTTTTGTGGCCAGTGATGACTTGGA 4541
Qy 4532 AAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGA 4591
Db 4542 T--------GGATCCCACCCATACTTACCTTTTAAATCTATGACC----------TCTTA 4583
Qy 4592 AGGATGCCCAGACATCAGCCTCCTTCTTTCACCC-CTTACCCCAAAGAGAAAGAGTTTGA 4650
Db 4584 AGGATGCGTCAACATCAGCGCCTCACTTTTCCTCTCTTGTCTCAAAGAGAAAGAGCTGGG 4643
Qy 4651 AACTC-GAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCT 4709
Db 4644 AACCCTGAAACCACGGTGGAGCTGAAGATTCGAAGGCTATGTGGGCGTGAACTGGCTCCT 4703





RESULT 19
US-10-995-561-13295
; Sequence 13295, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13295
; LENGTH: 81210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13295

Query Match 48.4%; Score 3105.6; DB 10; Length 81210;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3116; Conservative 6; Mismatches 5; Indels 1; Gaps 1;


Qy 3438 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAG 3497
Db 72269 CTGGGGCCACCTCTGGATCCCGTTCAGAAAACCACTTTATTGCAATGCRGAGGTTGAGAG 72328
Qy 3498 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 3557
Db 72329 GAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAA 72388
Qy 3558 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTC 3617
Db 72389 ATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTC 72448
Qy 3618 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 3677
Db 72449 AGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCAC 72508
Qy 3678 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 3737
Db 72509 AGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACT 72568
Qy 3738 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATT 3797
Db 72569 GCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAMGGCTGTGTTTAGATT 72628
Qy 3798 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 3857
Db 72629 GTATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCT 72688
Qy 3858 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 3917
Db 72689 CTTGAAACCTGATGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTT 72748
Qy 3918 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 3977
Db 72749 TGAACCTTAAAAGGTACTGGTACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGAT 72808
Qy 3978 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 4037
Db 72809 AAAGAATAATAATTAACCAACCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAAC 72868
Qy 4038 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 4097
Db 72869 TCATTTTCATATTGTAATCTATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATG 72928
Qy 4098 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 4157
Db 72929 TGTAATAATGTAACATGATTTCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAA 72988
Qy 4158 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 4217
Db 72989 GTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAG 73048
Qy 4218 TATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 4277
Db 73049 TATGGTAATAGCTTTAGTGAATYAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGT 73108
Qy 4278 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 4337
Db 73109 GTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTA 73168
Qy 4338 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 4397
Db 73169 AAAAACAATTAACTGCCCTCTGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCC 73228
Qy 4398 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 4457
Db 73229 TAAAAGTTCTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTAC 73288
Qy 4458 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTT 4517
Db 73289 CCAATGGAAAATATAATGATCAGCAAAAAGACTGGATTTGCAGAAG-TTTTTTTTTTTTT 73347
Qy 4518 CTTCATGCCTGATGAAAGCTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACC 4577
Db 73348 CTTCATGCCTGATGAAAGCTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACC 73407
Qy 4578 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 4637
Db 73408 TGAAAAGGGTCAGAAGGATGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAG 73467
Qy 4638 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 4697
Db 73468 AGAAAGAGTTTGAAACTCGAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATT 73527
Qy 4698 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 4757
Db 73528 AGCCTGGATCCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTC 73587
Qy 4758 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 4817
Db 73588 CATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAAC 73647
Qy 4818 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 4877
Db 73648 TCCCTGGCTGTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGC 73707
Qy 4878 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCC 4937
Db 73708 CATGGGAAACAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCC 73767
Qy 4938 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 4997
Db 73768 TACTATTTAAATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGC 73827
Qy 4998 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 5057
Db 73828 GACCTTAATTTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGAC 73887
Qy 5058 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 5117
Db 73888 AGGTTTTCCAAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCG 73947
Qy 5118 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 5177
Db 73948 TCTCCCGTCTTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTAT 74007
Qy 5178 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 5237
Db 74008 GCAATTCAGTGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTT 74067
Qy 5238 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 5297
Db 74068 TAAGTTTTACTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACT 74127
Qy 5298 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 5357
Db 74128 GTCAAACAGGTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATAC 74187
Qy 5358 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 5417
Db 74188 CATATGAATGAAACATGGGCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCT 74247
Qy 5418 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 5477
Db 74248 TTGGAAGATGCAGAAGCAATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCA 74307
Qy 5478 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 5537
Db 74308 AGCCCCAACTTTCTTATCCAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCC 74367
Qy 5538 AATTAAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 5597
Db 74368 AATTAAAAAACGAAAACCTGACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGT 74427
Qy 5598 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTA 5657

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Db      74428 GTTTCTAGAATCACAGCTCAAGCATTCTGTTTATCGCTCACTCTCCCCTTGTACAGCCTTA 74487

Qy       5658 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 5717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74488 TTTTGTTGGTGCTTTGCATTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGG 74547

Qy       5718 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 5777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74548 ATGAAACTTCTCAGTCCAGCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTAT 74607

Qy       5778 ATGACTGCATTTGTGGGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 5837
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      74608 ATGACTGCATTTGTGKGTGTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGG 74667

Qy       5838 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 5897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74668 CCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGAT 74727

Qy       5898 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 5957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74728 GACAATCAAAGCCGGCCTGAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCC 74787

Qy       5958 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 6017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74788 TTAAAATGTGGTCTGCCAATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAG 74847

Qy       6018 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 6077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74848 ATAAAATGATGTTATACATCAATATGTATATATGTATTTCTATATAGACTTGGAGAATAC 74907

Qy       6078 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 6137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74908 TGCCAAAACATTTATGACAAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGAT 74967

Qy       6138 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 6197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74968 AATCCCCACAGGCACATTAACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAA 75027

Qy       6198 TAATAAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 6257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75028 TAATAAAAAAGAAAGATACTTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAA 75087

Qy       6258 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 6317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75088 AACTAACTTGATAGGGTCTACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTT 75147

Qy       6318 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 6377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75148 TGTTTTAAAACGTGTAAATGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGT 75207

Qy       6378 TAAAAAAA 6385
              || |  ||
Db      75208 TATACTAA 75215


RESULT 20
US-11-121-086-99
; Sequence 99, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99
;   LENGTH: 134174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-99

  Query Match            48.4%;  Score 3101.6;  DB 17;  Length 134174;
  Best Local Similarity  98.9%;  Pred. No. 0;
  Matches 3134;  Conservative    0;  Mismatches   34;  Indels    2;  Gaps    1;

Qy       3218 CTGTCCCTGAGGAGGAGGACCTGGGCAAGAGGAACAGACACAGCTCGCAGACCTCTGAAG 3277
              |||| |  |||  | |  |  ||  |         |      ||||||||||||||||||||
Db       8814 CTGTGCAGGAGTTGTAATATTTGCTCTTCTCTCCCTCCTCCAGCTCGCAGACCTCTGAAG 8873

Qy       3278 AGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCA 3337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8874 AGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTCATCAAGAGAGAGGACGAGACCA 8933

Qy       3338 TTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACA 3397
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       8934 TTGAAGACATCGACATGATGGATGACATCGGCATAGACTCTTCAGACCTGGTGGAAGACA 8993

Qy       3398 GCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCC 3457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8994 GCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCACCTCTGGATCC 9053

Qy       3458 CGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTA 3517
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       9054 CGTTCAGAAAACCACTTTATTGCAATGCAGAGGTTGAGAGGAGGACTTGGTTGATGTTTA 9113

Qy       3518 AAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAATGAATGGGATATT 3577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9114 AAGAGAAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAATGAATGGGATATT 9173

Qy       3578 TTGAAATGAACTTTGTCAGTGTTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTG 3637
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       9174 TTGAAATGAACTTTGTCAGTGTTGCCTCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTG 9233

Qy       3638 TGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTT 3697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9234 TGAAGTTTGGAGATAGATGGATAAGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTT 9293

Qy       3698 CAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAGAACTTCAGCATTG 3757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9294 CAAGGACATTGGTGAGAGTCCAACAGACACAATTTATACTGCGACAGAACTTCAGCATTG 9353

Qy       3758 TAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGG 3817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9354 TAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTGTATTAACTATCTTCTTTGG 9413

Qy       3818 ACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCT 3877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9414 ACTTCTGAAGAGACCACTCAATCCATCCATGTACTTCCCTCTTGAAACCTGATGTCAGCT 9473

Qy       3878 GCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGG 3937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9474 GCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGG 9533

Qy       3938 TACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAA 3997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9534 TACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAATAATTAACCAA 9593

Qy       3998 CCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCT 4057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9594 CCTTGTTTAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCT 9653

Qy       4058 ATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAATGTAACATGATT 4117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9654 ATGTTTATAATACTACTACTGTTATCAGTAATGCTAAATGTGTAATAATGTAACATGATT 9713

Qy       4118 TCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAG 4177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9714 TCCCTCCAGAGAAAGCACAATTTAAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAG 9773

Qy       4178 TTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGA 4237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      9774 TTTTTGACATTTATATTAAATAACATGTTTCTCTATAAAGTATGGTAATAGCTTTAGTGA 9833

Qy      4238 ATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAAT 4297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9834 ATTAAATTTAGTTGAGCATAGAGAACAAAGTAAAAGTAGTGTTGTCCAGGAAGTCAGAAT 9893

Qy      4298 TTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAAAAAACAATTAACTGCCCTC 4357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9894 TTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAAAAAACAATTAACTGCCCTC 9953

Qy      4358 TGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAG 4417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9954 TGAAATAATGGGATTAGAAACAAACAAAACTCTTAAGTCCTAAAAGTTCTCAATGTAGAG 10013

Qy      4418 GCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGAAAATATAATGAT 4477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10014 GCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGAAAATATAATGAT 10073

Qy      4478 CAGCAAAAAGACTGGATTTGCAGAAG--TTTTTTTTTTTTTTCTTCATGCCTGATGAAAG 4535
             |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db     10074 CAGCAAAAAGACTGGATTTGCAGAAGTTTTTTTTTTTTTTTTCTTCATGCCTGATGAAAG 10133

Qy      4536 CTTTGGCAACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGA 4595
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10134 CTTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCAGAAGGA 10193

Qy      4596 TGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTC 4655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10194 TGCCCAGACATCAGCCTCCTTCTTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTC 10253

Qy      4656 GAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTC 4715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10254 GAGACCATAAAGATATTCTTTAGTGGAGGCTGGATGTGCATTAGCCTGGATCCTCAGTTC 10313

Qy      4716 TCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAA 4775
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10314 TCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGAGATTCTGAA 10373

Qy      4776 GTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATC 4835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10374 GTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCTGTTCTGATC 10433

Qy      4836 GGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATT 4895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10434 GGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAACAAATAATT 10493

Qy      4896 TGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGG 4955
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     10494 TGAACTTTGGAACAGGGTTGGCATTCAACCACGCAGGAAGCCTACTATTTAAATCCTTGG 10553

Qy      4956 CTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTC 5015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10554 CTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAATTTAACTTTC 10613

Qy      5016 CAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAA 5075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10614 CAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCCAAAAGTAAA 10673

Qy      5076 GATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTC 5135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10674 GATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTCTTCTGCCTC 10733

Qy      5136 CCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAG 5195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10734 CCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAGTGTTCCAAG 10793

Qy      5196 TCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATT 5255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10794 TCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTACTGATAATT 10853

Qy      5256 TGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTG 5315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10854 TGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAGGTTGGTGTG 10913

Qy      5316 GGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGG 5375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10914 GGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATACCATATGAATGAAACATGG 10973

Qy      5376 GCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCA 5435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10974 GCTGTGATTACTGCAATCACTGTGCTATCGGCAGATGATGCTTTGGAAGATGCAGAAGCA 11033

Qy      5436 ATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATC 5495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11034 ATAATAAAGTACTTGACTACCTACTGGTGTAATCTCAATGCAAGCCCCAACTTTCTTATC 11093

Qy      5496 CAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCT 5555
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11094 CAACTTTTTCATAGTAAGTGCGAAGACTGAGCCAGATTGGCCAATTAAAAACGAAAACCT 11153

Qy      5556 GACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCT 5615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11154 GACTAGGTTCTGTAGAGCCAATTAGACTTGAAATACGTTTGTGTTTCTAGAATCACAGCT 11213

Qy      5616 CAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCA 5675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11214 CAAGCATTCTGTTTATCGCTCACTCTCCCTTGTACAGCCTTATTTTGTTGGTGCTTTGCA 11273

Qy      5676 TTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCA 5735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11274 TTTTGATATTGCTGTGAGCCTTGCATGACATCATGAGGCCGGATGAAACTTCTCAGTCCA 11333

Qy      5736 GCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGGGT 5795
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     11334 GCAGTTTCCAGTCCTAACAAATGCTCCCACCTGAATTTGTATATGACTGCATTTGTGTGT 11393

Qy      5796 GTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCA 5855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11394 GTGTGTGTGTTTTCAGCAAATTCCAGATTTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCA 11453

Qy      5856 GAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCT 5915
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11454 GAAGAAAATTTGCCAATCTTTCCTACTTTCTATTTTTATGATGACAATCAAAGCCGGCCT 11513

Qy      5916 GAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCA 5975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11514 GAGAAACACTATTTGTGACTTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCA 11573

Qy      5976 ATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACA 6035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11574 ATCTGTACAAAATGGTCCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACA 11633

Qy      6036 TCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGAC 6095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11634 TCAATATGTATATATGTATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGAC 11693

Qy      6096 AAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATT 6155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11694 AAGCTGTATCACTGCCTTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATT 11753

Qy      6156 AACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATAC 6215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11754 AACTGTTGCACTTTTGAATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATAC 11813

Qy      6216 TTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAAACTAACTTGATAGGGTC 6275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11814 TTACATGTTCCCAAAACAATGGTGTGGTGAATGTGTGAGAAAAAACTAACTTGATAGGGTC 11873

Qy      6276 TACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAA 6335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11874 TACCAATACAAAATGTATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAAACGTGTAAA 11933

Qy      6336 TGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTAAAAAAA 6385
             |||||||||||||||||||||||||||||||||||||||||||||| |  ||
Db     11934 TGAAGATCTTTATATTTCAATAAATGATATATAATTTAAAGTTATACTAA 11983
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RESULT 21
US-10-995-561-313
; Sequence 313, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 313
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-313

  Query Match             11.5%;  Score 734.8;  DB 10;  Length 1047;
  Best Local Similarity   98.3%;  Pred. No. 2.2e-117;
  Matches  761;  Conservative    3;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          1 CCATTACTGTTGGAGCTACAGGGAGAGAAAC--AGGAGGAGAATGCAAGAGATCATTTGG 58
              |||||||||||||||||||||||||||||||  |||||||| ||||||||||||||| |
Db        257 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGG- 315

Qy         59 GAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 118
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 --AGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGG 373

Qy        119 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 178
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 AGGAGAAGTTTCCCAGAGCTATGGGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTC 433

Qy        179 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 238
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 TTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAATG 493

Qy        239 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 298
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 AAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAGTG 553

Qy        299 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAATG 358
              |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        554 AAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCYGATGTGGAAATCAGAAATG 613

Qy        359 AAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 418
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        614 AAGAAAACAACAGCGRCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCC 673

Qy        419 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 ACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAG 733

Qy        479 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GCAGGCACATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGA 793

Qy        539 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        794 CGGATTATTTAGTCATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTG 853

Qy        599 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        854 ATCCCGAGACTCCTGTAACCTTACACAACAGTGAGGGGGTGGTACCTGCCTCCTACGACA 913

Qy        659 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        914 GCAGACAGGGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCA 973

Qy        719 AAGGAAAGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACAT 772
              |||||||||||||||||||||||||||||:||||||||||||||||  || |
Db        974 AAGGAAAGAAGTTCCAGACCATCCCATTTAAYGTTTATGCTTTAAAAGGTACTT 1027


RESULT 22
US-11-076-427A-15
; Sequence 15, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, et al.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
;  TITLE OF INVENTION:  VESSEL ARTERIALIZATION
;  FILE REFERENCE: 28967/40008A
;  CURRENT APPLICATION NUMBER: US/11/076,427A
;  CURRENT FILING DATE:  2005-03-08
;  PRIOR APPLICATION NUMBER: US 60/551,581
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 5427
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (187)..(3507)
US-11-076-427A-15

  Query Match             10.4%;  Score 667.6;  DB 17;  Length 5427;
  Best Local Similarity   55.5%;  Pred. No. 1.2e-105;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||    |  ||  |   | ||| ||     | | | |  |||| ||   |||
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
                ||||   ||||  || | |    |  ||||  ||   |||  | |  |   | |||
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||| ||    || | |||  | |||   |      |||   ||  ||
Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              |  |   |||    |     ||  || || || ||   ||| || ||   ||
Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              || ||  | ||| | |   | ||||  ||       |||| | |||| ||   |  ||
Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

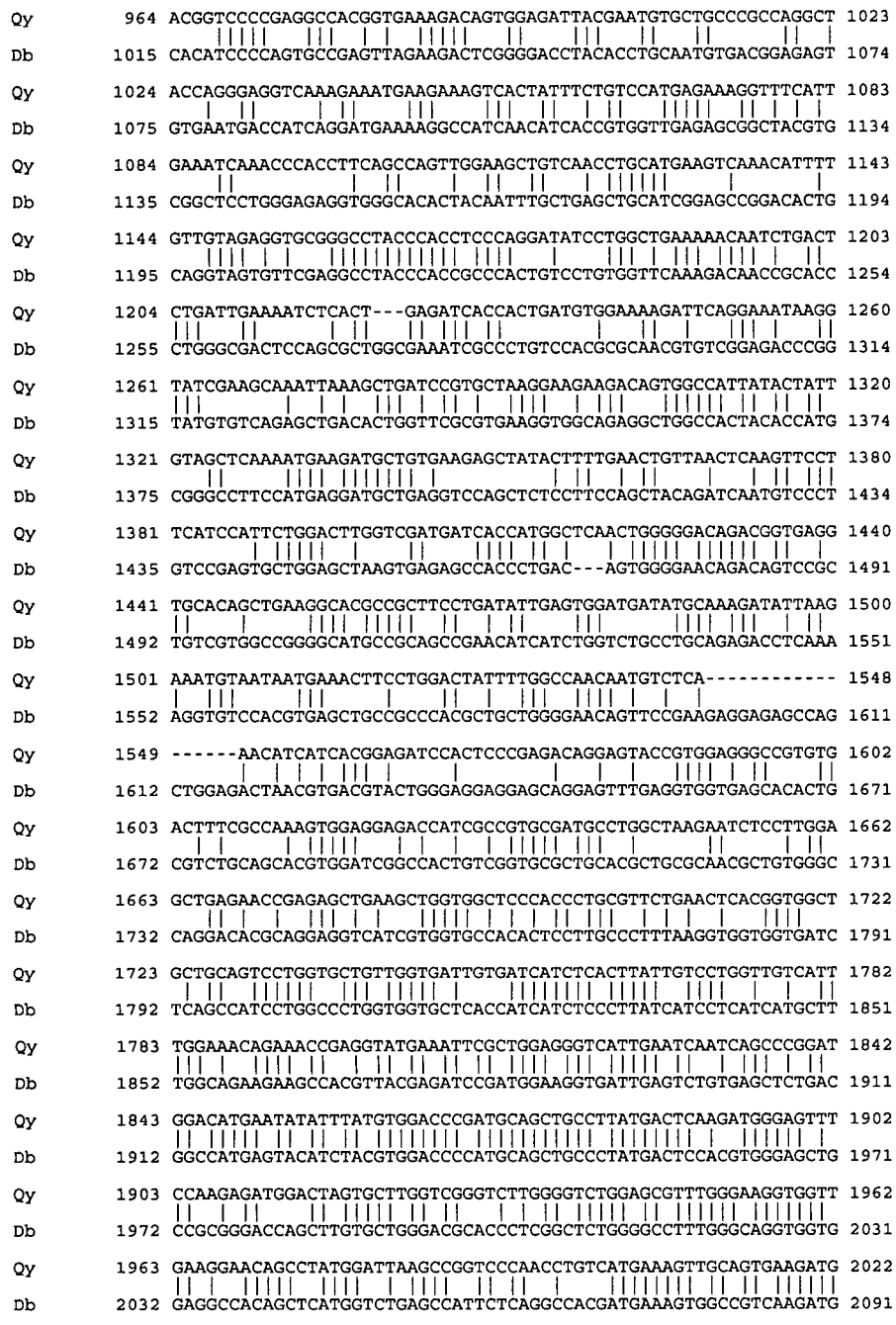
Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||     |   |   ||| |||||  |  |||||  |    | | |
Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

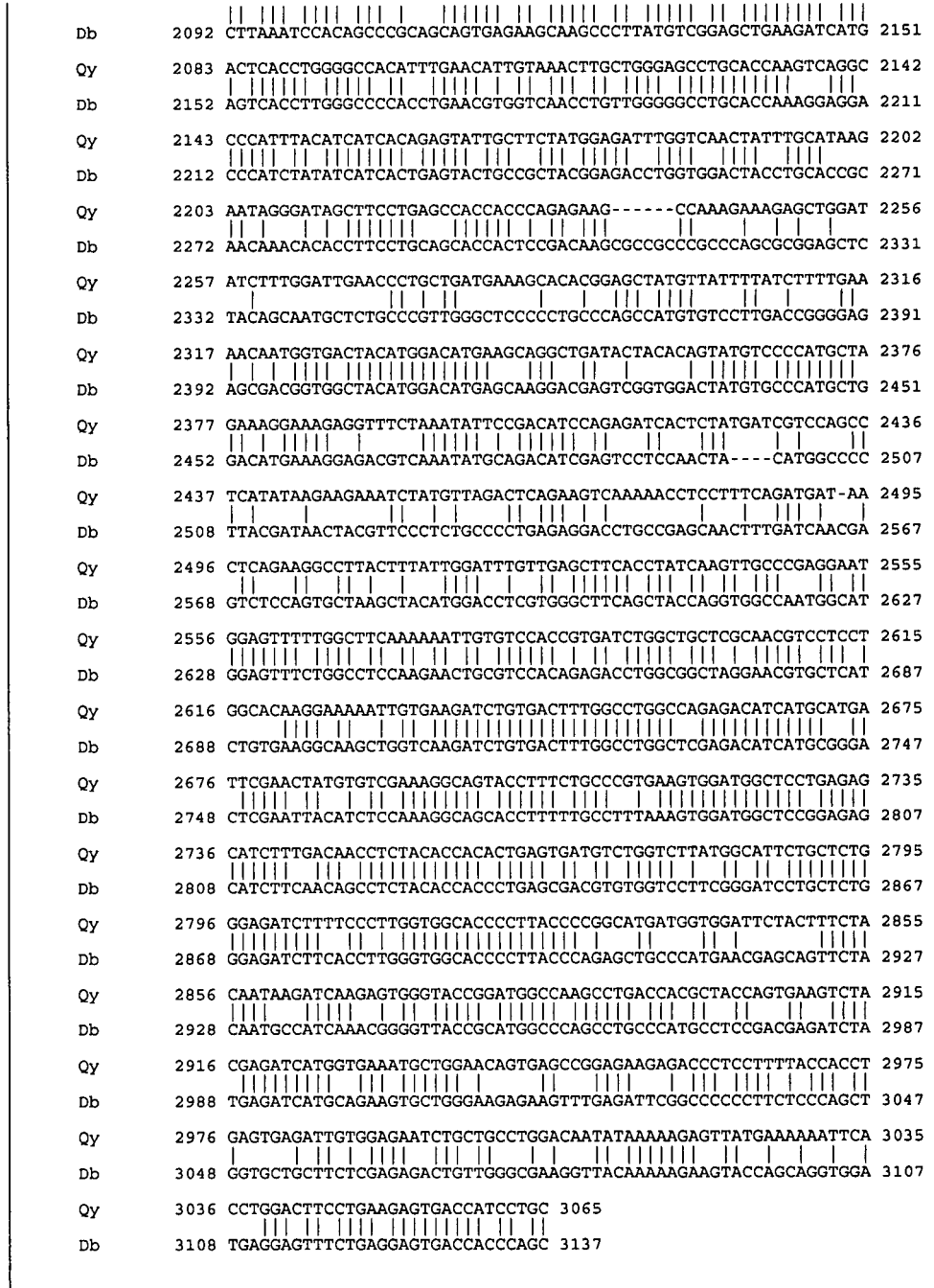
Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  |  |       | |   |||| ||      |  | |   ||||     |  |
Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
                || | ||  |  | || |||          || || |  ||     |||  ||   |
Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |    |||| |||||  || |  | ||||| |||||  |  |||  |  |   |
Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
                    |  ||  ||    ||  |    |  | |  |  | ||   ||
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014
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RESULT 23

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US-11-075-047A-118
; Sequence 118, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
;  APPLICANT: ALITALO, et al.
;  TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
;  FILE REFERENCE: 28967/39700A
;  CURRENT APPLICATION NUMBER: US/11/075,047A
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/550,907
;  PRIOR FILING DATE: 2004-03-07
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
;   LENGTH: 5427
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (187)..(3507)
US-11-075-047A-118

  Query Match            10.4%;  Score 667.6;  DB 18;  Length 5427;
  Best Local Similarity  55.5%;  Pred. No. 1.2e-105;
  Matches 1516;  Conservative    0;  Mismatches 1164;  Indels   50;  Gaps   10;

Qy        373 GGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCCCACACAGGGTTGTAC 432
              |||   ||    |  ||  |   | ||| ||    | | | |    |||| ||    |||
Db        421 GGCACCTTCTCCAGCGTGCTCACACTGACCAACCTCACTGGGCTAGACACGGGAGAATAC 480

Qy        433 ACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGAAGGCAGGCACATTTAC 492
              ||||    ||||  || | |    |  ||||  ||   |||  | |   |   | |||
Db        481 TTTTGCACCCACAATGACTCCCGTGGACTGGAGACCGA---TGAGCGGAAACGGCTCTAC 537

Qy        493 ATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTC 552
              |||| |||||||||  ||    || | |||  | |||    |       |||    ||  ||
Db        538 ATCTTTGTGCCAGATCCCACCGTGGGCTTCCTCCCTAATGATGCCGAGGAACTATTCATC 597

Qy        553 ATCGTGGAGGATGATGATTCTGCCATTATACCTTGTCGCACAACTGATCCCGAGACTCCT 612
              |  |  |||     |    ||  || || || ||   ||| || ||  ||
Db        598 TTTCTCACGGAAATAACTGAGATCACCATTCCATGCCGAGTAACAGACCCACAGCTGGTG 657

Qy        613 GTAACCTTACACAACAGTGAGGGGGTGGTA------CCTGCCTCCTACGACAGCAGACAG 666
              ||  ||  | ||| | |   | ||||  ||       |||| | |||| ||   |  ||
Db        658 GTGACACTGCACGAGAAGAAAGGGGACGTTGCACTGCCTGTCCCCTATGATCACCAACGT 717

Qy        667 GGCTTTAATGGGACCTTCACTGTAGGGCCCTATATCTGTGAGGCCACCGTCAAAGGAAAG 726
              ||||||  ||| | |||    |   |   ||| |||||  |  |||||  |    | | |
Db        718 GGCTTTTCTGGTATCTTTGAGGACAGAAGCTACATCTGCAAAACCACCATTGGGGACAGG 777

Qy        727 AAGTTCCAGACCATCCCATTTAATGTTTATGCTTTAAAAGCAACATCAGAGCTGGATCTA 786
              || |  |  |     | |   |||| ||     |  | |   ||||     |  |  |
Db        778 GAGGTGGATTCTGATGCCTACTATGTCTACAGACTCCAGGTGTCATC---CATCAACGTC 834

Qy        787 GAAATGGAAGCTCTTAAAACCGTGTATAAGTCAGGGGAAACGATTGTGGTCACCTGTGCT 846
              || | ||  |  | || |||          || || |  ||     |||  ||    |
Db        835 TCTGTGAACGCAGTGCAGACTGTGGTCCGCCAGGGTGAGAACATCACCCTCATGTGCATT 894

Qy        847 GTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAAG---GC 903
              ||  |    ||||| |||||  ||  |  | |||| |||||  |  |||  |  |   |
Db        895 GTGATCGGGAATGATGTGGTCAACTTCGAGTGGACATACCCCCGCAAAGAAAGTGGGCGG 954

Qy        904 AAAGGCATCACAATGCTGGAAGAAATCAAAGTCCCATCCATCAAATTGGTGTACACTTTG 963
                |     |  ||   ||    ||   |     |   | |  |    | ||   ||
Db        955 CTGGTGGAGCCGGTGACTGACTTCCTCTTGGATATGCCTTACCACATCCGCTCCATCCTG 1014

Qy        964 ACGGTCCCCGAGGCCACGGTGAAAGACAGTGGAGATTACGAATGTGCTGCCCGCCAGGCT 1023
              |||||   |||  | |  |||||   ||    |||   ||   ||      ||  |
Db       1015 CACATCCCCAGTGCCGAGTTAGAAGACTCGGGGACCTACACCTGCAATGTGACGGAGAGT 1074

Qy       1024 ACCAGGGAGGTCAAAGAAATGAAGAAAGTCACTATTTCTGTCCATGAGAAAGGTTTCATT 1083
              |  ||    | ||    |||   |||  ||  | ||   |||||  || | | |
Db       1075 GTGAATGACCATCAGGATGAAAAGGCCATCAACATCACCGTGGTTGAGAGCGGCTACGTG 1134

Qy       1084 GAAATCAAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTCAAACATTTT 1143
              ||          |  ||    |  ||  ||   | ||||||     |       |
Db       1135 CGGCTCCTGGGAGAGGTGGGCACACTACAATTTGCTGAGCTGCATCGGAGCCGGACACTG 1194

Qy       1144 GTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATATCCTGGCTGAAAAACAATCTGACT 1203
              ||||  |  |  |||||||||||| ||||    |     |||  | ||| |||| |  ||
Db       1195 CAGGTAGTGTTCGAGGCCTACCCACCGCCCACTGTCCTGTGGTTCAAAGACAACCGCACC 1254

Qy       1204 CTGATTGAAAATCTCACT---GAGATCACCACTGATGTGGAAAAGATTCAGGAAATAAGG 1260
              |||  ||       |  ||   || ||| ||          |   ||  |  ||| |  ||
Db       1255 CTGGGCGACTCCAGCGCTGGCGAAATCGCCCTGTCCACGCGCAACGTGTCGGAGACCCGG 1314

Qy       1261 TATCGAAGCAAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTATACTATT 1320
              |||       |  |  ||| | || |  ||||  | |||   ||||||  || || ||
Db       1315 TATGTGTCAGAGCTGACACTGGTTCGCGTGAAGGTGGCAGAGGCTGGCCACTACACCATG 1374

Qy       1321 GTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTTGAACTGTTAACTCAAGTTCCT 1380
              ||     |||| |||||| |          | ||  | ||    |  | || |||
Db       1375 CGGGCCTTCCATGAGGATGCTGAGGTCCAGCTCTCCTTCCAGCTACAGATCAATGTCCCT 1434

Qy       1381 TCATCCATTCTGGACTTGGTCGATGATCACCATGGCTCAACTGGGGGACAGACGGTGAGG 1440
                  |||||  |    ||   |||| || |  | ||||| ||||||  ||  |
Db       1435 GTCCGAGTGCTGGAGCTAAGTGAGAGCCACCCTGAC---AGTGGGGAACAGACAGTCCGC 1491

Qy       1441 TGCACAGCTGAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGATATTAAG 1500
              ||    |   |||| |||||  ||  | ||    |||       |||| |||  | ||
Db       1492 TGTCGTGGCCGGGGCATGCCGCAGCCGAACATCATCTGGTCTGCCTGCAGAGACCTCAAA 1551

Qy       1501 AAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAACAATGTCTCA------------ 1548
              |  |||     |||     |   ||  |  |||  ||||  |  |  |
Db       1552 AGGTGTCCACGTGAGCTGCCGCCCACGCTGCTGGGGAACAGTTCCGAAGAGGAGAGCCAG 1611

Qy       1549 ------AACATCATCACGGAGATCCACTCCCGAGACAGGAGTACCGTGGAGGGCCGTGTG 1602
                    |  | | | |||  |       |   |  |   ||||  | ||    ||
Db       1612 CTGGAGACTAACGTGACGTACTGGGAGGAGGAGCAGGAGTTTGAGGTGGTGAGCACACTG 1671

Qy       1603 ACTTTCGCCAAAGTGGAGGAGACCATCGCCGTGCGATGCCTGGCTAAGAATCTCCTTGGA 1662
              | |    | |||||   | |  |  | |||||  |||  |     ||     | ||
Db       1672 CGTCTGCAGCACGTGGATCGGCCACTGTCGGTGCGCTGCACGCTGCGCAACGCTGTGGGC 1731

Qy       1663 GCTGAGAACCGAGAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTGGCT 1722
              || |  |  ||| | |   ||||| | | | || |||  | | |  |  ||||
Db       1732 CAGGACACGCAGGAGGTCATCGTGGTGCCACACTCCTTGCCCTTTAAGGTGGTGGTGATC 1791

Qy       1723 GCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGGTTGTCATT 1782
              | ||  ||||||  |||  |||||  |     |||||||  |||||  ||||  |  | ||
Db       1792 TCAGCCATCCTGGCCCTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTT 1851

Qy       1783 TGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGAT 1842
              |||  |  |||| ||  | ||  ||  ||  ||  |||| |||  |||||  ||  | ||| | ||
Db       1852 TGGCAGAAGAAGCCACGTTACGAGATCCGATGGAAGGTGATTGAGTCTGTGAGCTCTGAC 1911

Qy       1843 GGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTT 1902
              || ||||| ||  ||  ||  |||||||| ||||||||||  ||||||||  |  |||||| |
Db       1912 GGCCATGAGTACATCTACGTGGACCCCATGCAGCTGCCCTATGACTCCACGTGGGAGCTG 1971

Qy       1903 CCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTT 1962
              ||  | ||   || ||||| || ||  | | || ||||| || ||||||  |||||||
Db       1972 CCGCGGGACCAGCTTGTGCTGGGACGCACCCTCGGCTCTGGGGCCTTTGGGCAGGTGGTG 2031

Qy       1963 GAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATG 2022
              || |  |||||  ||||  | ||||  ||  ||  |    ||||||||  || || ||||||
Db       2032 GAGGCCACAGCTCATGGTCTGAGCCATTCTCAGGCCACGATGAAAGTGGCCGTCAAGATG 2091

Qy       2023 CTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATG 2082
              || ||| |||| ||| |   |||||| || |||||  || |||||  || |||||||| |||
Db       2092 CTTAAATCCACAGCCCGCAGCAGTGAGAAGCAAGCCCTTATGTCGGAGCTGAAGATCATG 2151

Qy       2083 ACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGC 2142
              | |||||| ||||| ||  ||||| | || ||| ||  |||| ||||||||||    |||
Db       2152 AGTCACCTTGGGCCCCACCTGAACGTGGTCAACCTGTTGGGGGCCTGCACCAAAGGAGGA 2211
```

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Qy       2143 CCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAG 2202
             ||||| || |||||||| ||||| ||| ||| |||||  |||| ||||  ||||
Db       2212 CCCATCTATATCATCACTGAGTACTGCCGCTACGGAGACCTGGTGGACTACCTGCACCGC 2271

Qy       2203 AATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAG------CCAAAGAAAGAGCTGGAT 2256
             || |   | | |||||||   |||||| | || |||       ||    |  | |  |
Db       2272 AACAAACACACCTTCCTGCAGCACCACTCCGACAAGCGCCGCCCGCCCAGCGCGGAGCTC 2331

Qy       2257 ATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAA 2316
               |        || | ||       |   |  ||| ||||    ||  |    ||
Db       2332 TACAGCAATGCTCTGCCCGTTGGGCTCCCCCTGCCCAGCCATGTGTCCTTGACCGGGGAG 2391

Qy       2317 AACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTA 2376
             | | | |||| ||||||||||||||    |||  ||  |     | |||||  |||||||||
Db       2392 AGCGACGGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTG 2451

Qy       2377 GAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCC 2436
             || | |||||  |      |||||| | |||||| ||    ||   |||     | |    ||
Db       2452 GACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTA----CATGGCCCC 2507

Qy       2437 TCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGAT-AA 2495
             | |.  |      ||  | |    || ||| | |       |   | ||| |   |
Db       2508 TTACGATAACTACGTTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGA 2567

Qy       2496 CTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAAT 2555
               ||   ||  || |  |  ||||  |  || |||||| ||| || || |||   || ||
Db       2568 GTCTCCAGTGCTAAGCTACATGGACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCAT 2627

Qy       2556 GGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCT 2615
             |||||||  |||| || || || || |||||| | || ||||| ||| | |||||  ||| |
Db       2628 GGAGTTTCTGGCCTCCAAGAACTGCGTCCACAGAGACCTGGCGGCTAGGAACGTGCTCAT 2687

Qy       2616 GGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGA 2675
               |||| ||  | || |||||||||||||||||||||||  ||||||||||||  ||
Db       2688 CTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGGCTCGAGACATCATGCGGGA 2747

Qy       2676 TTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAG 2735
               ||||| ||  | || |||||||| |||||| |||| | ||||||||||||| |||||
Db       2748 CTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGGCTCCGGAGAG 2807

Qy       2736 CATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTG 2795
             ||||||  ||| |||||||||||| ||||| || || ||||| |  || || ||||||||
Db       2808 CATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCTG 2867

Qy       2796 GGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTA 2855
             ||||||||  || | |||||||||||||||| |  ||   || |      |||||
Db       2868 GGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTA 2927

Qy       2856 CAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTA 2915
             ||||  |||||  | || ||||| ||||||  ||||| ||  ||   ||  ||||
Db       2928 CAATGCCATCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTA 2987

Qy       2916 CGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCT 2975
             |||||||||  ||| |||||| |      ||   ||||   | ||| |||| | ||| ||
Db       2988 TGAGATCATGCAGAAGTGCTGGGAAGAGAAGTTTGAGATTCGGCCCCCCTTCTCCCAGCT 3047

Qy       2976 GAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCA 3035
             |     | || | ||||  ||| ||  | |   || |||||||  ||  |  |  |  |
Db       3048 GGTGCTGCTTCTCGAGAGACTGTTGGGCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGA 3107

Qy       3036 CCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
                ||| || |||| ||||||||| || ||
Db       3108 TGAGGAGTTTCTGAGGAGTGACCACCCAGC 3137


RESULT 24
US-09-925-065A-81823/c
; Sequence 81823, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81823
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-81823

  Query Match             10.1%;  Score 649.6;  DB 7;  Length 650;
  Best Local Similarity   99.8%;  Pred. No. 1e-102;
  Matches  649;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4707 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 4766
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 591

Qy       4767 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 4826
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 531

Qy       4827 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 4886
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 471

Qy       4887 CAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTA 4946
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        470 CAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCCTACTATTTA 411

Qy       4947 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 5006
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 351

Qy       5007 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 5066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 291

Qy       5067 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 5126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 231

Qy       5127 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 5186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 171

Qy       5187 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 5246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 111

Qy       5247 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 5306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 51

Qy       5307 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 5356
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          50 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 1


RESULT 25
US-10-301-480-183063/c
; Sequence 183063, Application US/10301480
```

```
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183063
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-183063

  Query Match             10.1%;  Score 649.6;  DB 11;  Length 650;
  Best Local Similarity   99.8%;  Pred. No. 1e-102;
  Matches  649;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4707 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 4766
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 591

Qy       4767 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 4826
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 531

Qy       4827 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 4886
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 471

Qy       4887 CAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTA 4946
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        470 CAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCCTACTATTTA 411

Qy       4947 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 5006
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 351

Qy       5007 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 5066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 291

Qy       5067 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 5126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 231

Qy       5127 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 5186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 171

Qy       5187 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 5246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 111

Qy       5247 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 5306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 51

Qy       5307 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 5356
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          50 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 1


RESULT 26
US-10-301-480-796472/c
; Sequence 796472, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 796472
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-796472

  Query Match             10.1%;  Score 649.6;  DB 12;  Length 650;
  Best Local Similarity   99.8%;  Pred. No. 1e-102;
  Matches  649;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4707 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 4766
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 CCTCAGTTCTCAAATGTGTGTGGCAGCCAGGATGACTAGATCCTGGGTTTCCATCCTTGA 591

Qy       4767 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 4826
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GATTCTGAAGTATGAAGTCTGAGGGAAACCAGAGTCTGTATTTTTCTAAACTCCCTGGCT 531

Qy       4827 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 4886
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 GTTCTGATCGGCCAGTTTTCGGAAACACTGACTTAGGTTTCAGGAAGTTGCCATGGGAAA 471

Qy       4887 CAAATAATTTGAACTTTGGAACAGGGTTGGAATTCAACCACGCAGGAAGCCTACTATTTA 4946
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        470 CAAATAATTTGAACTTTGGAACAGGGTTGGMATTCAACCACGCAGGAAGCCTACTATTTA 411

Qy       4947 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 5006
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AATCCTTGGCTTCAGGTTAGTGACATTTAATGCCATCTAGCTAGCAATTGCGACCTTAAT 351

Qy       5007 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 5066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TTAACTTTCCAGTCTTAGCTGAGGCTGAGAAAGCTAAAGTTTGGTTTTGACAGGTTTTCC 291

Qy       5067 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 5126
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 AAAAGTAAAGATGCTACTTCCCACTGTATGGGGGAGATTGAACTTTCCCCGTCTCCCGTC 231

Qy       5127 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 5186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 TTCTGCCTCCCACTCCATACCCCGCCAAGGAAAGGCATGTACAAAAATTATGCAATTCAG 171

Qy       5187 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 5246
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGTTCCAAGTCTCTGTGTAACCAGCTCAGTGTTTTGGTGGAAAAAACATTTTAAGTTTTA 111

Qy       5247 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 5306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 CTGATAATTTGAGGTTAGATGGGAGGATGAATTGTCACATCTATCCACACTGTCAAACAG 51

Qy       5307 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 5356
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          50 GTTGGTGTGGGTTCATTGGCATTCTTTGCAATACTGCTTAATTGCTGATA 1


RESULT 27
US-11-136-527-742
; Sequence 742, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 742
;   LENGTH: 1690
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-742

  Query Match             8.6%;  Score 549.6;  DB 17;  Length 1690;
  Best Local Similarity   63.6%;  Pred. No. 2.3e-85;
  Matches  872;  Conservative    0;  Mismatches  489;  Indels    9;  Gaps    2;

Qy       1702 CGTTCTGAACTCACGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCA 1761
Db          1 CCTTTCAAAGTGGTGGTGATCTCAGCCATCTTGGCCTTGGTGGTCCTTACTGTCATCTCT 60

Qy       1762 CTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTC 1821
Db         61 CTCATCATCCTCATCATGCTGTGGCAGAGGAAACCACGCTATGAGATCCGATGGAAGGTC 120

Qy       1822 ATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCT 1881
Db        121 ATTGAGTCTGTGAGCTCTGACGGCCATGAGTACATCTATGTGGATCCTGTGCAGTTGCCT 180

Qy       1882 TATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCT 1941
Db        181 TACGACTCCACCTGGGAGCTGCCACGGGACCAGCTTGTTCTGGGACGCACTCTTGGCTCT 240

Qy       1942 GGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTC 2001
Db        241 GGGGCTTTCGGACAGGTGGTGGAGGCCACGGCTCATGGTCTGAGCCACTCACAGGCCACC 300

Qy       2002 ATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTC 2061
Db        301 ATGAAAGTGGCTGTCAAGATGCTGAAATCTACAGCCAGAAGCAGTGAGAAGCAAGCCCTC 360

Qy       2062 ATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTG 2121
Db        361 ATGTCGGAGCTGAAGATCATGAGTCATCTCGGACCCCACCTGAACGTGGTCAACCTGCTG 420

Qy       2122 GGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGAT 2181
Db        421 GGGGCCTGTACCAAAGGAGGGCCCATCTACATTATCACGGAATACTGCCGTTATGGTGAC 480

Qy       2182 TTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCA 2241
Db        481 CTGGTGGACTACCTGCACCGAAACAAACACACCTTCCTGCAACGACACTCCAACAAGCAT 540

Qy       2242 AAGAAAGAGCTGGATATCTTTGGATTGAAC------CCTGCTGATGAAAGCACACGGAGC 2295
Db        541 TGTCCACCCAGCACTGAGCTCTACAGCAACGCCCTGCCGGTGGGGCTCTCCCTACCCAGC 600

Qy       2296 TATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACT 2355
Db        601 CACTTGAACCTGACTGGGGAGAGCGACGGTGGTTACATGGACATGAGCAAGGATGAATCT 660

Qy       2356 ACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGA 2415
Db        661 GTAGATTACGTGCCCATGTTGGACATGAAAGGACACATCAAATACGCGGACATCGAGTCC 720

Qy       2416 TCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAA 2475
Db        721 TCCAGCTACATGGCCCCTTACGATAACTATGTCCCATCTGCCCCTGA---AAGGACCTAT 777

Qy       2476 AACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACC 2535
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Db        778 CGTGCTACCTTAATCAACGACTCACCAGTGCTCAGCTACACGGACCTCGTGGGCTTCAGT 837

Qy       2536 TATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTG 2595
Db        838 TACCAAGTGGCCAATGGCATGGAATTCTTGGCCTCTAAGAATTGTGTTCACCGAGACCTG 897

Qy       2596 GCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTG 2655
Db        898 GCGGCCAGGAATGTGCTCATCTGTGAGGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTG 957

Qy       2656 GCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTG 2715
Db        958 GCTCGAGACATCATGCGGGACTCAAACTACATCTCCAAAGGCAGTACTTTCCTGCCTCTG 1017

Qy       2716 AAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGG 2775
Db       1018 AAGTGGATGGCCCCAGAGAGCATCTTCAACAGCCTCTACACCACCTTGAGTGATGTGTGG 1077

Qy       2776 TCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATG 2835
Db       1078 TCCTTTGGAATCCTACTCTGGGAAATCTTCACACTGGGTGGCACCCCTTACCCAGAGCTG 1137

Qy       2836 ATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGAC 2895
Db       1138 CCCATGAACGACCAGTTCTACAATGCCATCAAGAGGGGCTACCGCATGGCCCAACCTGCT 1197

Qy       2896 CACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAG 2955
Db       1198 CATGCCTCCGACGAGATCTATGAGATCATGCAGAAATGCTGGGAAGAAAAGTTTGAGACT 1257

Qy       2956 AGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAA 3015
Db       1258 CGGCCCCCCTTCTCTCAGCTGGTGCTGCTCCTGGAGAGGCTTCTGGGTGAAGGCTATAAA 1317

Qy       3016 AAGAGTTATGAAAAAATTCACCTGGACTTCCTGAAGAGTGACCATCCTGC 3065
Db       1318 AAGAAGTACCAGCAGGTGGATGAGGAGTTTCTGAGGAGTGACCATCCAGC 1367


RESULT 28
US-11-177-894-22
; Sequence 22, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: PDGFRA nucleotide sequence
US-11-177-894-22

  Query Match             8.4%;  Score 539.4;  DB 18;  Length 1176;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-83;
  Matches  540;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983
Db        211 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 270

Qy       1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043
Db        271 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 330

Qy       2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103
```

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Db        331 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 390

Qy       2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163

Db        391 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 450

Qy       2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223

Db        451 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 510

Qy       2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283

Db        511 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 570

Qy       2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343

Db        571 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 630

Qy       2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403

Db        631 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 690

Qy       2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463

Db        691 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGGC 750

Qy       2464 T 2464

Db        751 T 751
```

RESULT 29
US-11-177-894-25
; Sequence 25, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PDGFRA nucleotide sequence
US-11-177-894-25

Query Match 8.4%; Score 539.4; DB 18; Length 1176;
Best Local Similarity 99.8%; Pred. No. 1.3e-83;
Matches 540; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1924 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 1983

Db        211 GGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTA 270

Qy       1984 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 2043

Db        271 AGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCC 330

Qy       2044 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 2103

Db        331 AGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTG 390

Qy       2104 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 2163

Db        391 AACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAG 450

Qy       2164 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 2223

Db        451 TATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGC 510

Qy       2224 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 2283

Db        511 CACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAA 570

Qy       2284 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 2343

Db        571 AGCACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAG 630

Qy       2344 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 2403

Db        631 CAGGCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCC 690

Qy       2404 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGAC 2463

Db        691 GACATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGGC 750

Qy       2464 T 2464

Db        751 T 751
```

RESULT 30
US-11-136-527-7664
; Sequence 7664, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7664
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7664

Query Match 6.1%; Score 391; DB 17; Length 600;
Best Local Similarity 83.8%; Pred. No. 4.8e-58;
Matches 485; Conservative 0; Mismatches 75; Indels 19; Gaps 3;

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Qy       5824 TTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTT 5883

Db         22 TGGTTTCCTTTTGGCCTCCTGCAGAGTCCCTGGAAGGAAATTTACCAATTTTCTCTGCTT 81

Qy       5884 TC------TATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC--- 5934

Db         82 TCTATTCTTATTTTTATGATGACAATCAAAGCTGGCCCGAAGAACCCAATTTGTGACTTT 141

Qy       5935 ---TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGT 5991

Db        142 TTTTTTTTAAATAATCAGTGATGTCCTTAAAATGTGGTCTGCCAACCTGTACAAAATGGT 201

Qy       5992 CCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATG 6051

Db        202 CCTATATTTTTGAAGAGGGACGTGAGATAAAATGATGTTATACATCGATATGTATATATC 261

Qy       6052 TATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCC 6111

Db        262 TGTTGCTATGTAGACTTGGAGAATACTGCCAAAACGTGTATGACAAGCTGTATCACTGCC 321

Qy       6112 TTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTG 6171

Db        322 TTTGTTTATATTTTTTTAACTGTGATATTCCCCACAGGCACGTTAACTGTTGCACTTTTG 381
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Qy       6172 AATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAA 6231
              ||||||||||||||||||||||||   |||||| ||||| |||||||||||||||||| |
Db        382 AATGTCCAAAATTTATATTTTAGAAGGAATAAAGAGAAAAATACTTACATGTTCCCAACA 441

Qy       6232 CAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGT 6291
                |||||||| |||||||||||  ||||    | || |||||| ||||| ||| |||
Db        442 TGGTGGTGTGGTAAATGTGTGAGAGCAACTCCATAGAGAGGGTCTTCCAATCCAAGATGG 501

Qy       6292 ATTACGAATGCCCCTGTTCATGTTTTGTTTTAAA-------ACGTGTAAATGAAGATCT 6344
                || |  || ||| ||||||||||||  ||  |||       | |||||||| ||||||
Db        502 CTTCCAGATACCCGTGTTCATGTTTTGTTTAAAAAAAAAAAGAAGTGTAAATGGAGATCT 561

Qy       6345 TTATATTTCAATAAATGATATATAATTTAAAGTTAAAAA 6383
                |||||||||||||||||| ||| || ||   ||  |||
Db        562 TTATATTTCAATAAATGATTTATGATATATGATTTTAAA 600


RESULT 31
US-11-136-527-3568/c
; Sequence 3568, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3568
;   LENGTH: 629
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-3568

  Query Match             6.1%;  Score 391;  DB 17;  Length 629;
  Best Local Similarity   83.8%;  Pred. No. 4.9e-58;
  Matches  485;  Conservative    0;  Mismatches   75;  Indels   19;  Gaps    3;

Qy       5824 TTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTT 5883
              | |||||||||||||||||||| |||| |   |||| |||||| ||||| ||  || |||
Db        579 TGGTTTCCTTTTGGCCTCCTGCAGAGTCCCTGGAAGGAAATTTACCAATTTTCTCTGCTT 520

Qy       5884 TC------TATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC--- 5934
              ||      |||||||||||||||||||||| |||| ||  ||| | |||||||||
Db        519 TCTATTCTTATTTTTATGATGACAATCAAAGCTGGCCCGAAGAACCCAATTTGTGACTTT 460

Qy       5935 ---TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGT 5991
                  ||||||||  || ||||||||||||||||||||||||||| ||||||||||||||
Db        459 TTTTTTTTAAATAATCAGTGATGTCCTTAAAATGTGGTCTGCCAACCTGTACAAAATGGT 400

Qy       5992 CCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATG 6051
              ||||| ||| |||||||||| | ||||||||||||||||||| ||||||||||||
Db        399 CCTATATTTTTGAAGAGGGACGTGAGATAAAATGATGTTATACATCGATATGTATATATC 340

Qy       6052 TATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCC 6111
              | || |||| |||||||||||||||||||||| | ||||||||||||||||||||||
Db        339 TGTTGCTATGTAGACTTGGAGAATACTGCCAAAACGTGTATGACAAGCTGTATCACTGCC 280

Qy       6112 TTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTG 6171
              || |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Db        279 TTTGTTTATATTTTTTTAACTGTGATATTCCCCACAGGCACGTTAACTGTTGCACTTTTG 220

Qy       6172 AATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAA 6231
              |||||||||||||||||||||||   |||||| ||||| |||||||||||||||||| |
Db        219 AATGTCCAAAATTTATATTTTAGAAGGAATAAAGAGAAAAATACTTACATGTTCCCAACA 160

Qy       6232 CAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGT 6291
                |||||||| |||||||||||  ||||    | || |||||| ||||| ||| |||
Db        159 TGGTGGTGTGGTAAATGTGTGAGAGCAACTCCATAGAGAGGGTCTTCCAATCCAAGATGG 100

Qy       6292 ATTACGAATGCCCCTGTTCATGTTTTGTTTTAAA-------ACGTGTAAATGAAGATCT 6344
                || |  || ||| ||||||||||||  ||  |||       | |||||||| ||||||
Db         99 CTTCCAGATACCCGTGTTCATGTTTTGTTTAAAAAAAAAAAGAAGTGTAAATGGAGATCT 40

Qy       6345 TTATATTTCAATAAATGATATATAATTTAAAGTTAAAAA 6383
                |||||||||||||||||| ||| || ||   ||  |||
Db         39 TTATATTTCAATAAATGATTTATGATATATGATTTTAAA 1


RESULT 32
US-11-036-196-1270/c
; Sequence 1270, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Higgs, Brandon
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5089-US
;  CURRENT APPLICATION NUMBER: US/11/036,196
;  CURRENT FILING DATE:  2005-01-18
;  PRIOR APPLICATION NUMBER: US/10/152,319
;  PRIOR FILING DATE: 2002-05-22
;  PRIOR APPLICATION NUMBER: US 60/292,335
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/297,523
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,925
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,810
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,807
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,808
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: US 60/315,047
;  PRIOR FILING DATE: 2001-08-28
;  PRIOR APPLICATION NUMBER: US 60/324,928
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: US 60/330,867
;  PRIOR FILING DATE: 2001-11-01
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2221
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1270
;   LENGTH: 629
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. AI232379
US-11-036-196-1270

  Query Match             6.1%;  Score 391;  DB 18;  Length 629;
  Best Local Similarity   83.8%;  Pred. No. 4.9e-58;
  Matches  485;  Conservative    0;  Mismatches   75;  Indels   19;  Gaps    3;

Qy       5824 TTGTTTCCTTTTGGCCTCCTGCAAAGTCTCCAGAAGAAAATTTGCCAATCTTTCCTACTT 5883
              | |||||||||||||||||||| |||| |   |||| |||||| ||||| ||  || |||
Db        579 TGGTTTCCTTTTGGCCTCCTGCAGAGTCCCTGGAAGGAAATTTACCAATTTTCTCTGCTT 520

Qy       5884 TC------TATTTTTATGATGACAATCAAAGCCGGCCTGAGAAACACTATTTGTGAC--- 5934
              ||      |||||||||||||||||||||| |||| ||  ||| | |||||||||
Db        519 TCTATTCTTATTTTTATGATGACAATCAAAGCTGGCCCGAAGAACCCAATTTGTGACTTT 460

Qy       5935 ---TTTTTAAACGATTAGTGATGTCCTTAAAATGTGGTCTGCCAATCTGTACAAAATGGT 5991
                  ||||||||  || ||||||||||||||||||||||||||| ||||||||||||||
Db        459 TTTTTTTTAAATAATCAGTGATGTCCTTAAAATGTGGTCTGCCAACCTGTACAAAATGGT 400

Qy       5992 CCTATTTTTGTGAAGAGGGACATAAGATAAAATGATGTTATACATCAATATGTATATATG 6051
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                |||||  |||  ||||||||||| | ||||||||||||||||||||||| ||||||||||||
Db        399 CCTATATTTTTGAAGAGGGACGTGAGATAAAATGATGTTATACATCGATATGTATATATC 340

Qy       6052 TATTTCTATATAGACTTGGAGAATACTGCCAAAACATTTATGACAAGCTGTATCACTGCC 6111
                | ||  ||||  |||||||||||||||||||||||| | ||||||||||||||||||||
Db        339 TGTTGCTATGTAGACTTGGAGAATACTGCCAAAACGTGTATGACAAGCTGTATCACTGCC 280

Qy       6112 TTCGTTTATATTTTTTTAACTGTGATAATCCCCACAGGCACATTAACTGTTGCACTTTTG 6171
                || |||||||||||||||||||||||| ||||||||||||| ||||||||||||||||||
Db        279 TTTGTTTATATTTTTTTAACTGTGATATTCCCCACAGGCACGTTAACTGTTGCACTTTTG 220

Qy       6172 AATGTCCAAAATTTATATTTTAGAAATAATAAAAAGAAAGATACTTACATGTTCCCAAAA 6231
                ||||||||||||||||||||||||  |||||| ||||| ||||||||||||||||||| |
Db        219 AATGTCCAAAATTTATATTTTAGAAGGAATAAAGAGAAAAATACTTACATGTTCCCAACA 160

Qy       6232 CAATGGTGTGGTGAATGTGTGAGAAAAACTAACTTGATAGGGTCTACCAATACAAAATGT 6291
                 |||||||||  ||||||||||  ||||    | || |||||||  |||||  ||| |||
Db        159 TGGTGGTGTGGTAAATGTGTGAGAGCAACTCCATAGAGAGGGTCTTCCAATCCAAGATGG 100

Qy       6292 ATTACGAATGCCCCTGTTCATGTTTTTGTTTTAAA-------ACGTGTAAATGAAGATCT 6344
                || |  || ||| ||||||||||||  ||  |||       | |||||||| ||||||
Db         99 CTTCCAGATACCCGTGTTCATGTTTTGTTTAAAAAAAAAAAGAAGTGTAAATGGAGATCT 40

Qy       6345 TTATATTTCAATAAATGATATATAATTTAAAGTTAAAAA 6383
                ||||||||||||||||||  ||| || ||   ||  |||
Db         39 TTATATTTCAATAAATGATTTATGATATATGATTTTAAA 1


RESULT 33
US-11-136-527-2653
; Sequence 2653, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2653
;   LENGTH: 3816
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-2653

  Query Match             5.5%;  Score 351.8;  DB 17;  Length 3816;
  Best Local Similarity   54.2%;  Pred. No. 4e-51;
  Matches  710;  Conservative   51;  Mismatches  473;  Indels   75;  Gaps    3;

Qy       1715 CGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGG 1774
                || ||     ||   || ||||       |   |  ||   |||    | || || || |
Db       1621 CGCTGCTCATTGGCTTCGTGGTCACAGCCGGCTTGATGGGGATCATTGTGATGGTTCTTG 1680

Qy       1775 TTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCA 1834
                ||  |     |||||||| | |||||||| | |  |||| |||  | |||    || |
Db       1681 CCTACAAATATTTGCAGAAACCCATGTATGAAGTACAATGGAAGGTTGTCGAGGAGATAA 1740

Qy       1835 GCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGAT 1894
                 ||||  |  | ||| |||| | ||||::| |||:|| ||||||||:    | ||
Db       1741 ------ATGGGAACAATTATGTTTACATAGACCSRACGCARCTTCCTTATGAYCACAAAT 1794

Qy       1895 GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGA 1954
                ||||||||||  ||| |  | ||     ||||    |  :|||||  |||| || ||:||||
Db       1795 GGGAGTTTCCCAGAAACAGGCTGAGTTTTGGAAAGACMTTGGGAGCTGGTGCCTTYGGGA 1854

Qy       1955 AGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAG 2014
                |:|| |||||:|  || ||:||||| ||:|    |||  |  |:| |||||  :|||||
Db       1855 ARGTMGTTGARGCCACTGCMTATGGCTTRATTAAGTCGGATGCYGCCATGACRGTTGCCG 1914

Qy       2015 TGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGA 2074
                |||||||||| ||||| |  |||    |  |  |||| : | || || ||||| |||||||
Db       1915 TGAAGATGCTCAAACCAAGTGCCCATTTAACRGAAAGRGAGGCCCTAATGTCVGAACTGA 1974

Qy       2075 AGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCA 2134
                || |  |||   |||||||    ||  |||| ||:|| ||| |:|| ||:|| ||::|:
Db       1975 AGGTCCTGAGCTACCTGGGYAATCACATGAATATYGTSAACCTSCTTGGMGCRTGYMCSG 2034

Qy       2135 AGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATT 2194
                |  |:| ||||       ||:| ||||| ||:|| | |||||| ||| |  | || | :|
Db       2035 TGGGARGGCCCACCCTGGTCWTTACAGAATAYGTTGCTATGGTGATCTTTTGAATTTYT 2094

Qy       2195 TGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGG 2254
                ||   | :||  | ||   :|| |    |     | | |||  |:|       |:|
Db       2095 TGAGAAGRAAGCGTGACTCSTTTATTTTCTCAAAGCAAGAAGARCAGGCAGAMG------ 2148

Qy       2255 ATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTG 2314
                              : |   | || | | |   | |  :|       :  || | ||
Db       2149 ---------------CSGCACTTTATAAGAACCTTCTGCAYTCAAMGGAGYCTTCCTGTG 2193

Qy       2315 AAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGC 2374
                | | :     :|| ||:|||||||||:|||| |  | | |      :     : ||| |
Db       2194 ACAGYTCAAAYGARTAYATGGACATRAAGCCTGGCGTTTCCTACGTSGTRCCMACCAAGA 2253

Qy       2375 TAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAG 2434
                 ||| | :|
Db       2254 CAGACAARA----------------------------------------------GGA 2265

Qy       2435 CCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATA 2494
                 ||    | |   | |:    ||||   ||| || |    :  | |    || |||
Db       2266 GATCCGCAAGAATAGAYTYGTAYATAGAAAGAGACGTGACTCCYGCCATCATGGAAGATG 2325

Qy       2495 ACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAA 2554
                ||      |  ||     |   |||||| |||||||: |||| || || |||   || |
Db       2326 ACGAGCTGGYTCTGGACCTGGAWGATTTGCTGAGCTTYTCCTACCAGGTGGCCAAGGGCA 2385

Qy       2555 TGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCC 2614
                ||| ||| :| || || || ||:||| | ||| | ||| |||| ||   | ||  ||:|||
Db       2386 TGGCGTTCYTCGCCTCCAAGAAYTGTATTCACAGAGATTTGGCAGCCAGGAATATCYTCC 2445

Qy       2615 TGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATG 2674
                |  : || ||    ||    ||||| || || || ||:|| |||||||||||| | |||
Db       2446 TYAMTCACGGGCGGATCACAAAGATTTGCGATTTCGGSCTAGCCAGAGACATCAGGAATG 2505

Qy       2675 ATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGA 2734
                ||||||| || |||   ||||| | | |    |||||||||||||||||||| || ||||
Db       2506 ATTCGAATTACGTGGTMAAAGGAAATGCACGRCTGCCCGTGAAGTGGATGGCACCRGAGA 2565

Qy       2735 GCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCT 2794
                |||| ||  :|  | | |||||       |||||:|||||||| ||||| ||| | ||||
Db       2566 GCATTTTCARCTGCGTGTACACATTTGAAAGTGAYGTCTGGTCCTATGGGATTTTCCTCT 2625

Qy       2795 GGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCT 2854
                ||||| |:|| ||::|  ||  ||| ||| ||||| || |||  ||| ||:|| |  || |
Db       2626 GGGAGCTMTTCTCYYTAGGAAGCAGCCCCTACCCAGGGATGCCGGTCGAYTCCAAGTTTT 2685

Qy       2855 ACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCT 2914
                |||| | |||||||    || | ||| |||  ||  ||||| |||||  |     | | | |
Db       2686 ACAAGATGATCAAGGAAGGTTTCCGAATGCTCAGCCCTGAGCACGCGCCTGCCGCAATGT 2745

Qy       2915 ACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACC 2974
                | ||  | |||  ||  |||||  |    ||| ||  ||| || ||  | ||  | ||
Db       2746 ATGAAGTTATGAAGACTTGCTGGGATGCTGATCCCCTGAAAAGGCCAACATTCAAGCAGG 2805

Qy       2975 TGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTA 3023
                |   | || |  | |||||  | | |  | |        ||| | | |||
Db       2806 TTGTTCAGCTCATTGAGAAGCAGATCTCAGACAGCAGCAAACATATTTA 2854


RESULT 34
US-10-511-937-357
; Sequence 357, Application US/10511937
; Publication No. US20060088836A1
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; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 357
;   LENGTH: 5084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-357

  Query Match             5.2%;  Score 331.6;  DB 9;  Length 5084;
  Best Local Similarity   57.4%;  Pred. No. 1.3e-47;
  Matches  722;  Conservative    0;  Mismatches  464;  Indels   72;  Gaps    4;

Qy       1747 ATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAA 1806
Db       1624 ATGATGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGAAACCCATGTATGAA 1683

Qy       1807 ATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGAC 1866
Db       1684 GTACAGTGGAAGGTTGTTGAGGAGATAA------ATGGAAACAATTATGTTTACATAGAC 1737

Qy       1867 CCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGT 1926
Db       1738 CCAACACAACTTCCTTATGATCACAAATGGGAGTTTCCCAGAAACAGGCTGAGTTTTGGG 1797

Qy       1927 CGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGC 1986
Db       1798 AAAACCCTGGGTGCTGGAGCTTTCGGGAAGGTTGTTGAGGCAACTGCTTATGGCTTAATT 1857

Qy       1987 CGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGT 2046
Db       1858 AAGTCAGATGCGGCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCCCATTTGACA 1917

Qy       2047 GAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAAC 2106
Db       1918 GAACGGGAAGCCCTCATGTCTGAACTCAAAGTCCTGAGTTACCTTGGTAATCACATGAAT 1977

Qy       2107 ATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTAT 2166
Db       1978 ATTGTGAATCTACTTGGAGCCTGCACCATTGGAGGGCCCACCCTGGTCATTACAGAATAT 2037

Qy       2167 TGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 2226
Db       2038 TGTTGCTATGGTGATCTTTTGAATTTTTTGAGAAGAAAACGTGATTCATTTATTTGTTCA 2097

Qy       2227 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 2286
Db       2098 AAGCAGGAAGATC----------------------------------------------ATGC 2114

Qy       2287 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 2346
Db       2115 AGAAGCTGCACTTTATAAGAATCTTCTGCATTCAAAGGAGTCTTCCTGCAGCGATAG--- 2171

Qy       2347 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 2406
Db       2172 -----TACTAATGAGTACATGGACATGAAACCTGGAGTTTCTTATGTTGTCCCAACCAAG 2226

Qy       2407 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 2466
Db       2227 GCCGACAAAAGGAGATCTGTGAGAATAGGCTCATACA--------------TAGAAAGA 2271

Qy       2467 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 2526
Db       2272 GATGTGACTCCCGCCATCATGGAGGATGACGAGTTGGCCCTAGACTTAGAAGACTTGCTG 2331

Qy       2527 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 2586
Db       2332 AGCTTTTCTTACCAGGTGGCAAAGGGCATGGCTTTCCTCGCCTCCAAGAATTGTATTCAC 2391

Qy       2587 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 2646
Db       2392 AGAGACTTGGCAGCCAGAAATATCCTCCTTACTCATGGTCGGATCACAAAGATTTGTGAT 2451

Qy       2647 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 2706
Db       2452 TTTGGTCTAGCCAGAGACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGCTCGA 2511

Qy       2707 CTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGT 2766
Db       2512 CTACCTGTGAAGTGGATGGCACCTGAAAGCATTTTCAACTGTGTATACACGTTTGAAAGT 2571

Qy       2767 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826
Db       2572 GACGTCTGGTCCTATGGGATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCCTAT 2631

Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886
Db       2632 CCTGGAATGCCGGTCGATTCTAAGTTCTACAAGATGATCAAGGAAGGCTTCCGGATGCTC 2691

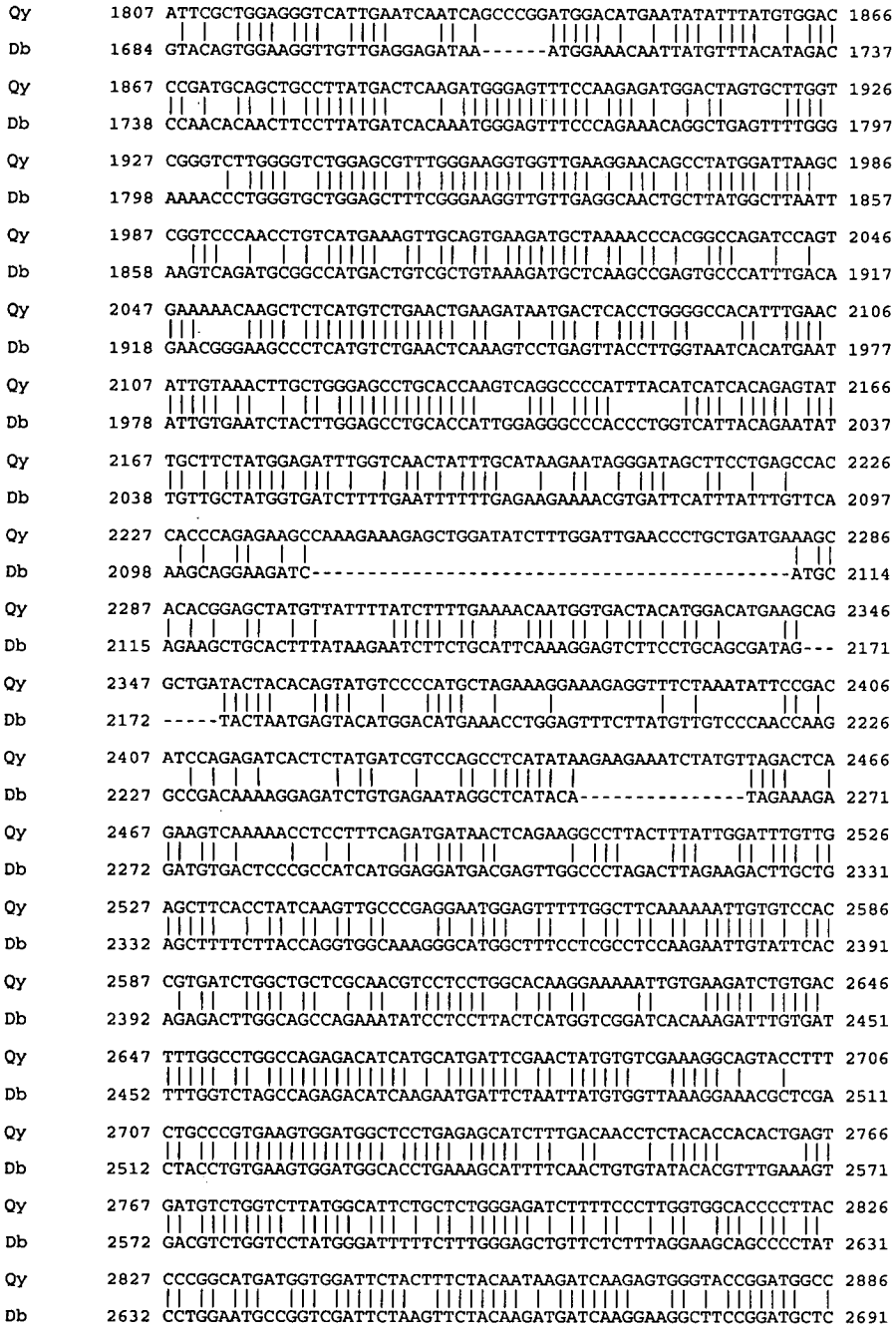
Qy       2887 AAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAG 2946
Db       2692 AGCCCTGAACACGCACCTGCTGAAATGTATGACATAATGAAGACTTGCTGGGATGCAGAT 2751

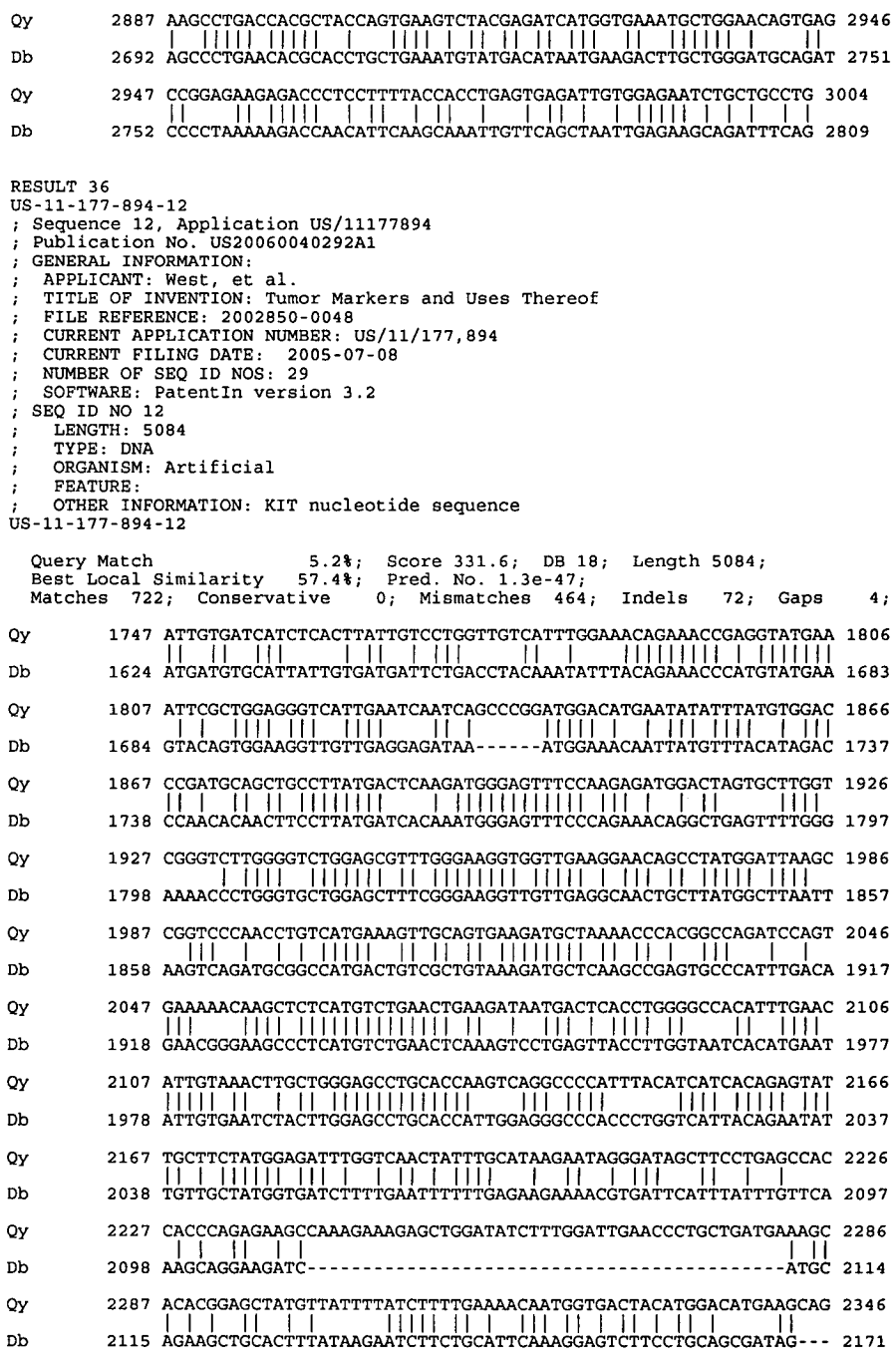
Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTG 3004
Db       2752 CCCCTAAAAAGACCAACATTCAAGCAAATTGTTCAGCTAATTGAGAAGCAGATTTCAG 2809


RESULT 35
US-11-148-770-29
; Sequence 29, Application US/11148770
; Publication No. US20060019280A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, LEI L.
;  APPLICANT:  FRAZIER, MARSHA L.
;  TITLE OF INVENTION: MUTATIONS IN KIT CONFER IMATINIB RESISTANCE IN
;  TITLE OF INVENTION:  GASTROINTESTINAL STROMAL TUMORS
;  FILE REFERENCE: UTXC:869US
;  CURRENT APPLICATION NUMBER: US/11/148,770
;  CURRENT FILING DATE:  2005-06-09
;  PRIOR APPLICATION NUMBER: 60/578,403
;  PRIOR FILING DATE: 2004-06-09
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 5084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-148-770-29

  Query Match             5.2%;  Score 331.6;  DB 17;  Length 5084;
  Best Local Similarity   57.4%;  Pred. No. 1.3e-47;
  Matches  722;  Conservative    0;  Mismatches  464;  Indels   72;  Gaps    4;

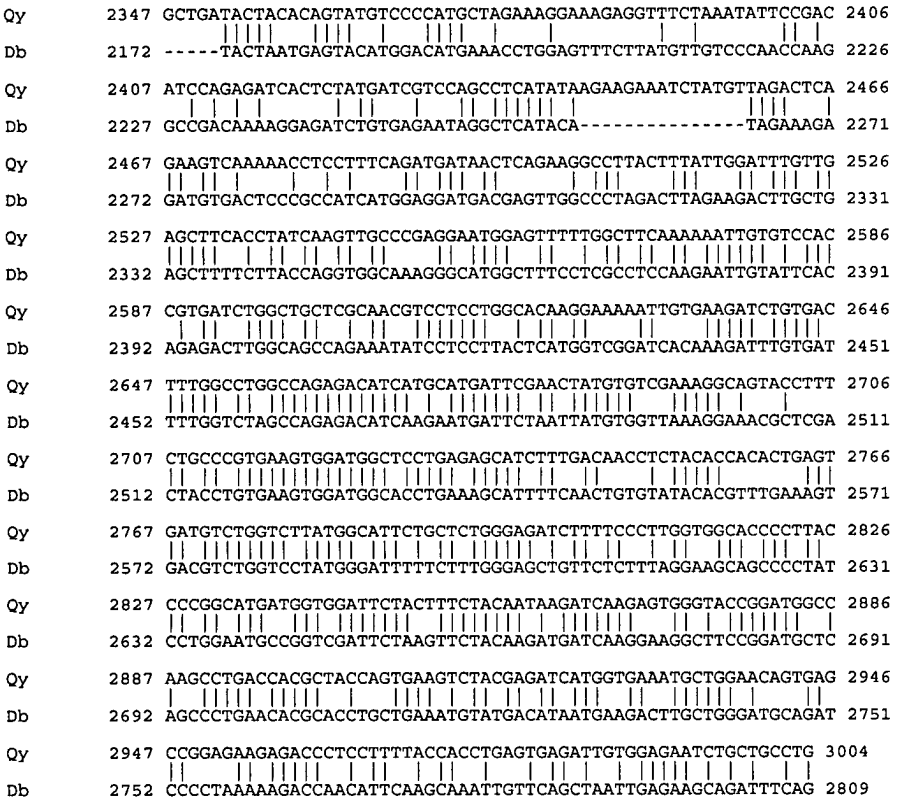
Qy       1747 ATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAA 1806
Db       1624 ATGATGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGAAACCCATGTATGAA 1683
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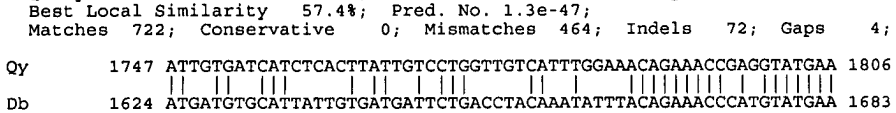
RESULT 36
US-11-177-894-12
; Sequence 12, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 5084
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT nucleotide sequence
US-11-177-894-12

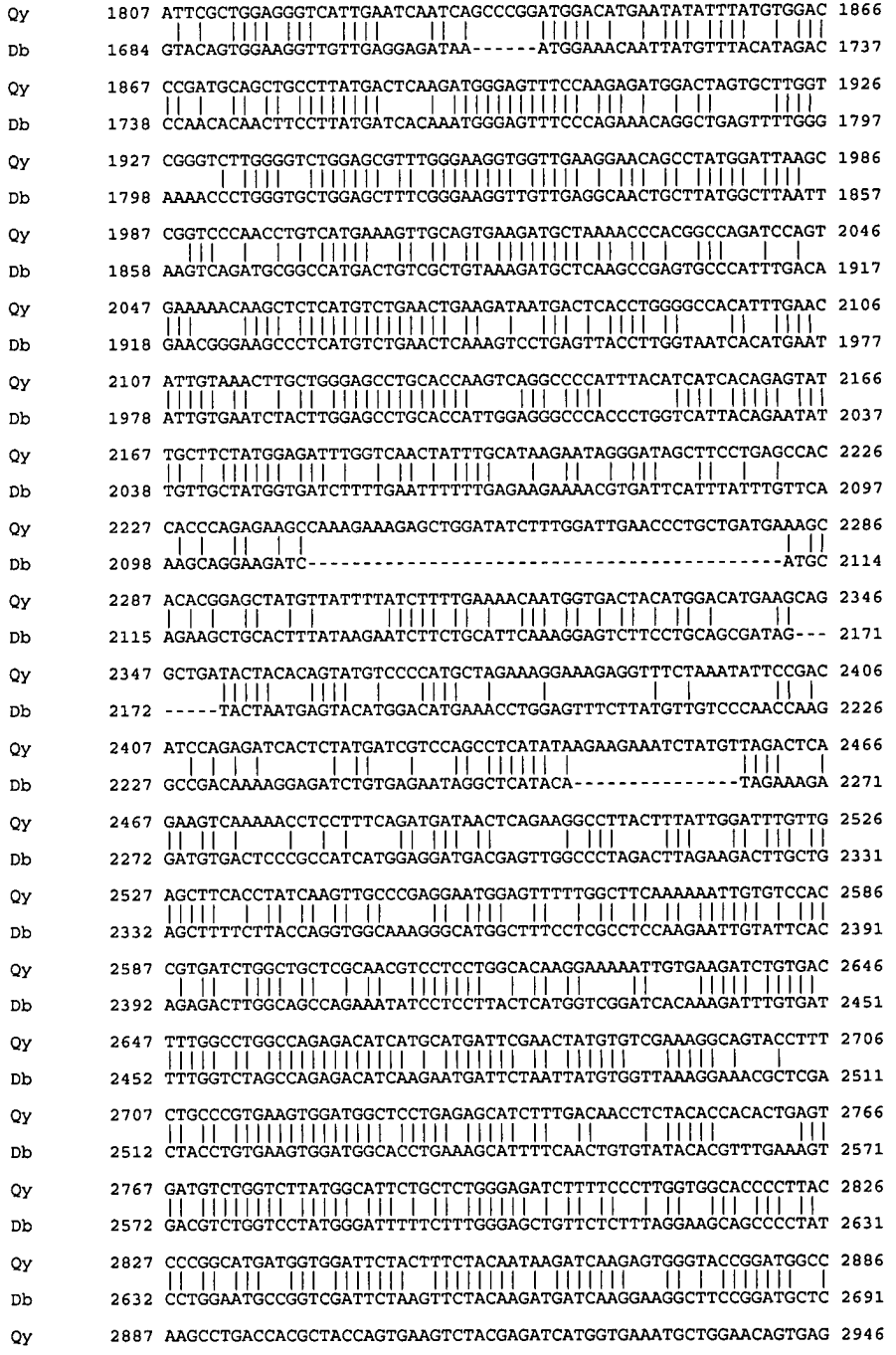
Query Match 5.2%; Score 331.6; DB 18; Length 5084;
Best Local Similarity 57.4%; Pred. No. 1.3e-47;
Matches 722; Conservative 0; Mismatches 464; Indels 72; Gaps 4;



RESULT 37
US-11-177-894-14
; Sequence 14, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
; APPLICANT: West, et al.
; TITLE OF INVENTION: Tumor Markers and Uses Thereof
; FILE REFERENCE: 2002850-0048
; CURRENT APPLICATION NUMBER: US/11/177,894
; CURRENT FILING DATE: 2005-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 5084
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KIT nucleotide sequence
US-11-177-894-14

Query Match 5.2%; Score 331.6; DB 18; Length 5084;
Best Local Similarity 57.4%; Pred. No. 1.3e-47;
Matches 722; Conservative 0; Mismatches 464; Indels 72; Gaps 4;





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Db       2692 AGCCCTGAACACGCACCTGCTGAAATGTATGACATAATGAAGACTTGCTGGGATGCAGAT 2751

Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTG 3004
Db       2752 CCCCTAAAAAGACCAACATTCAAGCAAATTGTTCAGCTAATTGAGAAGCAGATTTCAG 2809


RESULT 38
US-11-154-287-2
; Sequence 2, Application US/11154287
; Publication No. US20060058339A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA N.
;  APPLICANT:  HURT, CLARENCE R.
;  APPLICANT:  ZHANG, CHAO
;  APPLICANT:  ZHANG, JIAZHONG
;  TITLE OF INVENTION: COMPOUNDS MODULATING C-KIT ACTIVITY AND USES THEREFOR
;  FILE REFERENCE: 039363-2155
;  CURRENT APPLICATION NUMBER: US/11/154,287
;  CURRENT FILING DATE:  2005-06-16
;  PRIOR APPLICATION NUMBER: 60/682,076
;  PRIOR FILING DATE: 2005-05-17
;  PRIOR APPLICATION NUMBER: 60/682,058
;  PRIOR FILING DATE: 2005-05-17
;  PRIOR APPLICATION NUMBER: 60/580,898
;  PRIOR FILING DATE: 2004-06-17
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;   LENGTH: 5084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-154-287-2

  Query Match             5.2%;  Score 331.6;  DB 18;  Length 5084;
  Best Local Similarity   57.4%;  Pred. No. 1.3e-47;
  Matches  722;  Conservative    0;  Mismatches  464;  Indels   72;  Gaps    4;

Qy       1747 ATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAA 1806
Db       1624 ATGATGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGAAACCCATGTATGAA 1683

Qy       1807 ATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGAC 1866
Db       1684 GTACAGTGGAAGGTTGTTGAGGAGATAA------ATGGAAACAATTATGTTTACATAGAC 1737

Qy       1867 CCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGT 1926
Db       1738 CCAACACAACTTCCTTATGATCACAAATGGGAGTTTCCCAGAAACAGGCTGAGTTTTGGG 1797

Qy       1927 CGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGC 1986
Db       1798 AAAACCCTGGGTGCTGGAGCTTTCGGGAAGGTTGTTGAGGCAACTGCTTATGGCTTAATT 1857

Qy       1987 CGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGT 2046
Db       1858 AAGTCAGATGCGGCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCCCATTTGACA 1917

Qy       2047 GAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAAC 2106
Db       1918 GAACGGGAAGCCCTCATGTCTGAACTCAAAGTCCTGAGTTACCTTGGTAATCACATGAAT 1977

Qy       2107 ATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTAT 2166
Db       1978 ATTGTGAATCTACTTGGAGCCTGCACCATTGGAGGGCCCACCCTGGTCATTACAGAATAT 2037

Qy       2167 TGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 2226
Db       2038 TGTTGCTATGGTGATCTTTTGAATTTTTTGAGAAGAAAACGTGATTCATTTATTTGTTCA 2097

Qy       2227 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 2286
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Db       2098 AAGCAGGAAGATC----------------------------------------------ATGC 2114

Qy       2287 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 2346
Db       2115 AGAAGCTGCACTTTATAAGAATCTTCTGCATTCAAAGGAGTCTTCCTGCAGCGATAG--- 2171

Qy       2347 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 2406
Db       2172 -----TACTAATGAGTACATGGACATGAAACCTGGAGTTTCTTATGTTGTCCCAACCAAG 2226

Qy       2407 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 2466
Db       2227 GCCGACAAAAGGAGATCTGTGAGAATAGGCTCATACA--------------TAGAAAGA 2271

Qy       2467 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 2526
Db       2272 GATGTGACTCCCGCCATCATGGAGGATGACGAGTTGGCCCTAGACTTAGAAGACTTGCTG 2331

Qy       2527 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 2586
Db       2332 AGCTTTTCTTACCAGGTGGCAAAGGGCATGGCTTTCCTCGCCTCCAAGAATTGTATTCAC 2391

Qy       2587 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 2646
Db       2392 AGAGACTTGGCAGCCAGAAATATCCTCCTTACTCATGGTCGGATCACAAAGATTTGTGAT 2451

Qy       2647 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 2706
Db       2452 TTTGGTCTAGCCAGAGACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGCTCGA 2511

Qy       2707 CTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGT 2766
Db       2512 CTACCTGTGAAGTGGATGGCACCTGAAAGCATTTTCAACTGTGTATACACGTTTGAAAGT 2571

Qy       2767 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826
Db       2572 GACGTCTGGTCCTATGGGATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCCTAT 2631

Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886
Db       2632 CCTGGAATGCCGGTCGATTCTAAGTTCTACAAGATGATCAAGGAAGGCTTCCGGATGCTC 2691

Qy       2887 AAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAG 2946
Db       2692 AGCCCTGAACACGCACCTGCTGAAATGTATGACATAATGAAGACTTGCTGGGATGCAGAT 2751

Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTG 3004
Db       2752 CCCCTAAAAAGACCAACATTCAAGCAAATTGTTCAGCTAATTGAGAAGCAGATTTCAG 2809


RESULT 39
US-11-154-988-2
; Sequence 2, Application US/11154988
; Publication No. US20060058340A1
; GENERAL INFORMATION:
;  APPLICANT: IBRAHIM, PRABHA N.
;  APPLICANT:  HURT, CLARENCE R.
;  APPLICANT:  ZHANG, CHAO
;  APPLICANT:  ZHANG, JIAZHONG
;  TITLE OF INVENTION: COMPOUNDS MODULATING C-KIT ACTIVITY
;  FILE REFERENCE: 039363-2121
;  CURRENT APPLICATION NUMBER: US/11/154,988
;  CURRENT FILING DATE:  2005-06-16
;  PRIOR APPLICATION NUMBER: 60/580,898
;  PRIOR FILING DATE: 2004-06-17
;  PRIOR APPLICATION NUMBER: 60/682,076
;  PRIOR FILING DATE: 2005-05-17
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;   LENGTH: 5084
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
US-11-154-988-2

  Query Match             5.2%;  Score 331.6;  DB 18;  Length 5084;
  Best Local Similarity   57.4%;  Pred. No. 1.3e-47;
  Matches  722;  Conservative    0;  Mismatches  464;  Indels   72;  Gaps    4;

Qy       1747 ATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAA 1806
              ||  ||  |||     | ||  | |||      ||  |    ||||||||| | |||||||
Db       1624 ATGATGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGAAACCCATGTATGAA 1683

Qy       1807 ATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGAC 1866
              | |  |||| |||  ||||     || |       |||||  |   | |||  |||| | |||
Db       1684 GTACAGTGGAAGGTTGTTGAGGAGATAA------ATGGAAACAATTATGTTTACATAGAC 1737

Qy       1867 CCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGT 1926
              || |  || ||  ||||||||     | ||||||||||| |||  |   |  ||     ||||
Db       1738 CCAACACAACTTCCTTATGATCACAAATGGGAGTTTCCCAGAAACAGGCTGAGTTTTGGG 1797

Qy       1927 CGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGC 1986
                  ||||  ||||||| || |||||||| ||||| | ||| || |||||  ||||
Db       1798 AAAACCCTGGGTGCTGGAGCTTTCGGGAAGGTTGTTGAGGCAACTGCTTATGGCTTAATT 1857

Qy       1987 CGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGT 2046
                |||   |  | | |||||  || || || |||||||| || ||  |  |||    |  |
Db       1858 AAGTCAGATGCGGCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCCCATTTGACA 1917

Qy       2047 GAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAAC 2106
              |||    |||| |||||||||||||| ||  |  ||| | |||| ||    ||  ||||
Db       1918 GAACGGGAAGCCCTCATGTCTGAACTCAAAGTCCTGAGTTACCTTGGTAATCACATGAAT 1977

Qy       2107 ATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTAT 2166
              ||||| ||  |  || |||||||||||||    ||| ||||      |||| ||||| |||
Db       1978 ATTGTGAATCTACTTGGAGCCTGCACCATTGGAGGGCCCACCCTGGTCATTACAGAATAT 2037

Qy       2167 TGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 2226
              || | |||||| ||| |  | || | ||||   |  ||  | |||   ||  |  |
Db       2038 TGTTGCTATGGTGATCTTTTGAATTTTTTGAGAAGAAAACGTGATTCATTTATTTGTTCA 2097

Qy       2227 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 2286
              | |  ||  | |                                             | ||
Db       2098 AAGCAGGAAGATC---------------------------------------------ATGC 2114

Qy       2287 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 2346
              | | |  ||  | |      |||| || |  ||| || | || | || |     ||
Db       2115 AGAAGCTGCACTTTATAAGAATCTTCTGCATTCAAAGGAGTCTTCCTGCAGCGATAG--- 2171

Qy       2347 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 2406
                |||||   ||||  |   ||||  |    |       |   |      || |
Db       2172 -----TACTAATGAGTACATGGACATGAAACCTGGAGTTTCTTATGTTGTCCCAACCAAG 2226

Qy       2407 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 2466
                | | | |       | ||    |    || |||||| |                ||||   |
Db       2227 GCCGACAAAAGGAGATCTGTGAGAATAGGCTCATACA--------------TAGAAAGA 2271

Qy       2467 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 2526
              || || |     |  | |     || ||| ||       | |||    |||   || ||| ||
Db       2272 GATGTGACTCCCGCCATCATGGAGGATGACGAGTTGGCCCTAGACTTAGAAGACTTGCTG 2331

Qy       2527 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 2586
              |||||  | ||  || ||  ||   || ||||  ||  | || || || |||||| | |||
Db       2332 AGCTTTTCTTACCAGGTGGCAAAGGGCATGGCTTTCCTCGCCTCCAAGAATTGTATTCAC 2391

Qy       2587 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 2646
                | ||  |||| ||  | ||  |||||||  | || ||     ||    |||||  |||||
Db       2392 AGAGACTTGGCAGCCAGAAATATCCTCCTTACTCATGGTCGGATCACAAAGATTTGTGAT 2451

Qy       2647 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 2706
              ||||| || |||||||||||||| | ||||||| || ||||||   |||||  |   |
Db       2452 TTTGGTCTAGCCAGAGACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGCTCGA 2511

Qy       2707 CTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGACAACCTCTACACCACACTGAGT 2766
              || || |||||||||||||| ||||| ||||| ||  ||    | |||||       |||
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Db       2512 CTACCTGTGAAGTGGATGGCACCTGAAAGCATTTTCAACTGTGTATACACGTTTGAAAGT 2571

Qy       2767 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826
              || |||||||| ||||| ||| | || |||||| | || ||  | ||  ||| ||| ||
Db       2572 GACGTCTGGTCCTATGGGATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCCTAT 2631

Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886
              || || |||  ||| |||||||  |||||||| | |||||||    || | |||||||  |
Db       2632 CCTGGAATGCCGGTCGATTCTAAGTTCTACAAGATGATCAAGGAAGGCTTCCGGATGCTC 2691

Qy       2887 AAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAG 2946
              |  ||||| |||||  |    |||| | || || || |||   ||  |||||| |     ||
Db       2692 AGCCCTGAACACGCACCTGCTGAAATGTATGACATAATGAAGACTTGCTGGGATGCAGAT 2751

Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTG 3004
              ||    || |||||  | ||  | ||  |   | || |  | ||||| | | |  | |
Db       2752 CCCCTAAAAAGACCAACATTCAAGCAAATTGTTCAGCTAATTGAGAAGCAGATTTCAG 2809


RESULT 40
US-11-177-894-13
; Sequence 13, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;  APPLICANT: West, et al.
;  TITLE OF INVENTION: Tumor Markers and Uses Thereof
;  FILE REFERENCE: 2002850-0048
;  CURRENT APPLICATION NUMBER: US/11/177,894
;  CURRENT FILING DATE:  2005-07-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 5179
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: KIT nucleotide sequence
US-11-177-894-13

  Query Match             5.1%;  Score 328.4;  DB 18;  Length 5179;
  Best Local Similarity   57.2%;  Pred. No. 4.7e-47;
  Matches  720;  Conservative    0;  Mismatches  466;  Indels   72;  Gaps    4;

Qy       1747 ATTGTGATCATCTCACTTATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAA 1806
              ||  ||  |||     | ||  | |||      ||  |    ||||||||| | |||||||
Db       1679 ATGATGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGAAACCCATGTATGAA 1738

Qy       1807 ATTCGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATATATTTATGTGGAC 1866
              | |  |||| |||  ||||     || |       |||||  |   | |||  |||| | |||
Db       1739 GTACAGTGGAAGGTTGTTGAGGAGATAA------ATGGAAACAATTATGTTTACATAGAC 1792

Qy       1867 CCGATGCAGCTGCCTTATGACTCAAGATGGGAGTTTCCAAGAGATGGACTAGTGCTTGGT 1926
              || |  || ||  ||||||||     | ||||||||||| |||  |   |  ||     ||||
Db       1793 CCAACACAACTTCCTTATGATCACAAATGGGAGTTTCCCAGAAACAGGCTGAGTTTTGGG 1852

Qy       1927 CGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGC 1986
                  ||||  ||||||| || |||||||| ||||| | ||| || |||||  ||||
Db       1853 AAAACCCTGGGTGCTGGAGCTTTCGGGAAGGTTGTTGAGGCAACTGCTTATGGCTTAATT 1912

Qy       1987 CGGTCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACGGCCAGATCCAGT 2046
                |||   |  | | |||||  || || || |||||||| || ||  |  |||    |  |
Db       1913 AAGTCAGATGCGGCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCCCATTTGACA 1972

Qy       2047 GAAAAACAAGCTCTCATGTCTGAACTGAAGATAATGACTCACCTGGGGCCACATTTGAAC 2106
              |||    |||| |||||||||||||| ||  |  ||| | |||| ||    ||  ||||
Db       1973 GAACGGGAAGCCCTCATGTCTGAACTCAAAGTCCTGAGTTACCTTGGTAATCACATGAAT 2032

Qy       2107 ATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTAT 2166
              ||||| ||  |  || |||||||||||||    ||| ||||      |||| ||||| |||
Db       2033 ATTGTGAATCTACTTGGAGCCTGCACCATTGGAGGGCCCACCCTGGTCATTACAGAATAT 2092

Qy       2167 TGCTTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGCTTCCTGAGCCAC 2226
              || | |||||| ||| |  | || | ||||   |  ||  | |||   ||  |  |
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Db       2093 TGTTGCTATGGTGATCTTTTGAATTTTTTGAGAAGAAAACGTGATTCATTTATTTGTTCA 2152

Qy       2227 CACCCAGAGAAGCCAAAGAAAGAGCTGGATATCTTTGGATTGAACCCTGCTGATGAAAGC 2286

Db       2153 AAGCAGGAAGATC----------------------------------------------ATGC 2169

Qy       2287 ACACGGAGCTATGTTATTTTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAG 2346

Db       2170 AGAAGCTGCACTTTATAAGAATCTTCTGCATTCAAAGGAGTCTTCCTGCAGCGATAG--- 2226

Qy       2347 GCTGATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCTAAATATTCCGAC 2406

Db       2227 -----TACTAATGAGTACATGGACATGAAACCTGGAGTTTCTTATGTTGTCCCAACCAAG 2281

Qy       2407 ATCCAGAGATCACTCTATGATCGTCCAGCCTCATATAAGAAGAAATCTATGTTAGACTCA 2466

Db       2282 GCCGACAAAAGGAGATCTGTGAGAATAGGCTCATACA--------------TAGAAAGA 2326

Qy       2467 GAAGTCAAAAACCTCCTTTCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTG 2526

Db       2327 GATGTGACTCCCGCCATCATGGAGGATGACGAGTTGGCCATAGACTTAGAAGACTTGCTG 2386

Qy       2527 AGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAAAATTGTGTCCAC 2586

Db       2387 AGCTTTTCTTACCAGGTGGCAAAGGGCATGGCTTTCCTCGCCTCCAAGAATTGTATTCAC 2446

Qy       2587 CGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGAAAAATTGTGAAGATCTGTGAC 2646

Db       2447 AGAGACTTGGCAGCCAGAAATATCCTCCTTACTCATGGTCGGATCACAAAGATTTGTGAT 2506

Qy       2647 TTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTT 2706

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Db       2567 CTACCTGTGAAGTGGATGGCACATGAAAGCATTTTCAACTGTGTATACACGTTTGAAAGT 2626

Qy       2767 GATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTAC 2826

Db       2627 GACGTCTGGTCCTATGGGATTTTTCTTTGGGAGCTGTTCTCTTTAGGAAGCAGCCCCTAT 2686

Qy       2827 CCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCC 2886

Db       2687 CCTGGAATGCCGGTCGATTCTAAGTTCTACAAGATGATCAAGGAAGGCTTCCGGATGCTC 2746

Qy       2887 AAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAG 2946

Db       2747 AGCCCTGAACACGCACCTGCTGAAATGTATGACATAATGAAGACTTGCTGGGATGCAGAT 2806

Qy       2947 CCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATTGTGGAGAATCTGCTGCCTG 3004

Db       2807 CCCCTAAAAAGACCAACATTCAAGCAAATTGTTCAGCTAATTGAGAAGCAGATTTCAG 2864
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RESULT 41
US-11-121-086-98
; Sequence 98, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
;   LENGTH: 171732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-98

  Query Match             5.0%;  Score 322.6;  DB 17;  Length 171732;
  Best Local Similarity   98.8%;  Pred. No. 9.3e-46;
  Matches  325;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        177 TCTTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAA 236

Db     168638 TCCTTTTGCAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAA 168697

Qy        237 TGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAG 296

Db     168698 TGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAG 168757

Qy        297 TGAAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAA 356

Db     168758 TGAAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAA 168817

Qy        357 TGAAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGC 416

Db     168818 TGAAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGC 168877

Qy        417 CCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGA 476

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Qy        477 AGGCAGGCACATTTACATCTATGTGCCAG 505

Db     168938 AGGCAGGCACATTTACATCTATGTGCCAG 168966
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RESULT 42
US-10-517-905-19
; Sequence 19, Application US/10517905
; Publication No. US20060084142A1
; GENERAL INFORMATION:
;  APPLICANT: Oregon Health & Science University
;  APPLICANT:  Michael, Heinrich Charles
;  APPLICANT:  Corless, Christopher Lee
;  APPLICANT:  Fletcher, Jonathan Alfred
;  APPLICANT:  Demetri, George D.
;  TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
;  TITLE OF INVENTION:  ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
;  FILE REFERENCE: 899-65892-02
;  CURRENT APPLICATION NUMBER: US/10/517,905
;  CURRENT FILING DATE:  2004-12-10
;  PRIOR APPLICATION NUMBER: US 60/389,107
;  PRIOR FILING DATE: 2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/438,899
;  PRIOR FILING DATE: 2003-01-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 191150
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1)..(49)
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;   NAME/KEY: Intron
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;   LOCATION: (8525)..(8696)
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;   NAME/KEY: Intron
;   LOCATION: (8697)..(8787)
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;   NAME/KEY: exon
;   LOCATION: (8788)..(8977)
;   FEATURE:
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;   LOCATION: (8978)..(166510)
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;   OTHER INFORMATION: n = any nucleic acid
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;   FEATURE:
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;   LOCATION: (14335)..(14434)
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;   NAME/KEY: misc_feature
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;   NAME/KEY: misc_feature
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;   NAME/KEY: Unsure
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;   LOCATION: (59742)..(59744)
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;   NAME/KEY: Unsure
;   LOCATION: (59749)..(59755)
;   OTHER INFORMATION: n = any nucleic acid
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;   NAME/KEY: misc_feature
;   LOCATION: (59749)..(59755)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: (59759)..(59760)
;   OTHER INFORMATION: n = any nucleic acid
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;   OTHER INFORMATION: n is a, c, g, or t
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;   LOCATION: (59765)..(59766)
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;   LOCATION: (59776)..(59875)
;   OTHER INFORMATION: n = any nucleic acid
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;   NAME/KEY: misc_feature
;   LOCATION: (59776)..(59875)
;   OTHER INFORMATION: n is a, c, g, or t
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;   NAME/KEY: Unsure
;   LOCATION: (82745)..(82844)
;   OTHER INFORMATION: n = any nucleic acid
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;   NAME/KEY: misc_feature
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;   NAME/KEY: Unsure
;   LOCATION: (96508)..(96607)
;   OTHER INFORMATION: n = any nucleic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (96508)..(96607)
;   OTHER INFORMATION: n is a, c, g, or t
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;   NAME/KEY: Unsure
;   LOCATION: (147675)..(147774)
;   OTHER INFORMATION: n = any nucleic acid
;   FEATURE:
;   NAME/KEY: misc_feature
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;   LOCATION: (147675)..(147774)
;   OTHER INFORMATION: n is a, c, g, or t
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;   NAME/KEY: Unsure
;   LOCATION: (157152)..(157251)
;   OTHER INFORMATION: n = any nucleic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (157152)..(157251)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (161475)..(161574)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:

  Query Match             5.0%;  Score 322.6;  DB 13;  Length 191150;
  Best Local Similarity   98.8%;  Pred. No. 9.5e-46;
  Matches  325;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        177 TCTTCTCACAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAA 236
              || | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2320 TCCTTTTGCAGGGCTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCAAA 2379

Qy        237 TGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAG 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2380 TGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTGAGATGCTTTGGGGAGAG 2439

Qy        297 TGAAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAA 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2440 TGAAGTGAGCTGGCAGTACCCCATGTCTGAAGAAGAGAGCTCCGATGTGGAAATCAGAAA 2499

Qy        357 TGAAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGC 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2500 TGAAGAAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGC 2559

Qy        417 CCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGA 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2560 CCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACAGAAGAGAATGAGCTTGA 2619

Qy        477 AGGCAGGCACATTTACATCTATGTGCCAG 505
              |||||||||||||||||||||||||||||
Db       2620 AGGCAGGCACATTTACATCTATGTGCCAG 2648


RESULT 43
US-10-511-937-399
; Sequence 399, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 399
;   LENGTH: 3475
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-511-937-399

  Query Match             4.7%;  Score 302.6;  DB 9;  Length 3475;
  Best Local Similarity   55.6%;  Pred. No. 1.3e-42;
  Matches  695;  Conservative    0;  Mismatches  484;  Indels   72;  Gaps    3;

Qy       1779 CATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCC 1838
              ||  |  ||| || ||   ||||||||||  |       | |  |  |    | | || |
Db       1749 CAAGTACAAAAAGCAATTTAGGTATGAAAGCCAGCTACAGATGGTACAGGTGACCGGCTC 1808

Qy       1839 GGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGA 1898
                |  |||| ||  | || || ||    |   |        |||||    | ||||||
Db       1809 CTCAGATAATGAGTACTTCTACGTTGATTTCAGAGAATATGAATATGATCTCAAATGGGA 1868

Qy       1899 GTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGT 1958
              ||||||||||||     ||| | ||||  |||  | || || || || ||||| || ||
Db       1869 GTTTCCAAGAGAAAATTTAGAGTTTGGGAAGGTACTAGGATCAGGTGCTTTTGGAAAAGT 1928

Qy       1959 GGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAGTGAA 2018
              | |  | | |||||| |||||| | |||    |   |       ||  | ||||| || ||
Db       1929 GATGAACGCAACAGCTTATGGAATTAGCAAAACAGGAGTCTCAATCCAGGTTGCCGTCAA 1988

Qy       2019 GATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGAT 2078
                ||||| |||   |  ||      | ||||| | | || |||||||| ||||| |||||
Db       1989 AATGCTGAAAGAAAAAGCAGACAGCTCTGAAAGAGAGGCACTCATGTCAGAACTCAAGAT 2048

Qy       2079 AATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTC 2138
                |||||  || |||||    ||   ||| ||||| ||| ||||||| || |||||   |||
Db       2049 GATGACCCAGCTGGGAAGCCACGAGAATATTGTGAACCTGCTGGGGGCGTGCACACTGTC 2108

Qy       2139 AGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCA 2198
              ||| || ||||||  | ||    || || || | |||||| ||| |  |||||||| |
Db       2109 AGGACCAATTTACTTGATTTTTGAATACTGTTGCTATGGTGATCTTCTCAACTATCTAAG 2168

Qy       2199 TAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATAT 2258
                |  || || || |  || |  ||         ||||||     ||| ||       | |
Db       2169 AAGTAAAAGAGAAAAATTTCACAGGACTTGGACAGAGATTTTCAAGGAA------CACAA 2222

Qy       2259 CTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTGAAAA 2318
                ||  | ||  |||| ||    ||      |  |  |    ||      ||    | |
Db       2223 TTTCAGTTTTTACCCCACTTTCCAATCACATCCAAATTCCAGCATGCCTGGTTCAAGAGA 2282

Qy       2319 CAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGCTAGA 2378
                |       ||  ||||  | | |
Db       2283 AGTTCAGATACACCCGGACTCGGATC---------------------------------- 2308

Qy       2379 AAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTC 2438
                              |||| |   | | ||  | ||   |  |    ||
Db       2309 ---------------AAATCTCAGGGCTTCATGGGAATTCATTTCACTCTGAAGATGAA 2352

Qy       2439 ATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATAACTC 2498
              ||  || | |||| | |                ||||  ||      ||| ||  |||
Db       2353 ATTGAATATGAAAACCA---------------AAAAGGCTGGAAGAAGAGGAGGACTT 2396

Qy       2499 AGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGA 2558
                | |  ||||| ||    ||| |  |  ||||  | ||||||||||||  |||||||||
Db       2397 GAATGTGCTTACATTTGAAGATCTTCTTTGCTTTGCATATCAAGTTGCCAAAGGAATGGA 2456

Qy       2559 GTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGC 2618
                ||| |||  |  ||     ||||| ||| | || ||||| ||  |  ||||| ||  |  |
Db       2457 ATTTCTGGAATTTAAGTCGTGTGTTCACAGAGACCTGGCCGCCAGGAACGTGCTTGTCAC 2516

Qy       2619 ACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTC 2678
              || || ||| | |||||||| |||||||||| ||||  |||| |||||  ||||||
Db       2517 CCACGGGAAAGTGGTGAAGATATGTGACTTTGGATTGGCTCGAGATATCATGAGTGATTC 2576

Qy       2679 GAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCAT 2738
                |||||||     | |||| | ||  |||||| || || |||||||| || || ||| |
Db       2577 CAACTATGTTGTCAGGGGCAATGCCCGTCTGCCTGTAAAATGGATGGCCCCCGAAAGCCT 2636

Qy       2739 CTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGA 2798
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Db       2637 GTTTGAAGGCATCTACACCATTAAGAGTGATGTCTGGTCATATGGAATATTACTGTGGGA 2696

Qy       2799 GATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAA 2858

Db       2697 AATCTTCTCACTTGGTGTGAATCCTTACCCTGGCATTCCGGTTGATGCTAACTTCTACAA 2756

Qy       2859 TAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGA 2918

Db       2757 ACTGATTCAAAATGGATTTAAAATGGATCAGCCATTTTATGCTACAGAAGAAATATACAT 2816

Qy       2919 GATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAG 2978

Db       2817 TATAATGCAATCCTGCTGGGCTTTTGACTCAAGGAAACGGCCATCCTTCCCTAATTTGAC 2876

Qy       2979 TGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAA 3029

Db       2877 TTCGTTTTTAGGATGTCAGCTGGCAGATGCAGAAGAAGCGATGTATCAGAA 2927


RESULT 44
US-10-821-234-735
; Sequence 735, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 735
;   LENGTH: 2919
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-735

  Query Match             4.5%;  Score 288;  DB 10;  Length 2919;
  Best Local Similarity   55.6%;  Pred. No. 4e-40;
  Matches  700;  Conservative    0;  Mismatches  465;  Indels   93;  Gaps    4;

Qy       1715 CGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGG 1774

Db       1550 CAGTGGTGGTCGCCTGCATGTCCATCATGGCCTTGCTGCTGCTGCTGCTCCTGCTGCTAT 1609

Qy       1775 TTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCA 1834

Db       1610 TGTACAAGTATAAGCAGAAGCCCAAGTACCAGGTCCGCTGGAAGATCATCGA------GA 1663

Qy       1835 GCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGAT 1894

Db       1664 GCTATGAGGGCAACAGTTATACTTTCATCGACCCCACGCAGCTGCCTTACAACGAGAAGT 1723

Qy       1895 GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGA 1954

Db       1724 GGGAGTTCCCCCGGAACAACCTGCAGTTTGGTAAGACCCTCGGAGCTGGAGCCTTTGGGA 1783

Qy       1955 AGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAG 2014

Db       1784 AGGTGGTGGAGGCCACGGCCTTTGGTCTGGGCAAGGAGGATGCTGTCCTGAAGGTGGCTG 1843

Qy       2015 TGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGA 2074

Db       1844 TGAAGATGCTGAAGTCCACGGCCCATGCTGATGAGAAGGAGGCCCTCATGTCCGAGCTGA 1903

Qy       2075 AGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCA 2134

Db       1904 AGATCATGAGCCACCTGGGCCAGCACGAGAACATCGTCAACCTTCTGGGAGCCTGTACCC 1963

Qy       2135 AGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATT 2194

Db       1964 ATGGAGGCCCTGTACTGGTCATCACGGAGTACTGTTGCTATGGCGACCTGCTCAACTTTC 2023

Qy       2195 TGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGG 2254

Db       2024 TGCGAAGGAAGGCTGAGGCCATGCTGGGACCC---------------------------- 2055

Qy       2255 ATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTG 2314

Db       2056 --AGCCTGAGCCCCGGCCAGGACCCCGAGGGAGGCGTCGACTATAAGAACATCCACCTCG 2113

Qy       2315 AAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGC 2374

Db       2114 AGAAGAAATATGTCCGCAGGG----------------------ACAGTGGCTTCTCCAGC 2151

Qy       2375 TAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAG 2434

Db       2152 CAGGGTGTGGACACCTATGTGGAGATGAGGCC---------------------------- 2183

Qy       2435 CCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATA 2494

Db       2184 -------TGTCTCCACTTCTTCAAATGACTCCTTCTCTGAGCAAGACCTGGACAAGGAGG 2236

Qy       2495 ACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAA 2554

Db       2237 ATGGACGGCCCCTGGAGCTCCGGGACCTGCTTCACTTCTCCAGCCAAGTAGCCCAGGGCA 2296

Qy       2555 TGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCC 2614

Db       2297 TGGCCTTCCTCGCTTCCAAGAATTGCATCCACCGGGACGTGGCAGCGCGTAACGTGCTGT 2356

Qy       2615 TGGCACAAGGAAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATG 2674

Db       2357 TGACCAATGGTCATGTGGCCAAGATTGGGGACTTCGGGCTGGCTAGGGACATCATGAATG 2416

Qy       2675 ATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGA 2734

Db       2417 ACTCCAACTACATTGTCAAGGGCAATGCCCGCCTGCCTGTGAAGTGGATGGCCCCAGAGA 2476

Qy       2735 GCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCT 2794

Db       2477 GCATCTTTGACTGTGTCTACACGGTTCAGAGCGACGTCTGGTCCTATGGCATCCTCCTCT 2536

Qy       2795 GGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCT 2854

Db       2537 GGGAGATCTTCTCACTTGGGCTGAATCCCTACCCTGGCATCCTGGTGAACAGCAAGTTCT 2596

Qy       2855 ACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCT 2914

Db       2597 ATAAACTGGTGAAGGATGGATACCAAATGGCCCAGCCTGCATTTGCCCCAAAGAATATAT 2656

Qy       2915 ACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCA 2972

Db       2657 ACAGCATCATGCAGGCCTGCTGGGCCTTGGAGCCCACCCACAGACCCACCTTCCAGCA 2714


RESULT 45
US-11-255-147-7
; Sequence 7, Application US/11255147
; Publication No. US20060094081A1
; GENERAL INFORMATION:
;  APPLICANT: SCHUBERT, CARSTEN
;  APPLICANT:  SPRINGER, BARRY A.
;  APPLICANT:  DECKMAN, INGRID
;  APPLICANT:  PATCH, RAYMOND J.
;  APPLICANT:  STRUBLE, GEOFFREY T.
;  APPLICANT:  MA, HONGCHANG
;  APPLICANT:  SCHALK-HIHI, CELINE
;  APPLICANT:  BRANDT, BENJAMIN M.
;  APPLICANT:  PETROUNIA, IOANNA
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;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE C-FMS KINASE DOMAIN:
;  TITLE OF INVENTION:  APPLICATIONS AND USE OF HETEROLOGOUS SUBSTITUTIONS OF
;  TITLE OF INVENTION:  KINASE INSERT DOMAINS FOR CRYSTALLIZATION
;  FILE REFERENCE: PRD2389USNP
;  CURRENT APPLICATION NUMBER: US/11/255,147
;  CURRENT FILING DATE:  2005-10-20
;  PRIOR APPLICATION NUMBER: 60/620,698
;  PRIOR FILING DATE: 2004-10-22
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
;   LENGTH: 3985
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-255-147-7

  Query Match             4.5%;  Score 288;  DB 14;  Length 3985;
  Best Local Similarity   55.6%;  Pred. No. 4.3e-40;
  Matches  700;  Conservative    0;  Mismatches  465;  Indels   93;  Gaps    4;

Qy       1715 CGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGG 1774
Db       1842 CAGTGGTGGTCGCCTGCATGTCCATCATGGCCTTGCTGCTGCTGCTGCTCCTGCTGCTAT 1901

Qy       1775 TTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCA 1834
Db       1902 TGTACAAGTATAAGCAGAAGCCCAAGTACCAGGTCCGCTGGAAGATCATCGA------GA 1955

Qy       1835 GCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGAT 1894
Db       1956 GCTATGAGGGCAACAGTTATACTTTCATCGACCCCACGCAGCTGCCTTACAACGAGAAGT 2015

Qy       1895 GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGA 1954
Db       2016 GGGAGTTCCCCCGGAACAACCTGCAGTTTGGTAAGACCCTCGGAGCTGGAGCCTTTGGGA 2075

Qy       1955 AGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAG 2014
Db       2076 AGGTGGTGGAGGCCACGGCCTTTGGTCTGGGCAAGGAGGATGCTGTCCTGAAGGTGGCTG 2135

Qy       2015 TGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGA 2074
Db       2136 TGAAGATGCTGAAGTCCACGGCCCATGCTGATGAGAAGGAGGCCCTCATGTCCGAGCTGA 2195

Qy       2075 AGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCA 2134
Db       2196 AGATCATGAGCCACCTGGGCCAGCACGAGAACATCGTCAACCTTCTGGGAGCCTGTACCC 2255

Qy       2135 AGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATT 2194
Db       2256 ATGGAGGCCCTGTACTGGTCATCACGGAGTACTGTTGCTATGGCGACCTGCTCAACTTTC 2315

Qy       2195 TGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGG 2254
Db       2316 TGCGAAGGAAGGCTGAGGCCATGCTGGGACCC---------------------------- 2347

Qy       2255 ATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTG 2314
Db       2348 --AGCCTGAGCCCCGGCCAGGACCCCGAGGGAGGCGTCGACTATAAGAACATCCACCTCG 2405

Qy       2315 AAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGC 2374
Db       2406 AGAAGAAATATGTCCGCAGGG----------------------ACAGTGGCTTCTCCAGC 2443

Qy       2375 TAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAG 2434
Db       2444 CAGGGTGTGGACACCTATGTGGAGATGAGGCC---------------------------- 2475

Qy       2435 CCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATA 2494
Db       2476 -------TGTCTCCACTTCTTCAAATGACTCCTTCTCTGAGCAAGACCTGGACAAGGAGG 2528

Qy       2495 ACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAA 2554
Db       2529 ATGGACGGCCCCTGGAGCTCCGGGACCTGCTTCACTTCTCCAGCCAAGTAGCCCAGGGCA 2588

Qy       2555 TGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCC 2614
Db       2589 TGGCCTTCCTCGCTTCCAAGAATTGCATCCACCGGGACGTGGCAGCGCGTAACGTGCTGT 2648

Qy       2615 TGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATG 2674
Db       2649 TGACCAATGGTCATGTGGCCAAGATTGGGGACTTCGGGCTGGCTAGGGACATCATGAATG 2708

Qy       2675 ATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGA 2734
Db       2709 ACTCCAACTACATTGTCAAGGGCAATGCCCGCCTGCCTGTGAAGTGGATGGCCCCAGAGA 2768

Qy       2735 GCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCT 2794
Db       2769 GCATCTTTGACTGTGTCTACACGGTTCAGAGCGACGTCTGGTCCTATGGCATCCTCCTCT 2828

Qy       2795 GGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCT 2854
Db       2829 GGGAGATCTTCTCACTTGGGCTGAATCCCTACCCTGGCATCCTGGTGAACAGCAAGTTCT 2888

Qy       2855 ACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCT 2914
Db       2889 ATAAACTGGTGAAGGATGGATACCAAATGGCCCAGCCTGCATTTGCCCCAAAGAATATAT 2948

Qy       2915 ACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCA 2972
Db       2949 ACAGCATCATGCAGGCCTGCTGGGCCTTGGAGCCCACCCACAGACCCACCTTCCAGCA 3006


RESULT 46
US-11-000-688-358
; Sequence 358, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
;  APPLICANT: BERTUCCI, Francois
;  APPLICANT:  HOULGATTE, Remi
;  APPLICANT:  BIRNBAUM, Daniel
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
;  FILE REFERENCE: 1423-R-03
;  CURRENT APPLICATION NUMBER: US/11/000,688
;  CURRENT FILING DATE:  2004-12-01
;  PRIOR APPLICATION NUMBER: US 60/525,987
;  PRIOR FILING DATE: 2003-12-01
;  NUMBER OF SEQ ID NOS: 1596
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
;   LENGTH: 3985
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial sequences:primer
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(3985)
;   OTHER INFORMATION: colony stimulating factor 1 receptor,
;   OTHER INFORMATION: formerly mcdonough feline sarcoma viral (v-fms)
;   OTHER INFORMATION: oncogene homolog(CSF1R) gene.
US-11-000-688-358

  Query Match             4.5%;  Score 288;  DB 17;  Length 3985;
  Best Local Similarity   55.6%;  Pred. No. 4.3e-40;
  Matches  700;  Conservative    0;  Mismatches  465;  Indels   93;  Gaps    4;

Qy       1715 CGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGG 1774
Db       1842 CAGTGGTGGTCGCCTGCATGTCCATCATGGCCTTGCTGCTGCTGCTGCTCCTGCTGCTAT 1901

Qy       1775 TTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCA 1834
Db       1902 TGTACAAGTATAAGCAGAAGCCCAAGTACCAGGTCCGCTGGAAGATCATCGA------GA 1955
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```
Qy       1835 GCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGAT 1894
Db       1956 GCTATGAGGGCAACAGTTATACTTTCATCGACCCCACGCAGCTGCCTTACAACGAGAAGT 2015

Qy       1895 GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGA 1954
Db       2016 GGGAGTTCCCCCGGAACAACCTGCAGTTTGGTAAGACCCTCGGAGCTGGAGCCTTTGGGA 2075

Qy       1955 AGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAG 2014
Db       2076 AGGTGGTGGAGGCCACGGCCTTTGGTCTGGGCAAGGAGGATGCTGTCCTGAAGGTGGCTG 2135

Qy       2015 TGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGA 2074
Db       2136 TGAAGATGCTGAAGTCCACGGCCCATGCTGATGAGAAGGAGGCCCTCATGTCCGAGCTGA 2195

Qy       2075 AGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCA 2134
Db       2196 AGATCATGAGCCACCTGGGCCAGCACGAGAACATCGTCAACCTTCTGGGAGCCTGTACCC 2255

Qy       2135 AGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATT 2194
Db       2256 ATGGAGGCCCTGTACTGGTCATCACGGAGTACTGTTGCTATGGCGACCTGCTCAACTTTC 2315

Qy       2195 TGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGG 2254
Db       2316 TGCGAAGGAAGGCTGAGGCCATGCTGGGACCC---------------------------- 2347

Qy       2255 ATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTG 2314
Db       2348 --AGCCTGAGCCCCGGCCAGGACCCCGAGGGAGGCGTCGACTATAAGAACATCCACCTCG 2405

Qy       2315 AAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGC 2374
Db       2406 AGAAGAAATATGTCCGCAGGG----------------------ACAGTGGCTTCTCCAGC 2443

Qy       2375 TAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAG 2434
Db       2444 CAGGGTGTGGACACCTATGTGGAGATGAGGCC---------------------------- 2475

Qy       2435 CCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATA 2494
Db       2476 -------TGTCTCCACTTCTTCAAATGACTCCTTCTCTGAGCAAGACCTGGACAAGGAGG 2528

Qy       2495 ACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAA 2554
Db       2529 ATGGACGGCCCCTGGAGCTCCGGGACCTGCTTCACTTCTCCAGCCAAGTAGCCCAGGGCA 2588

Qy       2555 TGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCC 2614
Db       2589 TGGCCTTCCTCGCTTCCAAGAATTGCATCCACCGGGACGTGGCAGCGCGTAACGTGCTGT 2648

Qy       2615 TGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATG 2674
Db       2649 TGACCAATGGTCATGTGGCCAAGATTGGGGACTTCGGGCTGGCTAGGGACATCATGAATG 2708

Qy       2675 ATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGA 2734
Db       2709 ACTCCAACTACATTGTCAAGGGCAATGCCCGCCTGCCTGTGAAGTGGATGGCCCCAGAGA 2768

Qy       2735 GCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCT 2794
Db       2769 GCATCTTTGACTGTGTCTACACGGTTCAGAGCGACGTCTGGTCCTATGGCATCCTCCTCT 2828

Qy       2795 GGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCT 2854
Db       2829 GGGAGATCTTCTCACTTGGGCTGAATCCCTACCCTGGCATCCTGGTGAACAGCAAGTTCT 2888

Qy       2855 ACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCT 2914
Db       2889 ATAAACTGGTGAAGGATGGATACCAAATGGCCCAGCCTGCATTTGCCCCAAAGAATATAT 2948
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Qy       2915 ACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCA 2972
Db       2949 ACAGCATCATGCAGGCCTGCTGGGCCTTGGAGCCCACCCACAGACCCACCTTCCAGCA 3006
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RESULT 47
US-11-136-527-3400
; Sequence 3400, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3400
; LENGTH: 3679
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3400

Query Match 4.3%; Score 275.6; DB 17; Length 3679;
Best Local Similarity 54.5%; Pred. No. 5.9e-38;
Matches 686; Conservative 0; Mismatches 479; Indels 93; Gaps 3;

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Qy       1715 CGGTGGCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTTATTGTCCTGG 1774
Db       1619 CGGTGGTGGTGGCCTGTATGTCTGTCATGTCTCTGCTGGTGCTACTGCTGTTGCTGCTCT 1678

Qy       1775 TTGTCATTTGGAAACAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCA 1834
Db       1679 TGTACAAGTACAAGCAGAAGCCGAAGTACCAGGTGCGCTGGAAGATCATCGA------GA 1732

Qy       1835 GCCCGGATGGACATGAATATATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGAT 1894
Db       1733 GATACGAAGGCAATAGCTACACCTTCATTGACCCTACTCAGTTGCCCTACAATGAGAAGT 1792

Qy       1895 GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGA 1954
Db       1793 GGGAGTTCCCTCGGAACAACCTGCAGTTTGGTAAGACTCTAGGAGCCGGTGCCTTTGGGA 1852

Qy       1955 AGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGGTCCCAACCTGTCATGAAAGTTGCAG 2014
Db       1853 AGGTGGTGGAGGCTACAGCCTTTGGTCTGGGCAAAGAAGATGCAGTGCTGAAGGTGGCTG 1912

Qy       2015 TGAAGATGCTAAAACCCACGGCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGA 2074
Db       1913 TGAAGATGCTAAAGTCCACGGCTCATGCTGATGAGAAGGAGGCCCTGATGTCAGAGCTGA 1972

Qy       2075 AGATAATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCA 2134
Db       1973 AGATCATGAGTCACCTGGGACAGCACGAGAATATAGTCAACCTCTTGGGAGCCTGTACTC 2032

Qy       2135 AGTCAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATT 2194
Db       2033 ACGGAGGACCTGTCCTGGTCATCACTGAATACTGCTGCTATGGAGACCTACTCAACTTTC 2092

Qy       2195 TGCATAAGAATAGGGATAGCTTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGG 2254
Db       2093 TCCGAAGGAAGGCCGAGGCTATGCT--------------AGGACCCAGCCTGAGTCCTGG 2138

Qy       2255 ATATCTTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATTTTATCTTTTG 2314
Db       2139 TCAGGACTCCGAGGGAGACTCCAGCTACAAGAACATCCACCTGGAGAAGAAATATGTGCG 2198

Qy       2315 AAAACAATGGTGACTACATGGACATGAAGCAGGCTGATACTACACAGTATGTCCCCATGC 2374
Db       2199 CAGGGACAGTGGCTTCTCCAGTCAGGGTGTAGACACCTACGTGGAGATGAGGCCTGTCTC 2258
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Qy       2375 TAGAAAGGAAAGAGGTTTCTAAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAG 2434
Db       2259 GACTTCTTCAAGTGACTCCTTCTTTAAGCAAGATCTGGACAAAGAACCGAGCCGGCC--- 2315

Qy       2435 CCTCATATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTTTCAGATGATA 2494
Db       2316 ------------------------------------------------------------ 2315

Qy       2495 ACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAA 2554
Db       2316 ----------CCTGGAGCTCTGGGACCTGCTCCACTTCTCCAGCCAAGTGGCTCAGGGCA 2365

Qy       2555 TGGAGTTTTTGGCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCC 2614
Db       2366 TGGCCTTCCTTGCTTCTAAAAACTGCATCCACCGGGACGTAGCAGCTCGAAACGTGCTGT 2425

Qy       2615 TGGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATG 2674
Db       2426 TGACCAGCGGACATGTGGCCAAGATTGGGGACTTTGGACTGGCTAGGGACATCATGAATG 2485

Qy       2675 ATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGA 2734
Db       2486 ACTCCAACTATGTTGTCAAGGGCAATGCCCGCCTGCCTGTAAAGTGGATGGCCCCAGAGA 2545

Qy       2735 GCATCTTTGACAACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCT 2794
Db       2546 GCATCTTGTACTGCGTCTACACAGTTCAGAGTGATGTGTGGTCCTACGGCATCCTCCTCT 2605

Qy       2795 GGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCT 2854
Db       2606 GGGAGATCTTCTCGCTTGGTCTGAACCCCTACCCCGGCATCCTAGTGAACAACAAGTTCT 2665

Qy       2855 ACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCT 2914
Db       2666 ACAAACTGGTGAAGGATGGATACCAAATGGCCCAGCCTGTATTTGCACCGAAGAACATAT 2725

Qy       2915 ACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCA 2972
Db       2726 ACAGCATCATGCAGTCCTGCTGGGACCTGGAGCCTACCAGAAGACCCACCTTCCAACA 2783
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RESULT 48
US-10-505-928-275
; Sequence 275, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 275
; LENGTH: 4450
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-275

Query Match 3.5%; Score 221.6; DB 9; Length 4450;
Best Local Similarity 65.2%; Pred. No. 1.3e-28;
Matches 326; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

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Qy       2506 CTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTG 2565
Db       3046 CTGACCATGGAAGATCTTGTCTGCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCTG 3105

Qy       2566 GCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGA 2625
Db       3106 GCTTCCCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTCTGCTGTCGGAAAGC 3165

Qy       2626 AAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTAT 2685
Db       3166 GACGTGGTGAAGATCTGTGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCCGACTAC 3225

Qy       2686 GTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGAC 2745
Db       3226 GTCCGCAAGGGCAGTGCCCGGCTGCCCCTGAAGTGGATGGCCCCTGAAAGCATCTTCGAC 3285

Qy       2746 AACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTT 2805
Db       3286 AAGGTGTACACCACGCAGAGTGACGTGTGGTCCTTTGGGGTGCTTCTCTGGGAGATCTTC 3345

Qy       2806 TCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATC 2865
Db       3346 TCTCTGGGGGCCTCCCCGTACCCTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGCGTG 3405

Qy       2866 AAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATG 2925
Db       3406 AGAGACGGCACAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCATACGCCACATCATG 3465

Qy       2926 GTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATT 2985
Db       3466 CTGAACTGCTGGTCCGGAGACCCCAAGGCGAGACCTGCATTCTCGGACCTGGTGGAGATC 3525

Qy       2986 GTGGAGAATCTGCTGCCTGG 3005
Db       3526 CTGGGGGACCTGCTCCAGGG 3545
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RESULT 49
US-11-076-427A-11
; Sequence 11, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 4195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(3913)
US-11-076-427A-11

Query Match 3.4%; Score 220; DB 17; Length 4195;
Best Local Similarity 65.0%; Pred. No. 2.4e-28;
Matches 325; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

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Qy       2506 CTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTG 2565
Db       3044 CTGACCATGGAAGATCTTGTCTGCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCTG 3103

Qy       2566 GCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGA 2625
Db       3104 GCTTCCCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTCTGCTGTCGGAAAGC 3163

Qy       2626 AAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTAT 2685
Db       3164 GACGTGGTGAAGATCTGTGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCTGACTAC 3223

Qy       2686 GTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGAC 2745
Db       3224 GTCCGCAAGGGCAGTGCCCGGCTGCCCCTGAAGTGGATGGCCCCTGAAAGCATCTTCGAC 3283
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Qy       2746 AACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTT 2805
             ||   | |||||||| | |||||| || ||||| | |||   | || ||||||||||||||
Db       3284 AAGGTGTACACCACGCAGAGTGACGTGTGGTCCTTTGGGGTGCTTCTCTGGGAGATCTTC 3343

Qy       2806 TCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATC 2865
             || || || | | |||| ||||| || ||  | |  ||       |||| | |    | |
Db       3344 TCTCTGGGGGCCTCCCCGTACCCTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGGCTG 3403

Qy       2866 AAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATG 2925
             |      ||      ||||| |      || || |  || ||     |    |    |   ||||||
Db       3404 AGAGACGGCACAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCATACGCCGCATCATG 3463

Qy       2926 GTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATT 2985
              |||| ||||||  | | || ||  ||  ||||||  | || |  | |||   |||||
Db       3464 CTGAACTGCTGGTCCGGAGACCCCAAGGCGAGACCTGCATTCTCGGAGCTGGTGGAGATC 3523

Qy       2986 GTGGAGAATCTGCTGCCTGG 3005
              ||| | | ||||| |  ||
Db       3524 CTGGGGGACCTGCTCCAGGG 3543


RESULT 50
US-11-075-047A-5
; Sequence 5, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
;  APPLICANT: ALITALO, et al.
;  TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
;  FILE REFERENCE: 28967/39700A
;  CURRENT APPLICATION NUMBER: US/11/075,047A
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/550,907
;  PRIOR FILING DATE: 2004-03-07
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 4195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (20)..(3913)
US-11-075-047A-5

  Query Match             3.4%;  Score 220;  DB 18;  Length 4195;
  Best Local Similarity   65.0%;  Pred. No. 2.4e-28;
  Matches  325;  Conservative    0;  Mismatches  175;  Indels    0;  Gaps    0;

Qy       2506 CTTACTTTATTGGATTTGTTGAGCTTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTG 2565
             || ||  |    ||| |  |  ||| || ||  || || ||| |||| |||||||  ||
Db       3044 CTGACCATGGAAGATCTTGTCTGCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCCTG 3103

Qy       2566 GCTTCAAAAAATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCACAAGGA 2625
             |||||    ||| ||  ||||| | || |||||||||||| ||| | || ||| |  || |
Db       3104 GCTTCCCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTCTGCTGTCGGAAAGC 3163

Qy       2626 AAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGACATCATGCATGATTCGAACTAT 2685
              |  | |||||||||||||||||||||||| ||| | ||||||     |  ||  |  ||||
Db       3164 GACGTGGTGAAGATCTGTGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCTGACTAC 3223

Qy       2686 GTGTCGAAAGGCAGTACCTTTCTGCCCGTGAAGTGGATGGCTCCTGAGAGCATCTTTGAC 2745
             ||    || |||||| ||   |||||| |||||||||||||| ||||| |||||||| |||
Db       3224 GTCCGCAAGGGCAGTGCCCGGCTGCCCCTGAAGTGGATGGCCCCTGAAAGCATCTTCGAC 3283

Qy       2746 AACCTCTACACCACACTGAGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTT 2805
             ||   | |||||||| | |||||| || ||||| | |||   | || ||||||||||||||
Db       3284 AAGGTGTACACCACGCAGAGTGACGTGTGGTCCTTTGGGGTGCTTCTCTGGGAGATCTTC 3343

Qy       2806 TCCCTTGGTGGCACCCCTTACCCCGGCATGATGGTGGATTCTACTTTCTACAATAAGATC 2865
             || || || | | |||| ||||| ||  ||  | |  ||       |||| | |    | |
Db       3344 TCTCTGGGGGCCTCCCCGTACCCTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGGCTG 3403

Qy       2866 AAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCTACCAGTGAAGTCTACGAGATCATG 2925
             |      ||      ||||| |      || || |  || ||     |    |    |   ||||||
Db       3404 AGAGACGGCACAAGGATGAGGGCCCCGGAGCTGGCCACTCCCGCCATACGCCGCATCATG 3463

Qy       2926 GTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTACCACCTGAGTGAGATT 2985
              |||| ||||||  | | || ||  ||  ||||||  | || |  | |||   |||||
Db       3464 CTGAACTGCTGGTCCGGAGACCCCAAGGCGAGACCTGCATTCTCGGAGCTGGTGGAGATC 3523

Qy       2986 GTGGAGAATCTGCTGCCTGG 3005
              ||| | | ||||| |  ||
Db       3524 CTGGGGGACCTGCTCCAGGG 3543


Search completed: May 16, 2006, 02:36:47
Job time : 1841 secs
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